

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 13, 2005, 12:24:56 ; Search time 4928 Seconds
(without alignments)
17317.389 Million cell updates/sec

Title: US-10-036-342-56

Perfect score: 2242

Sequence: 1 gaatgaataactccgaagcc.....aaaaaaaaaaaaaaaaaa 2242

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

EST:*

1: gb_est1.*

2: gb_est2.*

3: gb_est3.*

4: gb_est4.*

5: gb_est5.*

6: gb_est6.*

7: gb_est7.*

8: gb_est8.*

9: gb_est9.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2098.6	93.6	2105	3	CR610360 full-length
2	1445.2	64.5	1528	3	BC004271 Homo sapi
3	1007.8	45.0	2814	3	AK085308 Mus muscu
4	978.2	43.6	1107	5	BA422767 BX422767
5	952	42.5	1006	5	BA422768 BX422768
6	872.4	38.9	928	5	BA432016 BX432016
7	860.4	38.4	913	5	BA453730 BX453730
8	786.2	35.1	882	4	BA489822 BX489822
9	782.2	34.9	884	4	BA489822 BX489822
10	774	34.5	799	4	BA489822 BX489822
11	761.2	34.0	1054	5	BA489822 BX489822
12	741.8	33.1	887	4	BA489822 BX489822
13	736	32.8	807	4	BA489822 BX489822
14	735.4	32.8	804	4	BA489822 BX489822
15	726.6	32.4	742	1	BA489822 BX489822
16	714	31.8	772	4	BA489822 BX489822
17	712.8	31.8	806	4	BA489822 BX489822
18	712.4	31.8	763	4	BA489822 BX489822
19	712.2	31.8	730	4	BA489822 BX489822
20	710	31.7	748	4	BA489822 BX489822
21	705.6	31.5	932	4	BA489822 BX489822
22	698.4	31.2	842	4	BA489822 BX489822
23	695.2	31.0	959	4	BA489822 BX489822
24	680.2	30.3	753	4	BA489822 BX489822

25	673	30.0	806	4	BG705311	603687817
26	672.4	30.0	720	4	BI604230	603248596
27	669.8	29.9	770	4	BI549771	603194507
28	657.8	29.3	684	4	BG202268	RST21623
29	647.4	28.9	967	4	BI597577	603243712
30	642.4	28.7	666	4	BI604126	603244067
31	641.4	28.6	674	4	BI598229	603245407
32	641.4	28.6	775	4	BI598812	603245594
33	634.4	28.3	656	4	CV026334	4241 Full
34	626	27.9	664	4	BI821574	603036607
35	621.4	27.7	633	2	AW300615	xs88f03.x
36	613	27.3	632	2	AW300620	xs88h03.x
37	612	27.3	630	4	BM669584	UI-E-DX1-
38	611.6	27.3	668	1	AI480056	tm71f08.x
39	607	27.1	675	4	BG201754	RG2121096
40	601.2	26.8	823	7	CK462570	933379 MA
41	592	26.4	602	4	BM691429	UI-E-C11-
42	587.6	26.2	710	2	BE386438	601273841
43	580.6	25.9	600	1	AI589129	tf81d02.x
44	567	25.3	567	5	EX110726	EX110726
45	566	25.2	583	5	BP308439	BP308439
46	566	25.2	593	5	EX094414	EX094414
47	555.4	24.8	582	5	BP348168	BP348168
48	553.4	24.7	581	5	BP215955	BP215955
49	553	24.7	582	5	BP217415	BP217415
50	545	24.3	581	2	BF920454	QV2-NT014
51	543	24.2	630	2	BE386547	601274221
52	541.6	24.2	550	4	BM662490	UI-E-C11-
53	540.4	24.1	580	2	AW961851	EST373924
54	538.4	24.0	577	5	BP195392	BP195392
55	537.2	24.0	870	7	CN167186	999299 MA
56	532	23.7	582	5	BP349556	BP349556
57	522.2	23.3	648	7	CO048865	ILLUMIGEN
58	522.2	23.3	968	7	CN802889	ILLUMIGEN
59	517.4	23.1	539	1	AI911546	cy73d05.x
60	515	23.0	843	7	CK462211	932995 MA
61	503.2	22.4	846	4	BG705992	6032669127
62	486.8	21.7	576	5	BP212677	BP212677
63	484.4	21.6	2039	3	AK003779	Mus muscu
64	474.6	21.2	1816	3	CR682050	Tetraodon
65	474.4	21.2	543	4	EG186833	RST5810 A
66	471.6	21.0	2106	3	AY569013	Rattus no
67	458	20.4	908	1	AV726263	AV726263
68	456.4	20.4	491	4	BI667376	603292152
69	455.8	20.3	1631	3	CR692581	Tetraodon
70	454	20.2	454	1	AI361251	qy42e02.x
71	451.2	20.1	911	4	BI490778	603031554
72	443.4	19.8	658	4	BI667905	603292996
73	442	19.7	450	1	AI498527	tm54d04.x
74	433.8	19.3	782	7	CK481274	AGENCOURT
75	428	19.1	428	1	AV725146	AV725146
76	424.4	18.9	438	4	BM698797	UI-E-DX1-
77	422.8	18.9	426	2	AW901919	QV0-NN102
78	411.6	18.4	527	7	CR556283	KFE2p459J
79	410.4	18.3	590	5	EX642327	DKF2p686P
80	408	18.2	665	7	CN788490	4122831 B
81	400.6	17.9	1078	6	CD509748	CD509748
82	393.6	17.6	773	7	CO568592	AGENCOURT
83	391.4	17.5	420	5	EX508591	DKF2p686J
84	370.4	16.5	755	2	BE967591	601648661
85	369.4	16.5	677	6	BY179686	BY179686
86	366.2	16.3	1072	9	AY399851	Mus muscu
87	363.2	16.2	1230	6	CD503184	CD503184
88	360.4	16.1	1105	6	CD503183	CD503183
89	359.6	16.0	481	7	CR541003	CR541003
90	357.4	15.9	479	1	AY681198	AY681198
91	356	15.9	435	7	H41544	YB171408.s1
92	351	15.7	638	7	CO687244	CO687244
93	349.2	15.6	1094	7	CK025984	CK025984
94	348.8	15.6	923	5	EX710383	EX710383
95	345.8	15.4	675	6	BY179688	BY179688
96	344.4	15.4	1072	9	AY399849	AY399849
97	342.6	15.3	754	7	CK467341	CK467341

98	337.4	15.0	926	5	BX720898	BX720898	BX720898	171	270.8	12.1	746	7	CF785757	AGENCYCOURT
99	336.8	15.0	350	4	BI040121	CM4-NT028	BI040121	172	269.8	12.0	852	5	BX716093	BX716093
100	331.2	14.8	864	6	CB756269	AGENCYCOURT	CB756269	173	269.8	12.0	1025	5	BX103493	BX103493
101	330.6	14.7	753	7	CK465239	936327 MA	CK465239	174	269.8	12.0	700	7	CK941754	CK941754
102	328.8	14.7	644	2	BF784109	602110065	BF784109	175	268.8	12.0	726	5	BP689154	BP689154
103	320.2	14.3	866	7	CR409817	CR409817	CR409817	176	268.8	12.0	833	7	CO887829	CO887829
104	319.2	14.2	503	7	CR775127	DXZP2459G	CR775127	177	268.8	12.0	1028	6	CD325531	CD325531
105	318.6	14.2	568	4	BI489676	603032149	BI489676	178	268.4	12.0	761	7	CF287146	CF287146
106	317.6	14.2	872	6	CD302224	AGENCYCOURT	CD302224	179	268.4	12.0	783	5	BP694287	BP694287
107	312.6	13.9	851	4	BJ727946	BJ727946	BJ727946	180	268	12.0	771	5	BQ572787	BQ572787
108	311	13.9	838	7	CK948185	4072988 B	CK948185	181	267.8	11.9	761	3	CO888750	CO888750
109	310.6	13.9	855	5	BX705230	BX705230	BX705230	182	267	11.9	873	3	CNS09BV4	CNS09BV4
110	310.6	13.9	1425	3	CF635434	Tetraodon	CF635434	183	266.6	11.9	879	5	BU702948	BU702948
111	310.2	13.8	799	5	BU7373789	603813418	BU7373789	184	266.4	11.9	790	5	BU702948	BU702948
112	309	13.8	1423	3	CR654499	Tetraodon	CR654499	185	266	11.9	830	5	EX695126	EX695126
113	307	13.7	817	7	CR409263	CR409263	CR409263	186	266	11.9	843	7	CA408839	CA408839
114	306	13.6	855	7	CR447198	CR447198	CR447198	187	266	11.9	1054	1	AL541127	AL541127
115	305.8	13.6	1139	6	CD509342	CD495-G08	CD509342	188	265.4	11.8	927	7	CF222834	CF222834
116	304.8	13.6	794	5	BP695482	BP695482	BP695482	189	265	11.8	863	5	BP440876	BP440876
117	304.8	13.6	830	6	CB756718	AGENCYCOURT	CB756718	190	264.8	11.8	852	6	CD253810	CD253810
118	303.6	13.5	925	5	EX847091	EX847091	EX847091	191	264.4	11.8	813	4	EG972422	EG972422
119	300.6	13.4	1002	5	BQ059645	AGENCYCOURT	BQ059645	192	264.4	11.8	827	7	CF152238	CF152238
120	299.6	13.4	808	7	CR448386	CR448386	CR448386	193	264.4	11.8	888	6	CD360807	CD360807
121	298.2	13.3	827	5	BU473464	603761940	BU473464	194	264.2	11.8	860	5	EX439667	EX439667
122	298	13.3	847	6	CD519704	AGENCYCOURT	CD519704	195	263.6	11.8	858	5	BF743988	BF743988
123	297.6	13.3	910	7	CR409264	CR409264	CR409264	196	263.6	11.8	901	7	CF547608	CF547608
124	295.8	13.2	677	4	BJ618720	BJ618720	BJ618720	197	262.6	11.7	854	5	BF721390	BF721390
125	295	13.2	1006	5	BQ053384	AGENCYCOURT	BQ053384	198	262.6	11.7	873	7	CF548329	CF548329
126	294.2	13.1	349	1										

[illegible]

390	390	230	10.3	796	4	BG969419	BG969419	6028371010
391	391	230	10.3	979	5	BX334817	BX334817	6028371010
392	392	229.6	10.2	883	4	BG830550	BG830550	6027671339
393	393	229.4	10.2	782	7	CK477054	CK477054	AGENCOURT
394	394	229.2	10.2	710	7	CK655704	CK655704	AGENCOURT
395	395	229	10.2	749	5	BX713335	BX713335	AGENCOURT
396	396	229	10.2	868	5	BQ731362	BQ731362	AGENCOURT
397	397	229	10.2	898	5	BQ731295	BQ731295	AGENCOURT
c	398	228.6	10.2	476	5	BQ600323	BQ600323	MI-P-E7-a
399	399	228.5	10.2	899	7	CK179097	CK179097	BS7168417
c	400	228.2	10.2	801	6	CB243686	CB243686	UI-CP-FNO
401	401	228	10.2	626	1	AL798771	AL798771	AL798771
402	402	227.8	10.2	733	1	AL799073	AL799073	AL799073
403	403	227.8	10.2	740	6	CD241411	CD241411	AGENCOURT
404	404	227.6	10.2	630	7	CK656035	CK656035	AGENCOURT
405	405	227.6	10.2	682	4	BJ011823	BJ011823	AGENCOURT
406	406	227.6	10.2	730	1	AU122560	AU122560	AGENCOURT
407	407	227.6	10.2	741	7	CR449131	CR449131	AGENCOURT
c	408	227.6	10.2	764	6	BQ629087	BQ629087	56095585J
409	409	227.6	10.2	1026	5	BQ604099	BQ604099	AGENCOURT
410	410	226.4	10.1	577	6	CA368367	CA368367	644544 NC
411	411	226.4	10.1	769	7	CF780942	CF780942	AGENCOURT
c	412	226.4	10.1	795	7	CF226425	CF226425	AGENCOURT
413	413	226.4	10.1	871	5	BU465721	BU465721	603370496
414	414	226.4	10.1	837	5	BU104329	BU104329	603005106
415	415	226.2	10.1	898	7	CF548542	CF548542	AGENCOURT
416	416	226.2	10.1	1052	2	BF123719	BF123719	601760465
417	417	226	10.1	791	5	BQ231478	BQ231478	AGENCOURT
418	418	226	10.1	884	7	CF548058	CF548058	AGENCOURT
419	419	225.8	10.1	719	4	B1647157	B1647157	603279970
420	420	225.8	10.1	868	7	CF548457	CF548457	AGENCOURT
421	421	225.8	10.1	905	7	CF548312	CF548312	AGENCOURT
422	422	225.2	10.0	886	7	CF548417	CF548417	AGENCOURT
c	423	224.6	10.0	790	6	CD494230	CD494230	CDA09-F02
424	424	224.6	10.0	824	4	BG966406	BG966406	602832909
425	425	224.6	10.0	857	6	CA481726	CA481726	AGENCOURT
426	426	224.2	10.0	624	6	CA369346	CA369346	645767 NC
427	427	224.2	10.0	701	5	BX705552	BX705552	603705552
c	428	224.2	10.0	723	5	BX705553	BX705553	603705553
429	429	224	10.0	424	8	AQ172837	AQ172837	HS-3195_B
430	430	223.8	10.0	580	5	BQ388116	BQ388116	NISC mm27
431	431	223.6	10.0	868	5	BQ377132	BQ377132	AGENCOURT
432	432	223.6	10.0	891	5	BQ719033	BQ719033	AGENCOURT
433	433	223.6	10.0	940	5	BQ931553	BQ931553	AGENCOURT
434	434	223.6	10.0	1035	5	BQ071435	BQ071435	AGENCOURT
435	435	223.4	10.0	846	1	AL558847	AL558847	AGENCOURT
436	436	223.4	10.0	1070	4	BW478777	BW478777	AGENCOURT
437	437	223.2	10.0	673	4	AU168761	AU168761	AGENCOURT
438	438	223.2	10.0	920	6	CD326949	CD326949	AGENCOURT
c	439	223	9.9	734	4	BX099757	BX099757	602884944
440	440	223	9.9	897	5	BX698935	BX698935	602884944
c	441	222.8	9.9	701	7	CO427568	CO427568	UI-M-HW0-
442	442	222.4	9.9	710	7	CR421233	CR421233	CR421233
443	443	222.2	9.9	682	1	AU168761	AU168761	AGENCOURT
444	444	222.2	9.9	803	5	BX621679	BX621679	AGENCOURT
445	445	222.2	9.9	828	4	B164181	B1144181	602907909
446	446	222	9.9	336	5	BX337838	BY337838	602884944
447	447	222	9.9	774	1	AU124688	AU124688	AGENCOURT
c	448	222	9.9	837	5	BUI55063	BUI55063	AGENCOURT
449	449	221.8	9.9	1248	4	BW478998	BW478998	AGENCOURT
450	450	221.6	9.9	940	5	BUI181659	BUI181659	AGENCOURT
c	451	221.4	9.9	760	5	BX713336	BX713336	602884944
452	452	221.2	9.9	707	5	BX7129380	BX729380	602884944
453	453	221	9.9	622	5	BQ263633	BQ263633	fz92b10.Y
454	454	220.8	9.8	628	6	CD331000	CD331000	StrFu537.
455	455	220.8	9.8	632	1	AL780091	AL780091	AGENCOURT
456	456	220.8	9.8	700	4	BJ711597	BJ711597	AGENCOURT
457	457	220.6	9.8	708	7	CF290591	CF290591	AGENCOURT
c	458	220.4	9.8	703	5	BW393339	BW393339	602859649
459	459	220.4	9.8	741	4	B1093456	B1093456	602859649
460	460	220.4	9.8	928	5	B0944083	B0944083	AGENCOURT
461	461	220.2	9.8	895	2	BF781470	BF781470	602107060
462	462	220	9.8	630	4	BJ002427	BJ002427	AGENCOURT

463	220	9.8	681	5	BQ749288
464	220	9.8	684	4	BJ499488
465	220	9.8	774	7	CK473942
466	220	9.8	902	6	CA481212
467	219.8	9.8	721	5	BW411097
C 468	219.8	9.8	802	7	CF785300
469	219.6	9.8	710	5	BQ606950
470	219.2	9.8	1003	7	CK654652
471	219.2	9.8	807	5	BQ887905
C 472	218.8	9.8	704	5	BW394011
C 473	218.8	9.8	708	5	BW658699
C 474	218.8	9.8	726	5	BW021837
475	218.8	9.8	829	7	CK654300
476	218.6	9.8	894	7	CF921318
C 477	218.4	9.7	230	1	AA912388
478	218.4	9.7	608	7	CNT18092
479	218.4	9.7	608	7	CNT22893
480	218.2	9.7	787	7	CNT19667
481	218.2	9.7	792	7	CF288088
C 482	218.2	9.7	888	4	BJ739881
483	218.2	9.7	937	5	BQ931787
484	217.6	9.7	653	5	BW316137
485	217.6	9.7	688	5	BW39876
486	217.4	9.7	699	7	CNT18998
487	217.2	9.7	622	6	CB578576
488	217.2	9.7	890	5	BQ730800
489	217.2	9.7	1053	2	BF783214
490	216.8	9.7	608	7	CNT24040
491	216.8	9.7	925	5	BA416871
492	216.6	9.7	633	2	BX660858
493	216.6	9.7	803	7	CF150037
494	216.4	9.7	733	6	CB955223
495	216.4	9.7	832	7	CF547624
496	216.4	9.7	901	5	BQ899283
497	216.2	9.6	535	2	BE809990
498	216.2	9.6	638	4	AG387059
499	215.8	9.6	516	1	AL958443
500	215.8	9.6	788	6	CD494236
501	215.8	9.6	812	4	BG430236
C 502	215.4	9.6	619	7	CNO96709
503	215.4	9.6	658	4	BW706132
C 504	215.4	9.6	734	5	BW107210
505	215.4	9.6	756	7	CR764595
506	215.4	9.6	788	7	CO571255
507	215.2	9.6	674	1	AL643379
508	215	9.6	922	5	BQ334601
C 509	215	9.6	1057	6	CD325481
C 510	214.6	9.6	683	5	BW107164
511	214.6	9.6	1246	4	BI256948
512	214.4	9.6	763	7	CF284139
513	214	9.5	700	2	BE277832
514	214	9.5	762	7	CV113414
515	213.8	9.5	958	4	BG696332
516	213.8	9.5	739	7	CNO45436
517	213.8	9.5	780	4	BG972155
518	213.8	9.5	800	2	BF780312
C 519	213.6	9.5	657	5	BW414303
520	213.6	9.5	734	7	CF250811
521	213.6	9.5	737	7	CF250785
522	213.6	9.5	864	2	BE792913
523	213.4	9.5	575	1	AL786362
524	213.4	9.5	686	1	AL651853
525	213.4	9.5	926	7	CK181922
526	213.2	9.5	668	5	BP013710
527	213	9.5	625	4	BW706374
528	213	9.5	644	4	BJ706039
529	213	9.5	741	6	CA356209
530	213	9.5	759	7	CV121029
C 531	212.8	9.5	685	5	BW414404
C 532	212.8	9.5	716	1	AI746433
C 533	212.8	9.5	796	7	CNO57213
C 534	212.4	9.5	638	6	CA290993
535	212.4	9.5	785	6	CA958654

BQ743280	UI-N-FD-01
BQ749488	BJ4399488
CK473842	AG499488
CA481212	AGENCOURT
BW411097	BW411097
CF778530	AGENCOURT
BQ609050	AGENCOURT
BQ654652	AGENCOURT
BQ887905	AGENCOURT
BW394011	BW394011
BW065869	BW065869
BW021837	BW021837
CK654300	AGENCOURT
FA821328	EST659870.s
CF911238	o195d06.s
CN718092	E0758G07
CN728233	E0484H10
CV113667	AGENCOURT
CF788088	AGENCOURT
BJ733981	BJ733981
BQ937187	AGENCOURT
BW336137	BW336137
BW333876	BW333876
CV116998	AGENCOURT
CB578856	AMGNNUC.N
BQ730800	AGENCOURT
BQ783214	6021092323
EX742400	E0871H11
EX7416871	E0871H11
BW660858	BW660858
CF150037	AGENCOURT
CB955223	AGENCOURT
CF547624	AGENCOURT
BQ892983	AGENCOURT
BQ809290	218200 MAR
BG387059	6025447559
AL958443	AL958443
CD494236	CD490-F059
BG430236	6024952323
CN096709	EC2CAA11D
BW706132	BW706132
BW107210	BW107210
CR764595	DKF2p46399
CO571255	AGENCOURT
AL643379	AL643379
BQ934601	AGENCOURT
BW107164	BW107164
BI256948	6023755557
CF284139	AGENCOURT
BE277832	6011200404
CV113414	AGENCOURT
BG696332	6026594909
CN045436	v11_p56.d
BG972155	6028409122
BW780312	6021030221
BW414303	BW414303
CF250811	esao17_d01
CF250785	esao17_d00
BE792913	6015852556
AL786262	AL786262
AL651852	AL651852
CK181922	EST771242
BW013710	BW013710
BW706374	BW706374
BJ706039	BJ706039
CA356209	628308 NCN
CV121029	AGENCOURT
BW414404	BW414404
AL746433	ul07a02.x
CN057213	Salamadene
CD229039	5606875339
CA958654	pw86C10.Y

C	536	212.4	9.5	865	5	BX701141	BX701141	609	203.4	9.1	634	4	BU703336	BU703336
	537	212	9.5	866	2	BE751341	BE751341	610	203	9.1	623	7	CF914941	CF914941
C	538	212	9.5	915	2	CF821317	ES769869	611	203	9.1	645	7	CN694040	CN694040
	539	211.8	9.4	820	7	CN059607	Salamande	612	202.8	9.0	635	6	CK967185	CK967185
	540	211.6	9.4	805	4	BG770068	602745196	613	202.4	9.0	632	6	CA367208	CA367208
	541	211.4	9.4	679	1	AL658957	AL658957	614	202.4	9.0	853	5	BU160527	BU160527
	542	211.4	9.4	783	6	CB955558	AGENCOURT	615	202.4	9.0	934	5	BQ734438	BQ734438
	543	211.4	9.4	851	2	BF780226	BF780226	616	202	9.0	856	7	CN832267	CN832267
	544	211.4	9.4	945	2	BF781937	602103891	617	201.8	9.0	636	7	CK953554	CK953554
	545	211.2	9.4	651	2	BF160757	601769161	618	201.8	9.0	658	1	AL642334	AL642334
	546	211.2	9.4	718	7	CF704644	CCAAC13TR	619	201.8	9.0	674	1	AL636340	AL636340
	547	211	9.4	531	1	AV615674	AV615674	620	201.8	9.0	864	5	BU856566	BU856566
	548	211	9.4	643	5	BW440526	BW440526	621	201.6	9.0	772	6	CB952724	CB952724
	549	211	9.4	1041	2	BE542903	601068037	622	201.4	9.0	841	7	CF149212	CF149212
	550	210.6	9.4	724	5	BF145282	BP145282	623	201.2	9.0	516	4	BF1314198	BF1314198
	551	210.6	9.4	798	7	CF288087	AGENCOURT	624	201.2	9.0	610	6	CD216482	CD216482
	552	210.2	9.4	584	5	BP339351	BP339351	625	201.2	9.0	783	7	CF785301	CF785301
C	553	210.2	9.4	755	6	CD629089	602030685J	626	201	9.0	616	7	CN17268	CN17268
	554	210.2	9.4	1103	2	BF343673	602015326	627	201	9.0	644	7	CV026061	CV026061
	555	210	9.4	874	7	CF717716	CCAGJ45TF	628	201	9.0	737	7	CF257777	CF257777
	556	210	9.4	972	6	CD326976	AGENCOURT	629	200.8	9.0	689	4	BU631204	BU631204
	557	209.8	9.4	633	5	BW372925	BW372925	630	200.4	8.9	584	4	BM192106	BM192106
C	558	209.8	9.4	635	1	BW413732	BW413732	631	200.4	8.9	844	7	CF692291	CF692291
	559	209.8	9.4	656	5	AV899385	AV899385	632	200.2	8.9	654	7	CK959536	CK959536
	560	209.4	9.3	629	5	BW389564	BW389564	633	200.2	8.9	694	2	BF785894	BF785894
C	561	209.4	9.3	685	6	CA339172	CA339172	634	200.2	8.9	850	6	CD099076	CD099076
	562	209.2	9.3	774	1	AL553318	AL553318	635	200	8.9	605	2	BF787465	BF787465
	563	209.2	9.3	912	5	BU184087	AGENCOURT	636	200	8.9	607	4	BU003826	BU003826
C	564	209	9.3	646	5	BW414025	BW414025	637	200	8.9	751	4	BG757710	BG757710
	565	208.8	9.3	661	5	BX620105	BX620105	638	200	8.9	817	6	CB198887	CB198887
C	566	208.8	9.3	721	5									

682	195.2	8.7	888	6	CD7886311	EST659992	755	187.4	8.4	623	4	BM767401	BM767401	K-EST0049
683	195.2	8.7	1039	5	BM9208511	AGENCOURT	756	187.4	8.4	624	7	BM767277	K-EST0049	
684	195	8.7	566	4	BJ527376	BJ527376	757	187.4	8.4	627	7	BM761477	32823327	
685	195	8.7	766	7	CN054222	Salamande	758	187.4	8.4	628	7	CF698751	CCAGS72TR	
686	194.8	8.7	581	5	BP345587	BP345587	759	187.4	8.4	629	7	CF715325	CCAHLOSTR	
687	194.6	8.7	537	5	CB156243	K-EST0214	760	187.2	8.3	507	1	AI891964	u157b07.Y	
688	194.6	8.7	948	5	BQ674071	AGENCOURT	761	187.2	8.3	565	1	AL797625	AL797625	
689	194.4	8.7	503	1	AL629120	AL629120	762	187.2	8.3	615	6	CD629088	56030685H	
690	194.4	8.7	975	2	BF344169	BF344169	763	187.2	8.3	565	6	CD629088	56030685H	
691	194.2	8.7	583	5	BP361478	BP361478	764	187.2	8.3	787	7	CF685180	CCAHF50TF	
692	194	8.7	794	7	CO811744	AGENCOURT	765	187	8.3	787	7	CF715316	CCAHLOSTR	
693	193.8	8.6	587	7	CO782995	CO782995	766	187	8.3	887	7	CF715316	CCAHLOSTR	
694	193.8	8.6	976	5	BQ642607	AGENCOURT	767	186.6	8.3	887	7	CF715316	CCAHLOSTR	
695	193.6	8.6	637	7	CV221795	Le_mxo_52	768	186.6	8.3	896	4	BI455589	BI455589	
696	193.6	8.6	823	7	CV110304	AGENCOURT	769	186.6	8.3	278	5	AV902970	AV902970	
697	193.6	8.6	903	7	CO401389	AGENCOURT	770	186.4	8.3	577	1	AV902970	AV902970	
698	193.6	8.6	1098	4	BM460650	AGENCOURT	771	186.4	8.3	531	6	CD629096	56083657H	
699	193.4	8.6	724	4	BM597846	BM597846	772	186.2	8.3	691	4	BM624990	170006874	
700	193.4	8.6	1169	6	CD256963	AGENCOURT	773	186.2	8.3	665	5	BM624990	170006874	
701	193.2	8.6	637	4	BI193364	BI193364	774	186.2	8.3	695	5	BM624990	170006874	
702	193.2	8.6	655	7	CF145688	CF145688	775	186	8.3	750	7	CF682795	CF682795	
703	193.2	8.6	870	4	BI086497	BI086497	776	185.8	8.3	639	2	BF784713	BF784713	
704	193	8.6	619	7	CN694924	CN694924	777	185.8	8.3	470	4	BI088042	BI088042	
705	193	8.6	654	2	BF228658	BF228658	778	185.6	8.3	671	4	BI088042	BI088042	
706	192.8	8.6	671	4	BF491596	BF491596	779	185.6	8.3	502	1	AI930268	AI930268	
707	192.8	8.6	1021	4	BQ353535	BQ353535	780	185	8.3	1010	5	BQ057102	BQ057102	
708	192.8	8.6	1032	5	BQ62809	BQ62809	781	184.8	8.2	539	1	AI790788	AI790788	
709	192.6	8.6	645	5	BQ419972	BQ419972	782	184.8	8.2	527	7	CN361469	CN361469	
710	192.6	8.6	775	7	CO561624	AGENCOURT	783	184.6	8.2	583	4	BI533695	BI533695	
711	192.6	8.6	891	7	CO808963	AGENCOURT	784	184.4	8.2	626	1	AL799212	AL799212	
712	192.4	8.6	901	7	CN317115	CN317115	785	184.2	8.2	616	5	BQ387495	BQ387495	
713	192.4	8.6	929	5	BQ329286	BQ329286	786	184.2	8.2	667	2	BE285955	BE285955	
714	192.4	8.6	711	5	EG172039	EG172039	787	184.2	8.2	738	4	BG481133	BG481133	
715	192	8.6	787	4	BI092396	BI092396	788	184.2	8.2	790	4	BG171680	BG171680	
716	191.8	8.6	601	1	AI259827	AI259827	789	184	8.2	607	5	BQ396656	BQ396656	
717	191.8	8.6	699	2	BE159642	BE159642	790	184	8.2	859	5	BE160379	BE160379	
718	191.8	8.6	803	4	BJ715357	BJ715357	791	183.8	8.2	517	2	BE757521	BE757521	
719	191.4	8.5	351	2	BB797669	BB797669	792	183.6	8.2	660	6	BY745273	BY745273	
720	191.4	8.5	653	2	BE278298	BE278298	793	183.6	8.2	874	4	BG489861	BG489861	
721	191.4	8.5	827	7	CK93281	CK93281	794	183.4	8.2	533	4	BG016243	BG016243	
722	191.4	8.5	876	6	CD361073	AGENCOURT	795	183.4	8.2	1024	4	BG823747	BG823747	
723	191.2	8.5	605	7	CN687811	CN687811	796	183.2	8.2	777	4	BQ723643	BQ723643	
724	191.2	8.5	740	7	CF559690	CF559690	797	183.2	8.2	913	5	BQ734227	BQ734227	
725	191.2	8.5	896	7	CF659888	CF659888	798	183.2	8.2	936	4	BI869742	BI869742	
726	191	8.5	678	7	CR717108	CR717108	799	183.2	8.2	1034	4	BM459181	BM459181	
727	191	8.5	694	4	BM601243	BM601243	800	183	8.2	649	7	CR771095	CR771095	
728	190.6	8.5	621	6	CB515388	CB515388	801	183	8.2	561	6	BY738120	BY738120	
729	190.2	8.5	706	5	BM374533	BM374533	802	182.8	8.2	583	5	BP291610	BP291610	
730	190	8.5	809	4	BI100579	BI100579	803	182.8	8.2	598	1	AV857429	AV857429	
731	189.8	8.5	757	4	EG972086	EG972086	804	182.8	8.2	660	6	CD629095	CD629095	
732	189.8	8.5	1098	4	BM423500	BM423500	805	182.8	8.2	978	2	BE563299	BE563299	
733	189.6	8.5	615	5	BQ389484	BQ389484	806	182.6	8.1	928	3	CNS093V5	CNS093V5	
734	189.6	8.5	721	4	BM608455	BM608455	807	182.4	8.1	669	8	AO765026	AO765026	
735	189.4	8.4	704	5	BM608455	BM608455	808	182.4	8.1	697	7	CO575451	CO575451	
736	189.4	8.4	782	4	BG751936	BG751936	809	182.4	8.1	774	5	BP443845	BP443845	
737	189.4	8.4	824	5	BX612964	BX612964	810	182.2	8.1	481	5	BP443845	BP443845	
738	189.2	8.4	805	7	CN054326	CN054326	811	182	8.1	552	4	BI535835	BI535835	
739	189	8.4	586	6	BY704039	BY704039	812	182	8.1	1033	4	BG756004	BG756004	
740	189	8.4	701	7	CN054966	CN054966	813	181.8	8.1	799	1	AU051366	AU051366	
741	188.2	8.4	514	4	BE302753	BE302753	814	181.6	8.1	606	2	BE389639	BE389639	
742	188.2	8.4	646	5	BQ390223	BQ390223	815	181.2	8.1	594	4	BG831059	BG831059	
743	188.2	8.4	664	5	BQ399549	BQ399549	816	181.2	8.1	658	5	BQ523740	BQ523740	
744	188	8.4	633	4	BI891469	BI891469	817	181.2	8.1	948	1	AL559600	AL559600	
745	188	8.4	636	7	CN792550	CN792550	818	181	8.1	529	6	CD629097	CD629097	
746	188	8.4	699	4	EG697206	EG697206	819	181	8.1	843	7	CO739134	CO739134	
747	188	8.4	809	4	BJ717492	BJ717492	820	181	8.1	1016	5	BUI92922	BUI92922	
748	188	8.4	792	5	EX10761	EX10761	821	181	8.1	816	9	CNS06D4R	CNS06D4R	
749	187.8	8.4	622	6	CA958827	CA958827	822	180.8	8.1	513	2	BE807936	BE807936	
750	187.6	8.4	639	6	CA588972	CA588972	823	180.8	8.1	623	2	BE278056	BE278056	
751	187.6	8.4	765	7	BI107765	BI107765	824	180.8	8.1	629	2	AW767024	AW767024	
752	187.4	8.4	588	7	CR767439	CR767439	825	180.8	8.1	1049	4	BG482070	BG482070	
753	187.4	8.4	611	2	AV969267	AV969267	826	180.6	8.1	986	7	CF827130	CF827130	
754	187.4	8.4	623	4	BM741213	K-EST0013	827	180.4	8.0	555	7	CN792727	CN792727	

828	180.4	8.0	626	2	BE734407	BE734407	601565668	901	170.4	7.6	587	5	BP311411	BP311411
829	180.4	8.0	634	6	CD692703	CD692703	EST92226 h	902	170.4	7.6	648	5	CD684533	CD684533
830	180.2	8.0	661	6	CD760973	CD760973	GE3ZSM100	903	170.4	7.6	768	5	EX705231	EX705231
831	180.2	8.0	748	4	BJ725647	BJ725647	BJ725647	904	170.2	7.6	593	4	BJ490924	BJ490924
832	179.6	8.0	622	1	AL584429	AL584429	AL584429	905	169.8	7.6	595	4	BM192155	BM192155
833	179.4	8.0	583	7	CV339336	CV339336	MR0-BT300	906	169.8	7.6	627	4	BI650797	BI650797
834	179.2	8.0	751	4	BJ722914	BJ722914	BJ722914	907	169.8	7.6	744	7	CO140990	CO140990
835	179.2	8.0	759	7	CF698738	CF698738	CCAGS72TF	908	169.6	7.6	717	4	BG283253	BG283253
836	179	8.0	550	2	AW823784	AW823784	uf59c12.Y	909	169.4	7.6	681	1	AI667513	AI667513
837	179	8.0	1028	2	BE735191	BE735191	601569155	910	169.2	7.5	756	7	CR557665	CR557665
838	178.6	8.0	673	6	CB377511	CB377511	Cma8E1_37	911	169	7.5	599	7	CO334492	CO334492
839	178.6	8.0	892	2	BF686850	BF686850	602102803	912	168.8	7.5	808	6	CB993588	CB993588
840	178.6	8.0	1022	4	BM462965	BM462965	AGENCOURT	913	168.8	7.5	842	6	CD654434	CD654434
841	178.4	8.0	586	4	BJ694687	BJ694687	BJ694687	914	168.6	7.5	508	2	AW732427	AW732427
842	178.4	8.0	640	2	BE273961	BE273961	601104420	915	168.4	7.5	791	7	CK483116	CK483116
843	178	7.9	584	4	BI446157	BI446157	dal36806	916	168.4	7.5	881	5	EX713721	EX713721
844	178	7.9	672	1	AJ731921	AJ731921	AJ731921	917	168.2	7.5	584	5	BP366572	BP366572
845	178	7.9	849	7	CF692292	CF692292	CCAF109TR	918	168.2	7.5	748	7	CN052923	CN052923
846	177.8	7.9	652	6	BY754147	BY754147	BY754147	919	167.8	7.5	582	5	BP222244	BP222244
847	177.4	7.9	759	6	CB944443	CB944443	AGENCOURT	920	167.8	7.5	582	5	BP358484	BP358484
848	177.2	7.9	903	3	CNS09BXS	CNS09BXS	Single re	921	167.8	7.5	730	7	CF717962	CF717962
849	177	7.9	519	6	CD332789	CD332789	STPUs37	922	167.8	7.5	815	7	CF676543	CF676543
850	177	7.9	815	6	CB993122	CB993122	AGENCOURT	923	167.6	7.5	887	4	BG713945	BG713945
851	176.8	7.9	933	4	BI596767	BI596767	603242851	924	167.6	7.5	826	2	BE732082	BE732082
852	176.6	7.9	799	4	BM047828	BM047828	603629268	925	167.6	7.5	971	2	BE732082	BE732082
853	176.6	7.9	1020	2	BF568481	BF568481	602184489	926	167.4	7.5	590	5	BP213987	BP213987
854	176	7.9	692	7	CO641569	CO641569	USDA-PP 1	927	167.4	7.5	729	7	CF694870	CF694870
855	175.8	7.8	788	4	BM008636	BM008636	603618290	928	167.2	7.5	499	1	AI931441	AI931441
856	175.8	7.8	951	5	BQ643299	BQ643299	AGENCOURT	929	167.2	7.5	500	5	BQ694592	BQ694592
857	175.6	7.8	755	5	BQ415500	BQ415500	603668771	930	167.2	7.5	559	2	AW766410	AW766410
858	175.6	7.8	758	7	CN361478	CN361478	170005325	931	167.2	7.5	621	2	BE388035	BE388035
859	175.6	7.8	1380	2	BF686952	BF686952	602102727	932	167.2	7.5	798	7	CF691128	CF691128
860	175.4	7.8	553	4	BM744352	BM744352	K-EST0017	933	166.8	7.4	1001	9	CNS07E7E	CNS07E7E
861	175.2	7.8	736	4	BG327952	BG327952	602426975	934	166.4	7.4	785	7	CR438885	CR438885
862	175.2	7.8	854	4	BG336431	BG336431	602405373	935	166.2	7.4	786	6	CB601037	CB601037
863	174.8	7.8	466	4	BI100777	BI100777	602886075	936	166.2	7.4	785	7	CR438885	CR438885
864	174.8	7.8	584	5	BP367891	BP367891	BP367891	937	165.8	7.4	627	1	AV851172	AV851172
865	174.8	7.8	618	2	AW732305	AW732305	b02e05.Y	938	165.6	7.4	592	6	CD215111	CD215111
866	174.4	7.8	704	4	AU137269	AU137269	AU137269	939	165.6	7.4	723	2	BE733175	BE733175
867	173.8	7.8	602	5	BP459087	BP459087	BP459087	940	165.4	7.4	638	4	BG386055	BG386055
868	173.6	7.7	772	4	BG468148	BG468148	602509723	941	165	7.4	554	4	BG814445	BG814445
869	173.6	7.7	500	4	BI960884	BI960884	MONO1_2	942	165	7.4	637	7	CN058535	CN058535
870	173.6	7.7	562	4	BI536332	BI536332	393256 MA	943	164.6	7.3	525	7	CN677899	CN677899
871	173.4	7.7	605	1	AI530145	AI530145	u189f08.Y	944	164.6	7.3	525	6	CD629094	CD629094
872	173.2	7.7	546	1	AU167318	AU167318	AU167318	945	164.6	7.3	550	7	CN694605	CN694605
873	173.2	7.7	722	2	BE792388	BE792388	601585126	946	164.6	7.3	582	5	BP359215	BP359215
874	173.2	7.7	985	2	BE902224	BE902224	601675260	947	164.6	7.3	1068	5	BX421582	BX421582
875	173	7.7	583	5	BH0806250	BH0806250	haa3c01	948	164.4	7.3	515	6	CD544409	CD544409
876	173	7.7	610	2	BE336830	BE336830	ba97c08.Y	949	164.4	7.3	516	6	CA870665	CA870665
877	173	7.7	658	7	CV511319	CV511319	kc39h08.Y	950	164.4	7.3	662	2	AV956049	AV956049
878	173	7.7	968	2	BF100825	BF100825	601753760	951	164.2	7.3	666	4	BI485157	BI485157
879	172.8	7.7	495	4	BM583464	BM583464	170006872	952	164	7.3	496	2	AW823722	AW823722
880	172.8	7.7	716	6	BY742949	BY742949	BY742949	953	164	7.3	512	6	CA545416	CA545416
881	172.6	7.7	552	4	BI536323	BI536323	393244 MA	954	164	7.3	886	6	CB993636	CB993636
882	172.6	7.7	613	2	BE279711	BE279711	601158270	955	163.6	7.3	735	5	BQ642147	BQ642147
883	172.2	7.7	1094	6	CD325552	CD325552	AGENCOURT	956	163.4	7.3	976	4	BI668421	BI668421
884	172	7.7	623	1	AL798428	AL798428	AL798428	957	163	7.3	782	7	CF717723	CF717723
885	171.8	7.7	554	7	CF893264	CF893264	A0121804-	958	162.6	7.3	712	5	BW047812	BW047812
886	171.8	7.7	750	7	CO782086	CO782086	BL014A H0	959	162.4	7.2	465	7	CF919003	CF919003
887	171.6	7.7	670	6	BY739405	BY739405	BY739405	960	162.4	7.2	575	5	BP213753	BP213753
888	171.6	7.7	892	4	BG282995	BG282995	602406184	961	162.4	7.2	569	1	AI722207	AI722207
889	171.4	7.6	808	4	BG698032	BG698032	602659177	962	162.4	7.2	601	1	AL956138	AL956138
890	171	7.6	423	4	BJ496583	BJ496583	BJ496583	963	162.4	7.2	635	6	BY753314	BY753314
891	171	7.6	737	4	BJ718857	BJ718857	BJ718857	964	162.2	7.2	371	8	AQ390611	AQ390611
892	170.8	7.6	606	1	AL775869	AL775869	AL775869	965	162.2	7.2	419	4	CA371834	CA371834
893	170.8	7.6	810	2	AW331855	AW331855	S1F3 AGS-	966	162	7.2	765	6	BJ515070	BJ515070
894	170.6	7.6	621	5	BH05817	BH05817	haa22f08	967	162	7.2	887	7	CF819889	CF819889
895	170.6	7.6	685	7	CN058253	CN058253	Salamande	968	161.8	7.2	495	7	CO186932	CO186932
896	170.6	7.6	729	4	BG335695	BG335695	602404349	969	161.8	7.2	556	2	AW153789	AW153789
897	170.6	7.6	1080	7	CF109995	CF109995	Shultzomi	970	161.8	7.2	561	7	CN711499	CN711499
898	170.4	7.6	457	1	AL785742	AL785742	AL785742	971	161.6	7.2	403	6	CA043469	CA043469
899	170.4	7.6	571	7	CN622684	CN622684	ta9d0402	972	161.6	7.2	583	5	BP331989	BP331989
900	170.4	7.6	583	5	BP310616	BP310616	BP310616	973	161.6	7.2	662	7	CR557630	CR557630

974	161.4	7.2	495	2	BR853716	BB853716	BB853716	1047	155.2	6.9	581	5	BP252798	BP252798
975	161.4	7.2	536	7	CR873786	CR873786	SGP134949	1048	155.2	6.9	644	4	BM634771	BM634771
976	161.4	7.2	583	5	BP332465	BP332465	BP332465	1049	155	6.9	503	4	BM560120	BM560120
977	161	7.2	753	6	CB600403	CB600403	AGENCOURT	1050	155	6.9	790	7	CO958138	CO958138
978	161	7.2	786	4	BI1103676	BI1103676	602889170	1051	154.8	6.9	603	7	CO958138	CO958138
979	160.8	7.2	595	5	BQ667603	BQ667603	pb55h10.Y	1052	154.8	6.9	652	5	BN053995	BN053995
980	160.6	7.2	624	7	CK545211	CK545211	rswhb0_01	1053	154.8	6.9	684	6	CA806261	CA806261
981	160.6	7.2	676	2	BF059963	BF059963	HC_d11_09	1054	154.8	6.9	720	7	CK805313	CK805313
982	160.6	7.2	779	5	CK074911	CK074911	EX074911	1055	154.8	6.9	744	7	CF702965	CF702965
983	160.4	7.2	595	4	BM192252	BM192252	dai21d10.	1056	154.6	6.9	584	5	BP279614	BP279614
984	160.4	7.2	602	1	AL637057	AL637057	AL637057	1057	154.4	6.9	977	4	EG111505	EG111505
985	160.4	7.2	692	6	CB015029	CB015029	HC_d11_36	1058	154.2	6.9	427	2	BB845163	BB845163
986	160.2	7.1	790	7	CV486326	CV486326	AGENCOURT	1059	154.2	6.9	665	5	BP329009	BP329009
987	160	7.1	651	4	BM581674	BM581674	170006872	1060	154.2	6.9	701	6	CA806251	CA806251
988	160	7.1	670	5	BP010530	BP010530	BP010530	1061	154	6.9	619	5	BU412454	BU412454
989	160	7.1	682	5	BP010530	BP010530	BP010530	1062	153.8	6.9	602	2	BE279251	BE279251
990	160	7.1	868	4	BG325431	BG325431	602424122	1063	153.8	6.9	634	7	CK621045	CK621045
991	160	7.1	915	7	CF827129	CF827129	EST704511	1064	153.8	6.9	773	7	CK352038	CK352038
992	160	7.1	987	5	BQ989880	BQ989880	AGENCOURT	1065	153.6	6.9	456	7	CF139012	CF139012
993	159.8	7.1	554	4	BI892283	BI892283	2F637-3-0	1066	153.4	6.8	627	2	BF706298	BF706298
994	159.8	7.1	758	2	BE278462	BE278462	601156832	1067	153.4	6.8	647	4	BG970430	BG970430
995	159.6	7.1	525	6	CB127230	CB127230	K-EST0176	1068	153.2	6.8	581	5	BP357722	BP357722
996	159.6	7.1	414	1	AJ285538	AJ285538	4A3B-AAH	1069	153	6.8	675	7	CK514934	CK514934
997	159.4	7.1	601	6	CR435954	CR435954	CR435954	1070	153	6.8	834	5	BU243034	BU243034
998	159.4	7.1	828	6	CD781861	CD781861	EST653222	1071	153	6.8	628	4	BJ794651	BJ794651
999	159.4	7.1	828	6	CD781861	CD781861	EST653222	1072	152.8	6.8	768	7	CF694875	CF694875
1000	159.2	7.1	529	1	AI874574	AI874574	ul27h10.Y	1073	152.8	6.8	884	5	BO434981	BO434981
1001	159.2	7.1	650	4	BI230091	BI230091	GM15386.5	1074	152.6	6.8	532	4	BJ614514	BJ614514
1002	158.8	7.1	721	4	BJ818095	BJ818095	BJ818095	1075	152.6	6.8	595	5	EX604180	EX604180
1003	158.8	7.1	926	2	BE780974	BE780974	601469725	1076	152.2	6.8	571	7	CK491972	CK491972
1004	158.6	7.1	539	1	AL925409	AL925409	AL925409	1077	152.2	6.8	675	7	CK514934	CK514934
1005	158.6	7.1	563	1	AL675098	AL675098	AL675098	1078	152	6.8	834	5	BU243034	BU243034
1006	158.6	7.1	647	1	AJ272857	AJ272857	AJ272857	1079	151.8	6.8	495	4	BI813319	BI813319
1007	158.4	7.1	896	2	BF784952	BF784952	602110915	1080	151.6	6.8	553	4	BG814367	BG814367
1008	158.4	7.1	966	5	BQ668983	BQ668983	AGENCOURT	1081	151.4	6.8	630	6	CI913352	CI913352
1009	158.4	7.1	977	2	BE730867	BE730867	601569973	1082	151.4	6.8	637	5	BM339207	BM339207
1010	158.2	7.1	439	2	BB847422	BB847422	BB847422	1083	151.4	6.8	642	5	BM359381	BM359381
1011	158.2	7.1	654	5	BM359667	BM359667	BM359667	1084	151.4	6.8	644	5	BM339573	BM339573
1012	158	7.0	582	8	BZ139795	BZ139795	CH230-257	1085	151.2	6.7	722	6	BE563822	BE563822
1013	158	7.0	763	4	BJ040008	BJ040008	BJ040008	1086	151.2	6.7	752	4	BI544296	BI544296
1014	157.8	7.0	562	4	BJ040008	BJ040008	BJ040008	1087	151.2	6.7	767	7	CF685186	CF685186
1015	157.6	7.0	583	5	BP311888	BP311888	BP311888	1088	151.2	6.7	956	4	BG335749	BG335749
1016	157.6	7.0	585	1	AL780497	AL780497	AL780497	1089	151.2	6.7	581	5	BP362398	BP362398
1017	157.6	7.0	816	6	CK174615	CK174615	EST763935	1090	151	6.7	582	5	BP274868	BP274868
1018	157.6	7.0	754	1	AU133041	AU133041	AU133041	1091	151	6.7	582	5	BP200996	BP200996
1019	157.4	7.0	505	4	BG811431	BG811431	Gaf63c07.	1092	150.8	6.7	639	5	BM363347	BM363347
1020	157.2	7.0	583	4	BG814301	BG814301	Gaf65f11.	1093	150.8	6.7	949	4	EG250423	EG250423
1021	157.2	7.0	485	2	AW430635	AW430635	70387 MAR	1094	150.4	6.7	826	5	BU384402	BU384402
1022	157	7.0	583	2	AW430635	AW430635	70387 MAR	1095	150.4	6.7	558	2	BE018812	BE018812
1023	157	7.0	431	6	CB725416	CB725416	AMGNNUC:N	1096	150.2	6.7	413	7	CK611166	CK611166
1024	157	7.0	514	2	BE102647	BE102647	UT-R-BT1	1097	149.8	6.7	506	7	CO296350	CO296350
1025	157	7.0	520	6	CB721101	CB721101	AMGNNUC:C	1098	149.6	6.7	388	4	BG812158	BG812158
1026	157	7.0	749	7	CO565136	CO565136	AGENCOURT	1099	149.6	6.7	733	7	CK447267	CK447267
1027	157	7.0	776	2	AW335650	AW335650	S49G11 AG	1100	149.6	6.7	595	4	BM686163	BM686163
1028	156.6	7.0	489	7	CO299262	CO299262	EK174934.	1101	149.4	6.7	749	4	BM007332	BM007332
1029	156.6	7.0	643	2	BE977169	BE977169	bs60e10.Y	1102	149.4	6.7	510	4	BG579635	BG579635
1030	156.6	7.0	428	7	BN096710	BN096710	EC2CRA11D	1103	149	6.6	581	5	BP349274	BP349274
1031	156.4	7.0	632	6	CA807168	CA807168	ESG016c.E	1104	149	6.6	584	5	BP329637	BP329637
1032	156.4	7.0	715	2	BF784958	BF784958	602110921	1105	149	6.6	612	2	BE279718	BE279718
1033	156.2	7.0	499	4	BI312509	BI312509	Gaf92f10.	1106	148.8	6.6	651	7	CF140162	CF140162
1034	156.2	7.0	582	5	BP270540	BP270540	BP270540	1107	148.8	6.6	607	7	CF638567	CF638567
1035	156.2	7.0	698	6	CB015320	CB015320	HC_d11_40	1108	148.6	6.6	440	2	BB847141	BB847141
1036	156	7.0	495	5	BE255797	BE255797	BE255797	1109	148.4	6.6	602	6	CA869588	CA869588
1037	155.8	6.9	546	7	CF146611	CF146611	UT-HF-CBO	1110	148.2	6.6	464	5	BY241339	BY241339
1038	155.8	6.9	770	7	CF682805	CF682805	ESG0120b.	1111	148.2	6.6	464	5	BY241339	BY241339
1039	155.8	6.9	781	6	CF682805	CF682805	CAID156TR	1112	148.2	6.6	464	5	BY241339	BY241339
1040	155.8	6.9	436	2	BB847155	BB847155	BB847155	1113	148.2	6.6	464	5	BY241339	BY241339
1041	155.6	6.9	566	2	BP351687	BP351687	QV2-HT054	1114	148	6.6	582	5	BP313315	BP313315
1042	155.6	6.9	711	4	BU145550	BU145550	BU145550	1115	148	6.6	660	6	BY732874	BY732874
1043	155.4	6.9	604	4	BU699326	BU699326	BU699326	1116	147.8	6.6	602	6	CA869588	CA869588
1044	155.4	6.9	668	4	BU690166	BU690166	BU690166	1117	147.4	6.6	448	1	AJ663133	AJ663133
1045	155.4	6.9	544	4	BG814092	BG814092	daf63c07.	1118	147.4	6.6	464	5	BY241339	BY241339
1046	155.2	6.9	544	4	BG814092	BG814092	daf63c07.	1119	147.4	6.6	464	5	BY241339	BY241339

1120	147.4	6.6	569	5	BQ306973	MR0-BT200	BQ306973	1193	142.8	6.4	396	7	CK614195	CK614195	LPSC_H07
1121	147.4	6.6	582	5	BP346480	BP346480	BP346480	1194	142.8	6.4	500	2	BF786777	BF786777	602111350
1122	147.4	6.6	625	5	BI601335	603245078	BI601335	1195	142.6	6.4	500	2	BB853379	BB853379	BB853379
1123	147.2	6.6	524	4	BG814412	daf67a01.	BG814412	1196	142.6	6.4	553	7	CN721222	CN721222	E0818C10-
1124	147.2	6.6	878	5	BP383262	BP383262	BP383262	1197	142	6.3	455	5	BY060483	BY060483	BY060483
1125	147	6.5	718	6	CD488088	T04_D05_T	CD488088	1198	142	6.3	735	4	BJ816674	BJ816674	BJ816674
1126	146.8	6.5	449	2	BB846235	BB846235	BB846235	1199	141.8	6.3	385	7	CF723044	CF723044	AGENCOURT
1127	146.8	6.5	597	6	CA333238	had52c04.	CA333238	1200	141.8	6.3	385	7	CF781051	CF781051	AGENCOURT
1128	146.8	6.5	799	6	CB955554	AGENCOURT	CB955554	1201	141.8	6.3	385	7	CF781051	CF781051	AGENCOURT
1129	146.6	6.5	390	2	AW227075	umc4h03.Y	AW227075	1202	141.8	6.3	385	7	CF781692	CF781692	AGENCOURT
1130	146.6	6.5	509	5	BY243106	BY243106	BY243106	1203	141.8	6.3	395	7	CF782368	CF782368	AGENCOURT
1131	146.6	6.5	594	5	BQ387494	NISC_md24	BQ387494	1204	141.8	6.3	385	7	CF783476	CF783476	AGENCOURT
1132	146.6	6.5	603	5	BQ39548	NISC_md04	BQ39548	1205	141.8	6.3	385	7	CF783882	CF783882	AGENCOURT
1133	146.6	6.5	902	7	CK805288	AGENCOURT	CK805288	1206	141.8	6.3	385	7	CK653731	CK653731	AGENCOURT
1134	146.4	6.5	711	4	BJ726973	BJ726973	BJ726973	1207	141.8	6.3	395	7	CK654650	CK654650	AGENCOURT
1135	146.2	6.5	630	6	AL584454	AL584454	AL584454	1208	141.8	6.3	385	7	CK655526	CK655526	AGENCOURT
1136	146.2	6.5	690	6	CD305884	STR_Pu691.	CD305884	1209	141.8	6.3	417	4	BM771497	BM771497	K-BST0055
1137	146.2	6.5	1100	9	CNS060UM	AL411140_T7_end_of	AL411140	1210	141.8	6.3	581	5	BP359469	BP359469	BP359469
1138	146	6.5	445	7	CK343335	H3017D09-	CK343335	1211	141.6	6.3	425	4	BM675848	BM675848	BJ7602768
1139	146	6.5	519	4	BG552861	da80f11.	BG552861	1212	141.6	6.3	579	4	BJ702646	BJ702646	BJ702646
1140	146	6.5	528	4	BI314115	daf92f10.	BI314115	1213	141.6	6.3	582	5	BP360217	BP360217	BP360217
1141	146	6.5	570	5	BP291933	BP291933	BP291933	1214	141.4	6.3	765	4	BI770989	BI770989	603055326
1142	146	6.5	584	4	BJ702127	BJ702127	BJ702127	1215	141.2	6.3	581	5	BQ523739	BQ523739	NISC_n123
1143	145.8	6.5	427	7	CF144462	UI-HF-CB0	CF144462	1216	141	6.3	325	6	CA537596	CA537596	CO25E03-
1144	145.8	6.5	525	1	AL168590	AL168590	AL168590	1217	141	6.3	523	5	BQ520219	BQ520219	NISC_n103
1145	145.8	6.5	756	7	CF148234	AGENCOURT	CF148234	1218	141	6.3	575	7	CF638723	CF638723	D06_C04_F
1146	145.6	6.5	1262	6	CD325908	AGENCOURT	CD325908	1219	140.8	6.3	705	7	CF814415	CF814415	EST691797
1147	145.4	6.5	586	4	BI484773	RE67925.5	BI484773	1220	140.6	6.3	613	5	BM216183	BM216183	BM216183
1148	145.4	6.5	607	7	CK662144	LP22145.5	CK662144	1221	140.6	6.3	624	5	BM360046	BM360046	BM360046
1149	145.2	6.5	401	6	CD736173	4017553.1	CD736173	1222	140.6	6.3	727	6	CB994471	CB994471	AGENCOURT
1150	145.2	6.5	474	2	BB863141	BB863141	BB863141	1223	140.6	6.3	822	6	CB993805	CB993805	AGENCOURT
1151	145.2	6.5	693	6	CD783866	EST655227	CD783866	1224	140.4	6.3	430	4	BI541491	BI541491	455270_MA
1152	145	6.5	377	2	BF045811	BF250005A	BF045811	1225	140.4	6.3	497	1	AL790150	AL790150	AL790150
1153	145	6.5	593	4	BI533394	fr81e11.x	BI533394	1226	140.4	6.3	544	2	AW496517	AW496517	kd01c11.y
1154	145	6.5	725	6	CD759078	AGENCOURT	CD759078	1227	140.4	6.3	569	5	BP331618	BP331618	BP331618
1155	145	6.5	971	4	BG336618	602405730	BG336618	1228	140.4	6.3	690	6	CA769828	CA769828	ssalrga50
1156	144.8	6.5	966	5	BU165992	AGENCOURT	BU165992	1229	140.2	6.3	385	7	CF783475	CF783475	AGENCOURT
1157	144.6	6.4	378	6	CD565567	B0496009-	CD565567	1230	140.2	6.3	385	7	CF783883	CF783883	AGENCOURT
1158	144.6	6.4	512	4	BG553460	da84e05.	BG553460	1231	140.2	6.3	385	7	CN324782	CN324782	AGENCOURT
1159	144.4	6.4	458	2	BB847485	BB847485	BB847485	1232	140.2	6.3	501	2	BF607680	BF607680	MY1_00062
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1161	144.4	6.4	543	5	BQ389137	NISC_md05	BQ389137	1234	140.2	6.3	681	6	CA051088	CA051088	ssalrga53
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1163	144.4	6.4	642	6	CB281566	ru53a04.Y	CB281566	1236	140	6.2	509	2	BE890822	BE890822	601431269
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1175	143.6	6.4	414	5	BQ382045	kk41e08.Y	BQ382045	1248	139.6	6.2	521	4	BI966923	BI966923	id26c05.Y
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BB845506 BB845506
BP357837 BP357837
CN622280 tad88h05.
CR762563 DKFPZ469L
CN361484 170006000
CF732400 UI-M-HA0-
BB846498 BB846498
BX737649 BX737649
CR629731 DKFPZ469N
BF973920 602242064
BY079567 BY079567
CB267995 1006901.H
CF141464 UI-HF-CB0
CF688418 CCAFJ81TR
AA590890 vml7f08.r
BP360416 BP360416
AU004195 AU004195
CF784910 AGENCOURT
CR536868 DKFPZ459L
AW966517 EST378591
CB194729 EST378591
CF140203 CF140203
CR534333 CR534333
CK181921 CK181921
BY218179 BY218179
CV528496 dba55f10.
BB846508 BB846508
BP320056 BP320056
BB745052 BB745052
AW335275 S45C8 AGS
BF048496 dc29d01.x
CF237840 AGENCOURT
BM804222 AGENCOURT
BB843678 BB843678
BB847708 BB847708
BX625832 BX625832
BQ389136 NISC mq05
BM866749 mcs006xf
W82610 mfo5h12.r1
BQ398331 NISC.mo06
BJ707460 BJ707460
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CN622576 tad88h05.
BG668093 DRABVD02
BY160251 BY160251
BY047456 BY047456

RESULT 1
CR610360 2105 bp mRNA linear HTC 21-JUL-2004
LOCUS full-length cDNA clone CS0DN001YK12 of Adult brain of Homo sapiens
(human).
DEFINITION CR610360
ACCESSION CR610360.1 GI:50491167
VERSION HTC; CNSLIT_CDNA.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

REFERENCE
1 (bases 1 to 2105)
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
AUTHORS Full-length cDNA libraries and normalization
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Unpublished
JOURNAL Contact : Feng Liang Email : fliang@lifetech.com URL :
REMARK http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue
2 (bases 1 to 2105)
Genoscope.
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
source Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DN001YK12"
/tissue_type="Adult brain"
/plasmid="pCMVSPORT_6"
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Query Match 93.6%; Score 2098.6; DB 3; Length 2105;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2101; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 40 AATAGTCCACTATACACGCTCGTCTTCCTCCGGGGGACAAACGTGGGTACGGGCACAG 99
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Db 1 AATAGTCCACTATACACGCTCGTCTTCCTCCGGGGGACAAACGTGGGTACGGGCACAG 60
|||||
QY 100 AGAGATATTATATGTCACCTCTTGGGGCTTCATGGGACTCCCTCTGCCACATTTTTT 159
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ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	Strausberg,R.L., Reingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Hopkins,K., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Staptenton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Ussdin,T.B., Toshituki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullany,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butlerfield,Y.S., Krzywinski,M.I., Skalska,U., Smalls,D.E., Schnerbach,A., Schein,J.E., Jones,S.J. and Marra,M.A.
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED	12477932
REFERENCE	2 (bases 1 to 1528)
AUTHORS	Strausberg,R.
TITLE	Direct Submission
JOURNAL	Submitted (01-MAR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT	Contact: MGC help desk Email: cgapbs-f@mail.nih.gov Tissue Procurement: ATCC/DCTD/PPP cdNA Library Preparation: Ruben Laboratory cdNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada info@bcsc.bc.ca
FEATURES	source <p>Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 13 Row: f Column: 3 This clone has the following problem: retained intron. Location/Qualifiers 1..1528 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:3614507" /tissue_type="Skin, melanotic melanoma." /clone_lib="NIH MGC 20" /lab_host="DH10B-R" /note="Vector: pOTB"</p>
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Db 269 CTTGGGACACTCTGGGCTGTGAGAAAGCTCTTCCACTATAGACCTCCACCAGGATG 328
QY 343 AATTGTGACAGACGCTCAAGAGAGTGGGTGGCCATCGAGAGCGACTGTGCCAGCTGTGC 402
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QY 403 CTGCTTTACAGAACAGCTCTTACAGAAATGATGGCGTGGCTGGCGGACACGCTGACGCGCC 462
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QY 463 TGGGGCCCTGTGGCCCTCGTGGACATAGGCTCTGACGAGCTGCCCGATGGTTCAGATGC 522
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QY 523 TTCCAAATACCTCCGCTCATCTGCGCGAACTGGGGAGCGATCCACGAAAGGACCGTGT 582
Db 509 TCCCATACCTCTATCTTATGCTGAGCTGGGAAGTATCCCGAAGCCAACTGTAT 568
QY 583 GCTTCTACGGCCACTTGGACGTGCGAGCTCTGTCACCGGGCGATGGGTGGCTCACGGACC 642
Db 569 GCTTCTATGGGCACTGAGCGTGGAGCCAGCTCAGAAAGGACGAGCGGTGGCTCACGGACC 628
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Db 629 CCTACACACTGACAGAGGTGGATGGGAACCTGTATGGACGGGGAGCAACAGACAAAG 688
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Db 689 GCCCGCTCTGGCTTGGATCAATGCCGTGAGCACTTTCAGAGCTCTGCGACGAGATCTTC 748
QY 763 CTGTGAATATCAATTCATCAITGAGGGGATGGAAGAGCGTGGCTCTGTTCCTCGGAGG 822
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QY 823 AACTTGTGGAAGAAAGAGACCGATCTTCTCTGTGTGGATCAATGATGATTAATTTTCAG 882
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QY 883 ATAACTGTGTGATCAGCAAGAGGAGCGACCAATCACTTATGNAACCGGGGGAACAGCT 942
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QY 1363 AACAGGTGACACGACATCTTGAAGATGTGTCTTCCAAAAGAAATAGTTTCAACAGATGG 1422

Db 1349 AACAGGTAACCTCAGCATCTCGAAAGCTGTCTTCTCTAAAGGAATAGTTTCAACAGATGG 1408
QY 1423 TTGTTTTCATGACTCTAGGACTACACCGTGGATTGCAAAATATTGATGACACCCAGTATC 1482
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RESULT 4

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DEFINITION BX422767 Homo sapiens ADULT BRAIN Homo sapiens cDNA clone
CS0DN001YK12 3-PRIME, mRNA sequence.
ACCESSION BX422767
VERSION BX422767.2 GI:46932516
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1107)
AUTHORS Li, W. B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 13, 2003 this sequence version replaced gi:30655385.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 9111.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?S=CS0DN001BF06NP1&c=9111.f.

FEATURES

source
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was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6

Qy	40	AATAGCTCCCATATACAGACCTCGCTTCCTTCGGGGGCAACCTGGGTGAGGCAACAG	99
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Qy	220	GAATGGGTCGCTCCCTGCTGGCTG ---TGCTGCTGCTGCTGCTGAGCGCGCATGTTCT	276
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Qy	277	CCTCACCTCCCGCCCCCGCGCTGTAGAGAAAGTCTTCAGTACATGACCTCCATC	336

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Db 301 AGGATGAATTTGTGACAGCGCTGAAGAGTGGTGGCCATCGAGAGCGACTCTGTCCAGC 360
Qy 397 CTGTGCTCTGCTTCAGACAAGAGCTCTTCAGAATGATGGCGTGGCTGCCGACACGCTGC 456
Db 361 CTGTGCTCTGCTTCAGACAAGAGCTCTTCAGAATGATGGCGTGGCTGCCGACACGCTGC 420
Qy 457 AGCGCTGGGGGCGCGTGTGGCTCGGTGGACATGGGTCTCTCAGCAGCTGCCGATGGTC 516
Db 421 AGCGCTGGGGGCGCGTGTGGCTCGGTGGACATGGGTCTCTCAGCAGCTGCCGATGGTC 480
Qy 517 AGAGCTCTTCAATACCTCCCGTCACTCTGGCCGAACCTGGGAGGCGATCCCAAGAAAGGCA 576
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RESULT 6
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DEFINITION CS0DN001YK12 5-PRIME, mRNA sequence.
ACCESSION BX432016
VERSION BX432016.1 GI:30789074
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 928)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
```

end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Invitrogen.

This sequence belongs to sequence cluster 9111.f

For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CS0BAG0692A11_CS06609_1&c=9111.f

FEATURES

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	/dev_stage="adult"
	/clone_lib="Homo sapiens ADULT BRAIN"
	/notes="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

ORIGIN

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Qy 907	AGCAGCAATCACTTATGAAACCCGGGGAAACAGCTACTTTCATGGTGGAGTGAATGCA	966		
Db 59	AGCAGCAATCACTTACGGAAACCCGGGGAAACAGCTACTTTCATGGTGGAGTGAATGCA	118		
Qy 967	GAGACAGGATTTTCACTCAGGAACCTTTGGTGGCATCTTTCATGAACCAATGGCTGATC	1026		
Db 119	GAGACAGGATTTTCACTCAGGAACCTTTGGTGGCATCTTTCATGAACCAATGGCTGATC	178		
Qy 1027	TGTTTCTCTTCTCGGTAGCTGTGATCTGCTGTGTCATATCTTCTGGTCCCTGGATCT	1086		
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Qy 1087	ATGATGAAGTGGTTCCTCTTACAGAAGAGGAAATAAATACATACAAAGCCATCCATCTAG	1146		
Db 239	ATGATGAAGTGGTTCCTCTTACAGAAGAGGAAATAAATACATACAAAGCCATCCATCTAG	298		
Qy 1147	ACCTAGAAGAAATACCGGAATAGCAGCGGGTTGAGAAATTTCTGTCGATATAAGGAGG	1206		
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Qy 1207	AGATTCTAATGACCTCTGGAGGTACCATCTCTTCTTATTCATGGATCGAGGCGCGT	1266		
Db 359	AGATTCTAATGACCTCTGGAGGTACCATCTCTTCTTATTCATGGATCGAGGCGCGT	418		
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Db 599	ACCGTGGATTGCAAAATATTGTGACACCCAGTATCTCGCAGCAAAAAGAGCGATCAGAA	658		
Qy 1507	CAGTGTGGAAACAGAACCATGATATGATCCGGGATGGATCCACCATTTCCAAATTCGCCAAA	1566		

Wed Feb 16 11:38:00 2005

Db	659	CAGTGTGTTGGAACAGACAGATATGATCCGGATGGATCCACCAATTCCTCAATTCGCAAAA	718
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Db	719	TGTTCCAGAGATCGTCCACAGACGCTGGTCTTAATTCGCTGGAGCTCTTGATGATG	778
Qy	1627	GAGAACATTCGAGAAATCAACAGGTGGAACTACATAGAGGGAACCAAAATAT	1686
Db	779	GAGAACATTCGAGAAATCAACAGGTGGAACTACATAGAGGGAACCAAAATAT	837
Qy	1687	TTTGCTGCTTTTCTTAGAGATGGCCAGCTCCATTAATACAGAACTTCTAGTCTGA	1746
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Db	897	TCTGATCCACTGACAGATTTACCTGCCCCAC	927
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LOCUS			
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BX453730			
VERSION			
BX453730.1 GI:31024517			
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EST.			
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE			
1 (bases 1 to 913)			
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.			
Full-length cDNA libraries and normalization			
Unpublished (2001)			
Contact: Genoscope			
Genoscope - Centre National de Sequencage			
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE			
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr			
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime			
end enriched, double-strand cDNA was digested with Not I and cloned			
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library			
was not normalized. Library was constructed by Life Technologies, a			
division of Invitrogen.			
This sequence belongs to sequence cluster 9111.f			
For more information about this cluster, see			
http://www.genoscope.cns.fr/cdna?s=CS0BAI0532D09_CS05060_1&c=9111.f			
FEATURES			
source			
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/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA			
was primed with a NotI-oligo(dT) primer. Five prime end			
enriched, double-strand cDNA was digested with Not I and			
cloned into the Not I and EcoRV sites of the pCMVSPORT 6			
vector. Library was not normalized."			
ORIGIN			
Query Match			
Best Local Similarity 38.4%; Score 860.4; DB 5; Length 913;			
Matches 900; Conservative 0; Mismatches 12; Indels 3; Gaps 3;			
Qy	361	AGGAGTGGGTGGCCATCGAGAGCGACTCTGTCCAGCCCTGCTCGCTTCAGACAAGGC	420
Db	912	AAGAGTGGGTGGCCCTCGAGAGCGACTCTGTCCAGCNTG-GCCTCGCTCAAGACAAGGC	854
Qy	421	TTCTCAGAAATGATGGCCCTGCGGACACGCTGACGCGCCTGGGGGCCCTGTGGCCT	480
Db	853	TCCTCAGAAATGATGG-CGTGGCTGCGGACACGCTGACGCGCCTGGGGGCCCTGTGGCCT	795
Qy	481	CGGTGACATGGGTCTCTCAGCAGCTGCCCGATGGTCAGAGTCTTCCAAATACCTCCCGTCA	540
Db	794	CGGTGACATGGGTCTCTCAGCAGCTGCCCGAATGGTCAGAGTCTTCCAAATACCTCCCGTCA	735
Qy	541	TCCTGGCCGAATCTGGGAGCGATCCACGAAAGGACCGGTGTCTTCTACGGCCACTTGG	600
Db	734	TCCTGGCCGAATCTGGGAGCGATCCACGAAAGGACCGGTGTCTTCTACGGCCACTTGG	675
Qy	601	ACGTGACGCTGTGACCCGGGCGATGGGTGGCTCAGCGACCCCTATGTCTCAGCGAGG	660
Db	674	ACGTGACGCTGTGACCCGGGCGATGGGTGGCTCAGCGACCCCTATGTCTCAGCGAGG	615
Qy	661	TAGACGGGAAACTTTATGGAACGAGGAGCGACCGGACAAAGGCCCTGTCTGGCTTGA	720
Db	614	TAGACGGGAAACTTTATGGAACGAGGAGCGACCGGACAAAGGCCCTGTCTGGCTTGA	555
Qy	721	TCAATGCTGTGACGCGCTTCAGAGCCCTGGAGCAAGATCTTCTGTGAATATCAAAATCA	780
Db	554	TCAATGCTGTGAGCGCTTCAGAGCCCTGGAGCAAGATCTTCTGTGAATATCAAAATCA	495
Qy	781	TCATTGAGGGGATGGAAGAGCGCTGGCTCTGTGCTCCCTGGAGGAACTTTGTGAAAAA	840
Db	435	TCATTGAGGGGATGGAAGAGCGCTGGCTCTGTGCTCCCTGGAGGAACTTTGTGAAAAA	435
Qy	841	AGGACCGGATCTCTCTGTGTGACTACATCTGTAATTTAGATAAAGCTTTGGATCAGCC	900
Db	434	AGGACCGGATCTCTCTGTGTGACTACATCTGTAATTTAGATAAAGCTTTGGATCAGCC	375
Qy	901	AAAGGAGCCAGCAATCACTTATGAAACCCGGGGGAAACAGTACTTTCATGTTGAGGTGA	960
Db	374	AAAGGAGCCAGCAATCACTTACGAAACCCGGGGGAAACAGTACTTTCATGTTGAGGTGA	315
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Qy	1021	CTGATCTGGTGTCTTCTCGGTAGCCCTGAGTCTGCTGTTGTTGTTGTTGTTGTTGTTG	1080
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Qy	1081	GAATCTATGATGAGTGGTCTCTCTTACAGAGAGGAAATAAATACATACAAAGCCATCC	1140
Db	194	GAATCTATGATGAGTGGTCTCTCTTACAGAGAGGAAATAAATACATACAAAGCCATCC	135
Qy	1141	ATCTAGACCTAGAGAAATACCGGAATAGCAGCGGGTTGAGAAATTTCTGTTGATCTA	1200
Db	134	ATCTAGACCTAGAGAAATACCGGAATAGCAGCGGGTTGAGAAATTTCTGTTGATCTA	75
Qy	1201	AGGAGGAGATTCATATGACACCTCTCGAGGTACCCATCTCTTTCTATTTCATGGGATCGAGG	1260
Db	74	AGGAGGAGATTCATATGACACCTCTCGAGGTACCCATCTCTTTCTATTTCATGGGATCGAGG	16
Qy	1261	GGCGGTTTCATGAGC 1275	
Db	15	GGCGGTTTCATGAGC 1	
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LOCUS			
DEFINITION			
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BI489822			
VERSION			
BI489822.1 GI:15329050			
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EST.			
SOURCE			
Homo sapiens (human)			
ORGANISM			
Homo sapiens			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			

REFERENCE 1 (bases 1 to 882)
 NIH-MGC http://mgc.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM11430 row: k column: 13
 High quality sequence stop: 857.
 Location/Qualifiers
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 /note="Organ: pooled brain, lung, testis; Vector:
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 source anonymous pool of 6 male brains, age range 23-27; 1
 male lung, age 27; and 1 male testis, age 69. Library is
 oligo-dT primed and directionally cloned (EcoRV site is
 destroyed upon cloning). Average insert size 1.8 kb,
 insert size range 1-3 kb. Library is normalized and
 enriched for full-length clones and was constructed by C.
 Gruber (Invitrogen). Research Genetics tracking code
 021. Note: this is a NIH_MGC Library."

ORIGIN
 Query Match 35.1%; Score 786.2; DB 4; Length 882;
 Best Local Similarity 96.1%; Pred. No. 1.7e-176;
 Matches 849; Conservative 0; Mismatches 28; Indels 6; Gaps 4;
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 DB 61 TCTGCCACATTTTTGGAGGTGGGAAAGTTGCTAGAGGCTTCAGAACTCCAGCCTAATG 120
 QY 204 GATCCCAAACTGGGAGAAATGGCTGCTCCCTGCTGGCTG---TGCTGCTGCTGCTG 260
 DB 121 GATCCCAAACTGGGAGAAATGGCTGCTCCCTGCTGGCTGCTGCTGCTGCTGCTG 180
 QY 261 GAGCGCGCATGTTCTCTCCTCACCTCCCGCCCGCGCGCTGTAGAGAAAGTCTCCAG 320
 DB 181 GAGCGCGCATGTTCTCTCCTCACCTCCCGCCCGCGCGCTGTAGAGAAAGTCTCCAG 240
 QY 321 TACATTGACCTCCATCAGGATGAATTTGTGCAGACGCTGAAGAGTGGGTGGCCATCGAG 380
 DB 241 TACATTGACCTCCATCAGGATGAATTTGTGCAGACGCTGAAGAGTGGGTGGCCATCGAG 300
 QY 381 AGCGACTCTGTCCAGCTGTGCTGCTGCTTTCAGACAGAGCTCTTCAGAAATGATGGCGGTG 440
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 QY 441 GCTGCGGACACGCTGACGCGCTGGGGCGCGCTGCGCTCGGTGGACATGGGCTCTCCAG 500
 DB 361 GCTGCGGACACGCTGACGCGCTGGGGCGCGCTGCGCTCGGTGGACATGGGCTCTCCAG 420
 QY 501 CAGCTGCCCGATGTGTCAGAGTCTTCCAAATACCTCCCTCATCTCTGGCCGCACTGGGGAGC 560
 DB 421 CAGCTGCCCGATGTGTCAGAGTCTTCCAAATACCTCCCTCATCTCTGGCCGCACTGGGGAGC 480
 QY 561 GATCCCAAGAAAGCAGCGGTGTCTTACGGGCACCTTGAGCGCTGACGCTGCTGACCCGG 620

DB 481 GATCCCAAGAAAGCAGCGGTGTCTTCTACGGCCACTTGGACGCTGACGCTGCTGACCGG 540
 QY 621 GCGGATGGGTGGCTCAGGACCCCTATGTCTGACGAGGTAGACGGAACTTTATGGA 680
 DB 541 GCGGATGGGTGGCTCAGGACCCCTATGTCTGACGAGGTAGACGGAACTTTATGGA 600
 QY 681 CGAGGAGCGACCGACAAACAAAGGCCCTCTTGGCTTTGGATCAATGCTGTGAGCGCTTC 740
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 DB 661 AGAGCCCTGAGCAGAGATCTTCTGTGAATATCAATTCATTCATGAGGGATGGAAGAG 720
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 DB 721 GCTGGCTCTGTGCTCCCTGGAGGAACTTGTGAAAAAGA-AAAGACCGATTCTTCTCT-G 780
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 QY 919 CTTATGGAACCCGGGGAACAGCTACTTCTATGTTGGAGGTGAA 961
 DB 841 CTTATGGAACCCGGGGAAG-TACGTCACTGGGACAGTGAA 882

RESULT 9
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 LOCUS 602676657F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:4799126 5',
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 VERSION BG715910
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 884)
 NIH-MGC http://mgc.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
 Toshiyuki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM10688 row: a column: 15
 High quality sequence stop: 883.
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 /clone="IMAGE:4799126"
 /tissue_type="hypothalamus"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_96"
 /note="Organ: brain; Vector: pBluescriptR (modified
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 insert size 2.3 kb and normalized to 10^5. This is a
 primary library enriched for full-length clones and
 constructed using the Cap-trapper method (Carninci, in
 preparation). Library constructed by M. Brownstein
 (NHGRI/NHGR), National Institutes of Health). Note: this is

FEATURES
 source

ACCESSION		BI754224		GI:15745802	
VERSION		BI754224.1			
KEYWORDS		EST.			
SOURCE		Homo sapiens (human)			
ORGANISM		Homo sapiens			
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE		1 (bases 1 to 799)			
AUTHORS		NIH-MGC http://mgi.nci.nih.gov/.			
TITLE		National Institutes of Health, Mammalian Gene Collection (MGC)			
JOURNAL		Unpublished (1999)			
COMMENT		Contact: Robert Strausberg, Ph.D. Email: csapbs@mail.nih.gov Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: The I.M.A.G.E. Consortium (LLNL) cDNA Library Arrayed by: Incyte Genomics, Inc. DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM11490 row: 1 column: 06 High quality sequence stop: 797.			
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		/clone_lib="NIH_MGC_114"			
		/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH_MGC Library."			
ORIGIN		Query Match 34.5%; Score 774; DB 4; Length 799; Best Local Similarity 99.0%; Pred. No. 1.3e-173; Matches 790; Conservative 0; Mismatches 5; Indels 3; Gaps 1;			
Qy	155	TTTTGGAGGTTGGAAAGTTGCTAGAGGCTTCAGAACTCCAGCCTTAATGGATCCCAACT	214		
Db	2	TTTTGGAGGTTGGAAAGTTGCTAGAGGCTTCAGAACTCCAGCCTTAATGGATCCCAACT	61		
Qy	215	CGGAGAGATGGCTCCCTGCTGGCTG---TGCTGCTGCTGCTGCTGGAGCGGGCAT	271		
Db	62	CGGAGAGATGGCTCCCTGCTGGCTGCTGCTGCTGCTGCTGGAGCGGGCAT	121		
Qy	272	GTTCTCTCACTCCCGCCCGCGCTGTTAGAGAAAGTCTTCCAGTACATTGACCT	331		
Db	122	GTTCTCTCACTCCCGCCCGCGCTGTTAGAGAAAGTCTTCCAGTACATTGACCT	181		
Qy	332	CCATCAGGATGAATTTGTGCAGACGCTGAAGAGTGGGTGGCCATCGAGAGCGACTCTGT	391		
Db	182	CCATCAGGATGAATTTGTGCAGACGCTGAAGAGTGGGTGGCCATCGAGAGCGACTCTGT	241		
Qy	392	CCAGCTGTGCTCGCTTCAGACAAGAGCTTTCAGATGATGCGGTGGCGGAC	451		
Db	242	CCAGCTGTGCTCGCTTCAGACAAGAGCTTTCAGATGATGCGGTGGCGGAC	301		
Qy	452	GCTGACGCGCTGGGGCGGCTGTGGCTCGGTGGACATGGGTCTCTCAGCAGTGGCGGA	511		
Db	302	GCTGACGCGCTGGGGCGGCTGTGGCTCGGTGGACATGGGTCTCTCAGCAGTGGCGGA	361		
Qy	512	TGGTCAGAGTCTTCCAAATACCTCCCGTCATCTCGGCGGAACCTGGGAGCGATCCCAAG	571		
Db	362	TGGTCAGAGTCTTCCAAATACCTCCCGTCATCTCGGCGGAACCTGGGAGCGATCCCAAG	421		

ORIGIN		a NIH_MGC Library."		Query Match 34.9%; Score 782.2; DB 4; Length 884; Best Local Similarity 97.9%; Pred. No. 1.5e-175; Matches 857; Conservative 0; Mismatches 8; Indels 10; Gaps 6;	
Qy	136	GAGCTCCCTCTGCCACATTTTGGAGGTTGGGAAAGTTGCTAGAGGCTTCAGAACTCCA	195		
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Qy	196	GCTAATGATCCAAATCGGGAGATGGCTCGCTCCCTGCTGCTG---TGCTGCTGC	252		
Db	67	GCTAATGATCCAAATCGGGAGATGGCTCGCTCCCTGCTGCTGCTGCTGCTGCTGCTG	126		
Qy	253	TGCTGCTGAGCGCGGATTTCTCTCACCTCCCGCCCGCGCTGTTAGAGAAAG	312		
Db	127	TGCTGCTGAGCGCGGATTTCTCTCACCTCCCGCCCGCGCTGTTAGAGAAAG	186		
Qy	313	TCTTCCAGTACATTTGACCTCCATCAGGATGAATTTGTGCAGACGCTGAAGAGTGGTGG	372		
Db	187	TCTTCCAGTACATTTGACCTCCATCAGGATGAATTTGTGCAGACGCTGAAGAGTGGTGG	246		
Qy	373	CCATCAGAGCGACTCTGTCCAGCCTGTGCTCGCTTCAGACAGAGCTTTCAGAAAGA	432		
Db	247	CCATCAGAGC--CTCTGCTCAGCCTGTGCTCGCTTCAGACAGAGCTTTCAGAAAGA	304		
Qy	433	TGGCCGTGGCTGGGACACGCTCAGCGCTGGGGGCGGCTGTGGCTCGGTGGACATGG	492		
Db	305	TGGCCGTGGCTGGGACACGCTCAGCGCTGGGGGCGGCTGTGGCTCGGTGGACATGG	364		
Qy	493	GTCTCAGCAGCTGCCGATGCTCAGAGTCTTCCAAATACCTCCCGTTCATCTGGCGGAAC	552		
Db	365	GTCTCAGCAGCTGCCGATGCTCAGAGTCTTCCAAATACCTCCCGTTCATCTGGCGGAAC	424		
Qy	553	TGGGAGCGATCCACAGAAAGCAGCGTGTCTTACGCGCACTTGGACGCTGCAGCCTG	612		
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Qy	673	TTTATGACGAGGAGCGACCGACAAAGAGCGCTGTGGCTTGGATCAATGCTGTGA	732		
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Qy	733	GCGCTTCAGAGCCCTGGAGCAAGATCTTCTGTGAATATCAAAATTCATATTCAGGGGA	792		
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Qy	853	TCTCTGTGTGAGTACATTTGTAATTTTCAG--TAACTGTGATTCACCCAAAGGAGCCA	911		
Db	725	TCTCTGTGTGAGTACATTTGTAATTTTCAG--TAACTGTGATTCACCCAAAGGAGCCA	784		
Qy	912	GCAATCACTTATGAAACCGGGGAAACAGCTACTTCAATGTTGGAGGTGAAATGCGAGAC	971		
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LOCUS		603025522F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5196053 5',			
DEFINITION		mRNA sequence.			

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 QY 482 GCTACGACCGCCCTATGCTGACGAGGTAGACGGGAACCTTTATGACGAGGCGAC 541
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 DB |||||
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 DB |||||
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 DB |||||
 QY 662 TGCCCTGGAGGAACTTGTGGAAAGAAAGGACCGATTCTTCTGTGTGGACTACAT 721
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 DB |||||
 QY 782 GGGGAACAGCTACTTCAT 799
 DB |||||

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ACCESSION BM920701

VERSION BM920701.1 GI:19371080

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

TITLE NIH-MGC http://mgi.nci.nih.gov/.

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished (1999)

Contact: Robert Straubeberg, Ph.D.

Email: cgaaps-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: L1AM12785 row: d column: 23

High quality sequence stop: 583.

Location/Qualifiers

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/notes="Organ: pooled brain, lung, testis; Vector:

pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA

source anonymous pool of 6 male brains, age range 23-27; 1

male lung, age 27; and 1 male testis, age 69. Library is

oligo-dT primed and directionally cloned (EcoRV site is

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Gruber (Invitrogen). Research Genetics tracking code

ORIGIN 021. Note: this is a NIH_MGC Library."

Query Match 34.0%; Score 761.2; DB 5; Length 1054;

Best Local Similarity 96.0%; Pred. No. 1.6e-170;

Matches 835; Conservative 0; Mismatches 28; Indels 7; Gaps 5;

QY 2 AATGAATACCTCCGAAGCCGCTTGTTCACAGATGTGAATAGCTCCACATATACAGCCT 61

DB 1 AATGAATACCTCCGAAGCCGCTTGTTCACAGATGTGAATAGCTCCACATATACAGCCT 60

QY 62 CGTCTTCTTCCGGGGGCAACCGTGGTCAAGGCACAGAGAGATATTATATGTCAACCTC 121

DB 61 CGTCTTCTTCCGGGGGCAACCGTGGTCAAGGCACAGAGAGATATTATATGTCAACCTC 120

QY 122 TTGGGGCTTATGAGGACTCCCTCTGCCACATTTTTTTGGAGGTGGGAAGTTCCTAGAG 181

DB 121 TTGGGGCTTATGAGGACTCCCTCTGCCACATTTTTTTGGAGGTGGGAAGTTCCTAGAG 180

QY 182 GCTTCAGAACTCCAGACCTAATGGATCCAAACTCGGAGAGATGGCTCGCTCCCTGTGGC 241

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QY 242 TG---TGCTGCTGCTGCTGGAGCGCGCATGTTCTCTCTCACCTCCCGCCCGCCGCG 298

DB 241 TGCTGCTGCTGCTGCTGGAGCGCGCATGTTCTCTCTCACCTCCCGCCCGCCGCG 300

QY 299 GCTGTTAGAGAAAGTCTTCCAGTACATTGACCTCCATCAGATGAATTTGTGACAGCCT 358

DB 301 GCTGTTAGAGAAAGTCTTCCAGTACATTGACCTCCATCAGATGAATTTGTGACAGCCT 360

QY 359 GAAGGAGTGGGTGGCCATCCAGAGCGACTCTGTCCAGCCTGTGCTTCGCTTTCAGACAAGA 418

DB 361 GAAGGAGTGGGTGGCCATCCAGAGCGACTCTGTCCAGCCTGTGCTTCGCTTTCAGACAAGA 420

QY 419 GCTCTTCAGAAATGATGCGCTGGTGGACACGCTGACGCTGCGGGGCGCTGTGGC 478

DB 421 GCTCTTCAGAAATGATGCGCTGGTGGACACGCTGACGCGCTGGGGGCGCTGTGGC 480

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QY 718 GGAATCAATGCTGTGAGCGCTTTCAGAGCCCTGAGCAAGATCTTCTGTGAATATCAAT 777

DB 721 GGAATCAATGCTGTGAGCGCTTTCAGAGCCCTGAGCAAGATCTTCTGTGAATATCAAT 780

QY 778 TCATCA-TTGAGGGGATGGAAGGCTGGCTCTG-TTGGCCCTGGAGAACTTGTGG-AAA 834

DB 781 TCATCA-TTGAGGGGATGGAAGGCTGGCTCTG-TTGGCCCTGGAGAACTTGTGG-AAA 840

QY 835 AAGAAAAGGACCGAATCTTCTCTGTGGTGG 864

DB 841 AAGAAAAGGACCGAATCTTCTCTGTGGG 870

RESULT 12

BI600248 887 bp mRNA linear EST 07-SEP-2001
 LOCUS 603245955F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:528268 5',
 DEFINITION mRNA sequence.

366	Db	CCTCAGCAGCTGCCCGATGGTCAGAGTCTCCCAATACCTCCCGTCATCTTCCGCGCAACTG	425			
555	Qy	GGGAGCGATCCACGAAAGGACCGGTGTGCTTTACGGCCACTTTGGACGTGACGCTGCT	614			
426	Db	GGGAGCGATCCACGAAAGGACCGGTGTGCTTTACGGCCACTTTGGACGTGACGCTGCT	485			
615	Qy	GACCGGGCGATGGGTGGCTCACGGACCCCTATGTGTGTCGCGAGGTAGACGGGAACCTT	674			
486	Db	GACCGGGCGATGGGTGGCTCACGGACCCCTATGTGTGTCGCGAGGTAGACGGGAACCTT	545			
675	Qy	TATGACGAGGAGGACCGACGACAAAGAGCCCTGTCTGGCTTGGATCAATGCTGTGAGC	734			
546	Db	TATGACGAGGAGGACCGACGACAAAGAGCCCTGTCTGGCTTGGATCAATGCTGTGAGC	605			
735	Qy	GCCTTCAGAGCCCTGGAGCAAGATCTTCTGTG- AATATCAAAATTCATTCATTCAGGGAT	793			
606	Db	GCCTTCAGAGCCCTGGAGCAAGATCTTCTGTGNAATATCAAAATTCATTCATTCAGGGAT	665			
794	Qy	GGAGA- GCTGTGCTTGTTCCTCGGAGGACTTGTGAAAAGAGAAAGACCGATCT	852			
666	Db	GGAAGACGGCTGTGCTTGTTCCTCGGAGGACTTGTGAAAAGAGAAAGACCGATCT	724			
853	Qy	TCCTCTGTGTGGACT- ACATTTGTAATTTTCAGATAACCT- GTGGATTCAGCCAAAGAAACC	910			
725	Db	TCCTCTGTGTGGACTTCATTTTCAGATAAATTCATTTTCAGATAAATTCATTTTCAGAAACC	784			
911	Qy	AGC- AATCACTTATGGAACCCGGGGAGACAGTACTTATGTTGGAGCTGAAATCGACAG	969			
785	Db	AGCAATATCACTTATGGAACCCGGGGAGACAGTACTTATGTTGGAGCTGAAATCGGAG	844			
970	Qy	ACCAGGATTTTCACTCAGGAACCTTTGGTGGCATCCT	1006			
845	Db	ACAG- --ATTCACTTCAGGAACCTTTGGGGGCATCCT	878			
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LOCUS	602673107F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:4795945 5',					
DEFINITION	mRNA sequence.					
ACCESSION	RG708811					
VERSION	RG708811.1 GI:13986523					
KEYWORDS	EST.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.						
REFERENCE	1 (bases 1 to 807)					
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.					
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)					
JOURNAL	Unpublished (1999)					
COMMENT	Contact: Robert Strausberg, Ph.D. Email: csapbs-r@mail.nih.gov Tissue Procurement: Miklos Palkovits, M.D., Ph.D. cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN) cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM10679 row: m column: 02 High quality sequence stop: 757. Location/Qualifiers 1..807 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:4795945" /tissue_type="hypothalamus" /lab_host="DH10B" /clone_lib="NIH_MGC_96"					
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ORIGIN						
Query Match	33.1%; Score 741.8; DB 4; Length 887;					
Best Local Similarity	96.4%; Pred. No. 6.7e-166;					
Matches	845; Conservative 0; Mismatches 22; Indels 10; Gaps 8;					
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Qy	195	AGCCTAATGATCCCAACTCGGAGAAATGGCTGCGTCCCTGTGCTGTGCTGTGCTG	254			
Db	66	AGCCTAATGATCCCAACTCAGGAAATGGCTGCGTCCCTGTGCTGTGCTGTGCTG	125			
Qy	255	TTGCTGGAGCGGGATGTTCTCTCACTCCCGCCCGCCCGGCTGTTAGAGAAAGTC	314			
Db	126	TTGCTGGAGCGGGATGTTCTCTCACTCCCGCCCGCCCGGCTGTTAGAGAAAGTC	185			
Qy	315	TTCCAGTAGTACCTGACCTCCATCAGAGTAATTTGTGACAGCGCTGAGAGGTGGG	374			
Db	186	TTCCAGTAGTACCTGACCTCCATCAGAGTAATTTGTGACAGCGCTGAGAGGTGGG	245			
Qy	375	ATCGAGAGCGACTGTGTCAGCGCTGTGCTGCTTCAGACAGAGCTTCAGAAATG	434			
Db	246	ATCGAGAGCGACTGTGTCAGCGCTGTGCTGCTTCAGACAGAGCTTCAGAAATG	305			
Qy	435	GCCGTGGCTGGGACACGCTGCAGCGCTGGGGGCGCGTGTGGCTCGGTGACATGG	494			
Db	306	GCCGTGGCTGGGACACGCTGCAGCGCTGGGGGCGCGTGTGGCTCGGTGACATGG	365			
Qy	495	CCTCAGCAGCTGCCCGATGGTCAGAGTCTTCAATACCTCCCTCCCTTCCTGGCCG	554			

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Db GCCGTGGCTGCGGACACGCTGAGCGCTGGGGCCCTGTGGCTCGGTGGACATGGGT 365
495 CTTACGAGCTGCCGATGCTGAGAGTCTTCCATACCTCCGTCATCTCGGCGGACTG 554
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555 GGGAGCGATCCACGAAAGGACCGCTGTGCTTCTACGGCCACTTGGAGCTGAGCGCTGCT 614
Db GGGAGCGATCCACGAAAGGACCGCTGTGCTTCTACGGCCACTTGGAGCTGAGCGCTGCT 485
615 GACCGGGCGATGGGTGGCTACGAGCCCTTATGTGCTGACGAGGTAGAGCGGAACTT 674
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675 TATGACGAGGAGCGACCGACGACAAAGCCCTGCTTGGCTTGGATCAATGCTGTGAGC 734
Db TATGACGAGGAGCGACCGACGACAAAGCCCTGCTTGGCTTGGATCAATGCTGTGAGC 605
735 GCCTTCAGAGCCCTGGAGCAAGATCTTCTGTGAATATCAATTCATATTGAGGGGA-T 793
Db GCCTTCAGAGCCCTGGAGCAAGATCTTCTGTGAATATCAATTCATATTGAGGGGATT 665
794 GGAAGAGCTGGCTGCTTGGCTGGAGCACTTGTGGA-AGAAGAGGACCAATTCT 852
Db GGAAGAGCTGGCTGCTTGGCTGGAGCACTTGTGGA-AGAAGAGGACCAATTCT 725
853 TCTCTGGTGGACTACATTTGTAATTTTCAATTAACCTGTGGATCAGCCAAAGGAGCCAG 912
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913 CAATCACTTATGGAACC 929
Db CAATCACTTATGGAACC 801

RESULT 15
AI939620/c
LOCUS
DEFINITION
tm64d04.x5 NCI CGAP Brn25 Homo sapiens cDNA clone IMAGE:2162887 3',
similar to WP:R1186.1 CE12770 YEAST HYPOTHETICAL 52.9 KD PROTEIN
Like ;, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 (bases 1 to 742)
NCI/NINDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGP), Tumor Gene Index
Unpublished (1998)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonald, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

This read is a RESSEQUENCE of a previously sequenced human clone
Original clone citation: National Cancer Institute / National
Institute of Neurological Disorders and Stroke, Brain Tumor Genome
Anatomy Project (CGAP/BTGP), Tumor Gene Index
This read has been verified (found to hit its original self in the

correct orientation)
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Seq primer: -40UP from Gibco
High quality sequence stop: 462.
Location/Qualifiers
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strand cDNA was primed with a Not 1-oligo(dT) primer [5'
TGTACCAATCTGAAGTGGAGCGCGCATAGGTTTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT7T3 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."

ORIGIN
Query Match 32.4%; Score 726.6; DB 1; Length 742;
Best Local Similarity 98.7%; Pred. No. 2.7e-162;
Matches 732; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
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QY 1335 CTTCACTGAATGTCTGCGGTGGAAAAACAGGTGACACGACATCTTGAAGATGTGTC 1394
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QY 1395 TCCAAAAAGAAATAGTTCACAAAGATGTTTCTCATGACTCTAGGACTACACCGTGG 1454
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QY 1455 ATTGCAAAATATTGATGACACCCAGTATCTCGCAGCAAAAAGAGCGATCAGAACAGTGT 1514
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QY 1515 GGAACAGAACGATATGATCGGATGGATCCACATTTCCAAATGGCAAAATGTTCCAG 1574
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QY 1575 GAGATCGTCCACAGAGCGTGTGCTAAATTCGCTGGAGCTGTTGATGATGAGGAACAT 1634
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QY 1635 TCGCAGAAATGAGAAAATCAAGGTGGAACTACATAGAGGAAACCAATATTTCGTGCC 1694
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QY 1695 TTTTCTTATGAGATGCGGATGCTCCATTAATCAAGAACCTTCTAGTCTGATCTGATCC 1754
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||||| 82 TTGGGCTAGTAGTACATTTTCCTTCATTTAAATGCTCTGGGACATCTGGATCA 23
Qy 1875 GTAATAAAATATTTCAAAGGCA 1896
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Job time : 5072 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 13, 2005, 18:57:22 ; Search time 277 Seconds
(without alignments)
13243.799 Million cell updates/sec

Title: US-10-036-342-56

Perfect score: 2242

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : Issued Patents NA.*

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6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	612.8	27.3	672	4	US-09-621-976-97
2	467.4	20.8	2710	4	US-09-620-312B-931
3	373.2	16.6	1489	4	US-09-270-767-14369
4	292.8	13.1	300	4	US-09-513-999C-13950
5	224.8	10.0	1479	4	US-09-248-796A-652
6	96.4	4.3	273	1	US-08-204-740-5
7	96.4	4.3	273	3	US-09-081-167A-5
8	96.4	4.3	273	3	US-09-081-395-5
9	96.4	4.3	273	3	US-09-416-833-5
10	96.4	4.3	273	5	PCT-US95-02521-5
11	92.2	4.1	334	4	US-09-513-999C-22131
12	85.8	3.8	1374	4	US-09-583-110-2168
13	85.8	3.8	3766	3	US-08-961-527-225
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16	79.8	3.6	3820	3	US-09-221-017B-839
17	79.4	3.5	912	4	US-09-107-433-1041
18	77.8	3.5	474	4	US-09-621-976-557
19	76.8	3.4	409	4	US-09-513-999C-1625
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22	72	3.2	2852	3	US-09-344-441-2
23	69.4	3.1	1401	4	US-09-902-540-8465
24	69.4	3.1	7032	4	US-09-902-540-890
25	68.4	3.1	396	4	US-09-640-173-16
26	68.4	3.1	396	4	US-09-713-550-16
27	68.4	3.1	396	4	US-09-825-294-16

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Sequence 128, App	1925	3.0	67	4	US-09-148-545-128	Sequence 128, App
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Sequence 1, Appli	1781	3.0	66.4	4	US-09-818-512-1	Sequence 1, Appli
Sequence 66, Appl	1927	3.0	66.4	3	US-09-336-536-66	Sequence 66, Appl
Sequence 208, App	1378	3.0	66.2	3	US-09-149-476-208	Sequence 208, App
Sequence 24, Appl	2323	3.0	66.2	3	US-09-149-476-24	Sequence 24, Appl
Sequence 310, App	1181	2.9	66	3	US-09-149-476-310	Sequence 310, App
Sequence 186, App	1212	2.9	66	3	US-09-149-476-186	Sequence 186, App
Sequence 187, App	3116	2.9	66	4	US-09-311-021-187	Sequence 187, App
Sequence 1149, Ap	3145	2.9	65.8	4	US-09-949-016-1149	Sequence 1149, Ap
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Sequence 212, App	1985	2.9	64.2	4	US-09-906-618-212	Sequence 212, App
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Sequence 49, Appl	639	2.8	63.4	4	US-09-482-273-49	Sequence 49, Appl
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Sequence 26, Appl	700	2.8	63	3	US-09-152-060-26	Sequence 26, Appl
Sequence 14761, A	189	2.8	62.8	4	US-09-621-976-14761	Sequence 14761, A
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Sequence 7, Appli	1210	2.8	62.8	2	US-09-720-318A-3	Sequence 7, Appli
Sequence 33, Appl	1319	2.8	62.8	2	US-08-504-459-7	Sequence 33, Appl
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Sequence 801, App	194	2.8	62.4	4	US-09-621-976-801	Sequence 801, App

101	62.4	2.8	273	4	US-09-809-545A-31	Sequence 31, Appl	174	61.2	2.7	2407	3	US-09-921-259-7	Sequence 7, Appl
c 102	62.4	2.8	508	3	US-09-385-982-183	Sequence 183, App	175	61.2	2.7	2409	3	US-09-293-322C-8	Sequence 8, Appl
103	62.4	2.8	1248	4	US-09-489-847-101	Sequence 101, App	176	61.2	2.7	2409	4	US-09-839-437A-8	Sequence 8, Appl
104	62.4	2.8	1733	3	US-09-073-569-1	Sequence 1, Appl	177	61.2	2.7	2483	4	US-09-205-258-68	Sequence 68, Appl
105	62.4	2.8	1844	4	US-10-003-392-7	Sequence 7, Appl	178	61.2	2.7	2989	6	5378464-1	Patent No. 5378464
106	62.4	2.8	2082	2	US-08-785-310A-2	Sequence 2, Appl	179	61.2	2.7	2989	6	5378464-1	Patent No. 5378464
107	62.4	2.8	2447	2	US-09-014-969-14	Sequence 14, Appl	180	61.2	2.7	3366	4	US-09-595-141C-6	Sequence 6, Appl
108	62.4	2.8	259	4	US-09-621-976-16294	Sequence 16294, A	181	61.2	2.7	3366	4	US-09-595-526C-6	Sequence 6, Appl
c 109	62.2	2.8	396	4	US-09-640-173-53	Sequence 53, Appl	182	61.2	2.7	10442	4	US-09-595-526C-6	Sequence 6, Appl
c 110	62.2	2.8	396	4	US-09-713-550-53	Sequence 53, Appl	183	61.2	2.7	10442	4	US-09-595-526C-1	Sequence 1, Appl
c 111	62.2	2.8	396	4	US-09-825-294-53	Sequence 53, Appl	184	61.2	2.7	10474	4	US-09-596-141C-7	Sequence 7, Appl
c 112	62.2	2.8	396	4	US-09-970-966-53	Sequence 53, Appl	185	61.2	2.7	10474	4	US-09-595-141C-9	Sequence 9, Appl
113	62.2	2.8	441	4	US-09-601-537-10	Sequence 10, Appl	186	61.2	2.7	10474	4	US-09-595-526C-7	Sequence 7, Appl
114	62.2	2.8	997	4	US-09-907-794A-376	Sequence 376, App	187	61.2	2.7	10474	4	US-09-595-526C-9	Sequence 9, Appl
115	62.2	2.8	997	4	US-09-905-125A-376	Sequence 376, App	188	61	2.7	185	4	US-09-621-976-16779	Sequence 9, Appl
116	62.2	2.8	997	4	US-09-902-775A-376	Sequence 376, App	189	61	2.7	299	4	US-09-621-976-16226	Sequence 16226, A
117	62.2	2.8	997	4	US-09-906-700-376	Sequence 376, App	190	61	2.7	734	4	US-09-949-016-413	Sequence 413, App
118	62.2	2.8	997	4	US-09-903-603A-376	Sequence 376, App	191	61	2.7	1013	4	US-09-322-409-6	Sequence 6, Appl
119	62.2	2.8	997	4	US-09-904-920A-376	Sequence 376, App	192	61	2.7	1013	4	US-09-322-409-8	Sequence 8, Appl
120	62.2	2.8	997	4	US-09-909-064-376	Sequence 376, App	193	61	2.7	1013	4	US-09-451-527-6	Sequence 6, Appl
121	62.2	2.8	997	4	US-09-905-381A-376	Sequence 376, App	194	61	2.7	1013	4	US-09-451-527-8	Sequence 8, Appl
122	62.2	2.8	997	4	US-09-906-618-376	Sequence 376, App	195	61	2.7	1114	3	US-09-152-060-41	Sequence 41, Appl
123	62.2	2.8	1166	5	PCT-US96-12129B-1	Sequence 1, Appl	196	61	2.7	1271	4	US-09-905-558D-1	Sequence 1, Appl
124	62.2	2.8	1445	3	US-09-814-951A-1	Sequence 1, Appl	197	61	2.7	1459	4	US-09-537-654-3	Sequence 3, Appl
125	62.2	2.8	3080	3	US-09-099-041A-25	Sequence 25, Appl	198	61	2.7	1505	2	US-08-909-965C-13	Sequence 13, Appl
126	62.2	2.8	3080	3	US-09-245-281-25	Sequence 25, Appl	199	61	2.7	1579	4	US-09-403-463A-5	Sequence 5, Appl
127	62.2	2.8	3080	3	US-09-207-359B-25	Sequence 25, Appl	200	61	2.7	1651	4	US-09-800-729-41	Sequence 41, Appl
128	62.2	2.8	3080	3	US-09-340-620A-25	Sequence 25, Appl	201	61	2.7	1868	3	US-09-739-455-1	Sequence 1, Appl
129	62.2	2.8	3080	4	US-09-865-364-25	Sequence 25, Appl	202	61	2.7	2671	6	5168051-9	Patent No. 5168051
130	62.2	2.8	4121	4	US-09-601-537-9	Sequence 9, Appl	203	61	2.7	2671	6	5168051-9	Patent No. 5168051
131	62.2	2.8	4456	3	US-09-095-443-1	Sequence 1, Appl	204	60.8	2.7	91	4	US-09-621-976-14925	Sequence 14925, A
132	62	2.8	233	4	US-09-621-976-16559	Sequence 16559, A	205	60.8	2.7	612	4	US-09-270-767-11643	Sequence 11643, A
133	62	2.8	234	4	US-09-621-976-16557	Sequence 16557, A	206	60.8	2.7	1198	3	US-09-248-335-27	Sequence 27, Appl
134	62	2.8	235	4	US-09-621-976-16550	Sequence 16550, A	207	60.8	2.7	1582	3	US-08-545-136B-10	Sequence 10, Appl
135	62	2.8	1512	2	US-09-909-965C-8	Sequence 8, Appl	208	60.8	2.7	1582	3	US-08-545-136B-12	Sequence 12, Appl
136	62	2.8	1637	4	US-09-205-258-178	Sequence 178, App	209	60.8	2.7	1780	3	US-09-202-548B-5	Sequence 5, Appl
137	62	2.8	2045	3	US-09-152-060-22	Sequence 22, Appl	210	60.8	2.7	1780	4	US-09-942-858-5	Sequence 5, Appl
138	62	2.8	2285	2	US-08-967-101-136	Sequence 136, App	211	60.8	2.7	1780	4	US-10-461-180-5	Sequence 5, Appl
139	62	2.8	2285	3	US-08-592-541-136	Sequence 136, App	212	60.8	2.7	2634	3	US-09-463-238-3	Sequence 3, Appl
140	62	2.8	2285	3	US-09-124-698-136	Sequence 136, App	213	60.8	2.7	4086	4	US-09-702-705-1801	Sequence 1801, App
141	62	2.8	2285	3	US-09-127-480-136	Sequence 136, App	214	60.8	2.7	4086	4	US-09-736-457-1801	Sequence 1801, App
142	62	2.8	2285	3	US-09-124-523-136	Sequence 136, App	215	60.8	2.7	4086	4	US-09-671-325-1801	Sequence 1801, App
143	62	2.8	2285	4	US-09-636-796A-136	Sequence 136, App	216	60.6	2.7	1212	3	US-09-182-145-34	Sequence 34, Appl
c 144	61.8	2.8	396	4	US-09-640-173-10	Sequence 10, Appl	217	60.6	2.7	1212	3	US-09-182-145-35	Sequence 35, Appl
c 145	61.8	2.8	396	4	US-09-713-550-10	Sequence 10, Appl	218	60.6	2.7	1525	3	US-09-157-603-4	Sequence 4, Appl
c 146	61.8	2.8	396	4	US-09-825-294-10	Sequence 10, Appl	219	60.6	2.7	1525	3	US-09-587-436-4	Sequence 4, Appl
c 147	61.8	2.8	396	4	US-09-970-966-10	Sequence 10, Appl	220	60.6	2.7	1525	3	US-09-587-436-4	Sequence 4, Appl
c 148	61.8	2.8	467	2	US-08-841-349-18	Sequence 18, Appl	221	60.6	2.7	3334	4	US-08-927-165A-4	Sequence 2, Appl
c 149	61.8	2.8	467	2	US-09-431-184A-18	Sequence 18, Appl	222	60.4	2.7	3334	4	US-09-668-119-2	Sequence 2, Appl
150	61.6	2.7	231	4	US-09-621-976-16317	Sequence 16317, A	223	60.4	2.7	232	4	US-09-621-976-17701	Sequence 17701, A
151	61.6	2.7	231	4	US-09-621-976-16556	Sequence 16556, A	224	60.4	2.7	1037	4	US-09-489-847-112	Sequence 112, Appl
152	61.6	2.7	242	4	US-09-621-976-16320	Sequence 16320, A	225	60.4	2.7	1117	3	US-09-247-373B-33	Sequence 33, Appl
153	61.6	2.7	242	4	US-09-621-976-16324	Sequence 16324, A	226	60.4	2.7	1192	4	US-09-800-729-44	Sequence 44, Appl
154	61.6	2.7	331	4	US-09-621-976-16100	Sequence 16100, A	227	60.4	2.7	1192	4	US-09-439-554-23	Sequence 23, Appl
155	61.6	2.7	857	1	US-08-308-883-1	Sequence 1, Appl	228	60.4	2.7	1307	2	US-08-960-022-17	Sequence 17, Appl
156	61.6	2.7	857	1	US-08-730-163-1	Sequence 1, Appl	229	60.4	2.7	1454	3	US-09-372-422A-19	Sequence 19, Appl
157	61.6	2.7	857	3	US-08-256-799-1	Sequence 1, Appl	230	60.4	2.7	1522	3	US-09-413-574-1	Sequence 1, Appl
158	61.6	2.7	857	3	US-08-462-437-1	Sequence 1, Appl	231	60.4	2.7	2083	4	US-09-716-129-41	Sequence 41, Appl
159	61.6	2.7	990	4	US-09-800-729-79	Sequence 79, Appl	232	60.4	2.7	2442	4	US-09-575-081B-3	Sequence 3, Appl
160	61.6	2.7	1008	4	US-09-780-641-1	Sequence 1, Appl	233	60.4	2.7	3438	4	US-10-164-595-29	Sequence 29, Appl
161	61.6	2.7	1291	4	US-09-524-101D-5	Sequence 5, Appl	234	60.2	2.7	160	4	US-09-621-976-18071	Sequence 18071, A
162	61.6	2.7	1474	3	US-08-821-994-64	Sequence 64, Appl	235	60.2	2.7	162	4	US-09-621-976-18068	Sequence 18068, A
163	61.4	2.7	1492	4	US-09-369-247-23	Sequence 23, Appl	236	60.2	2.7	179	4	US-09-621-976-18054	Sequence 18054, A
164	61.4	2.7	1641	1	US-08-300-903A-8	Sequence 8, Appl	237	60.2	2.7	246	4	US-09-621-976-16288	Sequence 16288, A
165	61.4	2.7	1641	4	US-08-988-197-8	Sequence 8, Appl	238	60.2	2.7	250	4	US-09-621-976-18893	Sequence 18893, A
166	61.4	2.7	1641	4	US-10-385-072-8	Sequence 8, Appl	239	60.2	2.7	272	4	US-09-270-767-11902	Sequence 11902, A
167	61.4	2.7	1878	3	US-09-732-025-1	Sequence 1, Appl	240	60.2	2.7	1332	3	US-09-057-762-1	Sequence 1, Appl
168	61.4	2.7	3275	3	US-09-370-838-151	Sequence 151, App	241	60.2	2.7	1332	3	US-08-326-119A-1	Sequence 1, Appl
169	61.4	2.7	3275	4	US-09-854-133-151	Sequence 151, App	242	60.2	2.7	1692	4	US-09-821-803A-5	Sequence 5, Appl
170	61.4	2.7	5021	4	US-09-949-016-786	Sequence 786, App	243	60.2	2.7	1725	4	US-09-668-097A-21	Sequence 21, Appl
171	61.2	2.7	976	2	US-08-504-459-9	Sequence 9, Appl	244	60.2	2.7	1897	1	US-08-184-632-1	Sequence 1, Appl
172	61.2	2.7	1100	3	US-07-861-458C-4	Sequence 4, Appl	245	60.2	2.7	2378	3	US-08-803-870D-20	Sequence 20, Appl
173	61.2	2.7	2407	3	US-09-370-807-7	Sequence 7, Appl	246	60.2	2.7	2378	4	US-08-860-305D-1	Sequence 1, Appl

247	60.2	2.7	2438	4	US-09-393-634-4	Sequence 4, Appli	320	59.4	2.6	214	4	US-09-621-976-9843	Sequence 9843, Ap
248	60.2	2.7	3715	4	US-09-234-245-1	Sequence 1, Appli	c 321	59.4	2.6	342	4	US-09-270-767-13044	Sequence 13044, A
249	60.2	2.7	6409	4	US-09-967-908A-1	Sequence 1, Appli	322	59.4	2.6	427	4	US-09-461-325-107	Sequence 107, App
250	60.2	2.7	6409	4	US-10-159-151-1	Sequence 1, Appli	323	59.4	2.6	427	4	US-10-012-542-107	Sequence 107, App
251	60	2.7	146	4	US-09-621-976-8550	Sequence 8550, Ap	324	59.4	2.6	427	4	US-10-115-123-107	Sequence 107, App
252	60	2.7	147	4	US-09-621-976-8551	Sequence 8551, Ap	325	59.4	2.6	569	4	US-09-461-325-44	Sequence 44, Appl
253	60	2.7	157	4	US-09-621-976-10271	Sequence 10271, A	326	59.4	2.6	569	4	US-10-012-542-44	Sequence 44, Appl
254	60	2.7	390	4	US-09-621-976-15352	Sequence 15352, A	327	59.4	2.6	569	4	US-10-115-123-44	Sequence 44, Appl
255	60	2.7	763	3	US-09-743-207-3	Sequence 3, Appli	328	59.4	2.6	676	3	US-08-998-416-1142	Sequence 1142, Ap
256	60	2.7	960	3	US-09-248-335-57	Sequence 57, Appli	329	59.4	2.6	708	4	US-09-270-767-13081	Sequence 13081, A
257	60	2.7	1024	4	US-09-328-475C-50	Sequence 50, Appli	330	59.4	2.6	746	3	US-09-013-810-1	Sequence 1, Appli
258	60	2.7	1062	4	US-09-796-766-3	Sequence 3, Appli	331	59.4	2.6	949	4	US-09-489-847-35	Sequence 35, Appl
259	60	2.7	1277	4	US-09-461-325-20	Sequence 20, Appli	332	59.4	2.6	1486	4	US-09-461-325-73	Sequence 73, Appl
260	60	2.7	1277	4	US-10-012-542-20	Sequence 20, Appli	333	59.4	2.6	1486	4	US-10-012-542-73	Sequence 73, Appl
261	60	2.7	1277	4	US-10-115-123-20	Sequence 20, Appli	334	59.4	2.6	1486	4	US-10-115-123-73	Sequence 73, Appl
262	60	2.7	3350	2	US-08-663-566A-1	Sequence 1, Appli	335	59.4	2.6	1636	4	US-09-578-194-6	Sequence 6, Appli
263	60	2.7	3350	2	US-08-023-610-1	Sequence 1, Appli	336	59.4	2.6	1790	4	US-09-866-028-31	Sequence 31, Appl
264	60	2.7	3350	2	US-08-288-065A-1	Sequence 1, Appli	337	59.4	2.6	1790	4	US-09-866-028-31	Sequence 31, Appl
265	60	2.7	3350	2	US-08-362-240A-1	Sequence 1, Appli	338	59.4	2.6	1817	1	US-09-944-457-31	Sequence 31, Appl
266	60	2.7	3350	2	US-08-362-240A-1	Sequence 1, Appli	339	59.4	2.6	1817	1	US-08-473-981A-5	Sequence 5, Appli
267	59.8	2.7	109	4	PCT-US95-10245-1	Sequence 1, Appli	339	59.4	2.6	1817	2	US-08-473-981A-5	Sequence 5, Appli
268	59.8	2.7	194	4	US-09-621-976-14592	Sequence 14592, A	340	59.4	2.6	1864	3	US-09-149-476-130	Sequence 130, App
269	59.8	2.7	558	4	US-09-621-976-9596	Sequence 9596, Ap	341	59.4	2.6	8100	4	US-09-554-337-4	Sequence 4, Appli
270	59.8	2.7	593	3	US-09-043-861-3	Sequence 3, Appli	342	59.4	2.6	11517	1	US-07-920-281C-1	Sequence 1, Appli
271	59.8	2.7	593	3	US-09-385-982-262	Sequence 3, Appli	343	59.4	2.6	11517	3	US-08-466-277-1	Sequence 1, Appli
272	59.8	2.7	688	6	5498694-3	Sequence 82, App	344	59.4	2.6	11517	3	US-08-466-277-1	Sequence 1, Appli
273	59.8	2.7	748	1	US-08-361-467B-3	Patent No. 5498694	345	59.4	2.6	15538	4	US-09-554-337-1	Sequence 1, Appli
274	59.8	2.7	748	1	US-08-484-332C-3	Sequence 3, Appli	346	59.4	2.6	365	4	US-09-621-976-14699	Sequence 14699, A
275	59.8	2.7	903	5	PCT-US95-06406A-21	Sequence 3, Appli	347	59.2	2.6	339	1	US-07-885-970A-13	Sequence 13, Appl
276	59.8	2.7	1057	4	US-09-716-129-16	Sequence 21, Appli	348	59.2	2.6	339	1	US-08-298-687A-13	Sequence 13, Appl
277	59.8	2.7	1308	4	US-09-151-832-1	Sequence 16, Appli	c 349	59.2	2.6	339	1	US-08-530-797-12	Sequence 12, Appl
278	59.8	2.7	1414	4	US-09-501-115-5	Sequence 1, Appli	350	59.2	2.6	339	1	US-08-298-829-13	Sequence 13, Appl
279	59.8	2.7	1872	3	US-09-231-922-27	Sequence 5, Appli	c 351	59.2	2.6	339	2	US-08-787-335-12	Sequence 12, Appl
280	59.8	2.7	1938	3	US-09-232-200-68	Sequence 27, Appli	352	59.2	2.6	756	4	US-09-614-912-93	Sequence 93, Appl
281	59.8	2.7	1998	3	US-09-232-197-68	Sequence 68, Appli	353	59.2	2.6	1461	3	US-08-722-126A-4	Sequence 4, Appli
282	59.8	2.7	1998	3	US-09-232-197-68	Sequence 68, Appli	354	59.2	2.6	1461	5	PCT-US95-04258-4	Sequence 4, Appli
283	59.8	2.7	1998	3	US-09-232-195-68	Sequence 68, Appli	355	59.2	2.6	1662	4	US-09-668-097A-13	Sequence 13, Appl
284	59.8	2.7	2087	3	US-09-232-191-6	Sequence 68, Appli	356	59.2	2.6	1882	3	US-09-370-253-1	Sequence 1, Appli
285	59.8	2.7	2087	3	US-09-232-191-6	Sequence 6, Appli	357	59	2.6	147	4	US-09-621-976-10254	Sequence 10254, A
286	59.8	2.7	2087	3	US-09-232-197-6	Sequence 6, Appli	358	59	2.6	231	4	US-09-621-976-16456	Sequence 16456, A
287	59.8	2.7	2087	3	US-09-232-197-6	Sequence 6, Appli	359	59	2.6	231	4	US-09-621-976-10211	Sequence 10211, A
288	59.8	2.7	2087	4	US-09-232-195-6	Sequence 6, Appli	360	59	2.6	232	4	US-09-621-976-16050	Sequence 16050, A
289	59.8	2.7	2096	3	US-09-008-481A-10	Sequence 6, Appli	361	59	2.6	332	4	US-09-621-976-16053	Sequence 16053, A
290	59.8	2.7	2096	3	US-09-195-666A-16	Sequence 10, Appli	362	59	2.6	332	4	US-09-621-976-16032	Sequence 16032, A
291	59.8	2.7	2096	3	US-09-309-592-10	Sequence 10, Appli	363	59	2.6	333	4	US-09-621-976-16032	Sequence 16032, A
292	59.8	2.7	2096	3	US-09-635-705-16	Sequence 16, Appli	364	59	2.6	334	4	US-09-621-976-16044	Sequence 16044, A
293	59.8	2.7	2096	3	US-09-634-858A-16	Sequence 16, Appli	365	59	2.6	335	4	US-09-621-976-16061	Sequence 16061, A
294	59.8	2.7	2096	4	US-08-869-927C-16	Sequence 16, Appli	366	59	2.6	336	4	US-09-621-976-16013	Sequence 16013, A
295	59.8	2.7	2205	3	US-08-888-077A-41	Sequence 16, Appli	367	59	2.6	338	4	US-09-621-976-16041	Sequence 16041, A
296	59.8	2.7	2628	1	US-08-143-219-1	Sequence 41, Appli	368	59	2.6	347	4	US-09-621-976-16026	Sequence 16026, A
297	59.8	2.7	2674	3	US-08-143-219-1	Sequence 1, Appli	369	59	2.6	357	4	US-09-621-976-16058	Sequence 16058, A
298	59.8	2.7	2674	3	US-10-003-295-1	Sequence 1, Appli	370	59	2.6	359	4	US-09-621-976-16008	Sequence 16008, A
299	59.8	2.7	2674	3	US-09-553-839-9	Sequence 1, Appli	371	59	2.6	359	4	US-09-621-976-16019	Sequence 16019, A
300	59.8	2.7	2806	4	US-10-202-619-9	Sequence 9, Appli	372	59	2.6	362	4	US-09-621-976-16010	Sequence 16010, A
301	59.8	2.7	5173	1	US-08-242-677-1	Sequence 9, Appli	373	59	2.6	365	4	US-09-621-976-16042	Sequence 16042, A
302	59.6	2.7	215	4	US-09-621-976-15321	Sequence 15321, A	374	59	2.6	732	3	US-09-149-476-66	Sequence 66, Appl
303	59.6	2.7	1023	1	US-08-252-966B-16	Sequence 16, Appli	375	59	2.6	1129	3	US-09-227-357-40	Sequence 40, Appl
304	59.6	2.7	1046	1	US-08-361-467B-4	Sequence 4, Appli	376	59	2.6	1141	4	US-09-800-729-78	Sequence 78, Appl
305	59.6	2.7	1046	1	US-08-484-332C-4	Sequence 4, Appli	377	59	2.6	1190	4	US-09-390-207-1	Sequence 1, Appli
306	59.6	2.7	1406	4	US-10-000-489-81	Sequence 81, Appli	378	59	2.6	1297	4	US-09-800-729-80	Sequence 80, Appl
307	59.6	2.7	1509	3	US-09-149-476-179	Sequence 179, App	379	59	2.6	1359	3	US-09-387-574-11	Sequence 11, Appl
308	59.6	2.7	1606	4	US-09-820-004-1	Sequence 1, Appli	380	59	2.6	1359	3	US-09-668-096-11	Sequence 11, Appl
309	59.6	2.7	1827	4	US-09-720-318A-9	Sequence 9, Appli	381	59	2.6	1804	2	US-08-504-459-5	Sequence 5, Appli
310	59.6	2.7	1842	4	US-09-482-273-90	Sequence 90, Appli	382	59	2.6	1858	2	US-08-909-9650-11	Sequence 11, Appl
311	59.6	2.7	2026	2	US-08-993-228-3	Sequence 3, Appli	383	59	2.6	1872	3	US-09-801-052-1	Sequence 1, Appli
312	59.6	2.7	2038	4	US-09-885-723-6	Sequence 6, Appli	384	59	2.6	1872	4	US-10-020-121-1	Sequence 1, Appli
313	59.6	2.7	2218	4	US-09-205-258-103	Sequence 103, App	385	59	2.6	4860	4	US-09-949-016-296	Sequence 296, App
314	59.6	2.7	4239	4	US-09-815-048-1	Sequence 1, Appli	386	58.8	2.6	156	4	US-09-621-976-9095	Sequence 9095, Ap
315	59.4	2.6	100	4	US-09-621-976-12774	Sequence 12774, A	387	58.8	2.6	160	4	US-09-621-976-10335	Sequence 10335, A
316	59.4	2.6	150	4	US-09-621-976-8656	Sequence 8656, Ap	388	58.8	2.6	163	4	US-09-621-976-9608	Sequence 9608, Ap
317	59.4	2.6	160	4	US-09-621-976-18066	Sequence 18066, A	389	58.8	2.6	183	4	US-09-621-976-13606	Sequence 13606, A
318	59.4	2.6	165	4	US-09-621-976-8127	Sequence 8127, Ap	390	58.8	2.6	204	4	US-09-621-976-1323	Sequence 1323, Ap
319	59.4	2.6	196	4	US-09-644-460-40	Sequence 40, Appli	c 391	58.8	2.6	227	3	US-08-520-678A-28	Sequence 28, Appl
319	59.4	2.6	196	4	US-09-644-460-40	Sequence 40, Appli	c 392	58.8	2.6	227	3	US-08-897-126-28	Sequence 28, Appl

393	58.8	2.6	240	4	US-09-621-976-1324	Sequence 1324, Ap	466	58.6	2.6	991	3	US-09-247-373B-25	Sequence 25, Appl
394	58.8	2.6	249	4	US-09-621-976-1322	Sequence 1322, Ap	467	58.6	2.6	991	3	US-09-296-715-25	Sequence 25, Appl
395	58.8	2.6	263	3	US-09-091-097-26	Sequence 26, Appl	468	58.6	2.6	1411	3	US-08-964-127-5	Sequence 5, Appl
396	58.8	2.6	630	1	US-08-185-414E-1	Sequence 1, Appl	469	58.6	2.6	1411	3	US-09-436-692-5	Sequence 5, Appl
397	58.8	2.6	1069	3	US-09-373-432A-7	Sequence 7, Appl	470	58.6	2.6	1411	4	US-10-000-273-5	Sequence 5, Appl
398	58.8	2.6	1878	3	US-09-465-558-39	Sequence 39, Appl	471	58.6	2.6	1540	4	US-09-560-761B-3	Sequence 3, Appl
399	58.8	2.6	2822	4	US-09-907-794A-48	Sequence 48, Appl	472	58.6	2.6	1558	1	US-08-467-607-2	Sequence 2, Appl
400	58.8	2.6	2822	4	US-09-903-135A-48	Sequence 48, Appl	473	58.6	2.6	1558	2	US-08-469-362-2	Sequence 2, Appl
401	58.8	2.6	2822	4	US-09-902-775A-48	Sequence 48, Appl	474	58.6	2.6	1558	2	US-08-850-392-2	Sequence 2, Appl
402	58.8	2.6	2822	4	US-09-906-700-48	Sequence 48, Appl	475	58.6	2.6	1963	4	US-09-482-273-91	Sequence 91, Appl
403	58.8	2.6	2822	4	US-09-903-603A-48	Sequence 48, Appl	476	58.6	2.6	1965	4	US-09-482-273-27	Sequence 27, Appl
404	58.8	2.6	2822	4	US-09-904-920A-48	Sequence 48, Appl	477	58.6	2.6	2329	4	US-09-800-729-11	Sequence 11, Appl
405	58.8	2.6	2822	4	US-09-909-064A-48	Sequence 48, Appl	478	58.6	2.6	2445	6	5215909-9	Patent No. 5215909
406	58.8	2.6	2822	4	US-09-903-681A-48	Sequence 48, Appl	479	58.6	2.6	2445	6	5215909-9	Patent No. 5215909
407	58.8	2.6	2822	4	US-09-906-618-48	Sequence 48, Appl	480	58.6	2.6	2589	3	US-08-569-749-1	Sequence 1, Appl
408	58.8	2.6	3410	3	US-09-020-956-110	Sequence 110, App	481	58.6	2.6	2589	3	US-08-689-366-1	Sequence 1, Appl
409	58.8	2.6	3410	3	US-09-030-607-110	Sequence 110, App	482	58.6	2.6	2589	5	PCT-US96-12860-1	Sequence 1, Appl
410	58.8	2.6	3410	3	US-09-439-313-110	Sequence 110, App	483	58.6	2.6	2589	5	US-09-031-563-1	Sequence 1, Appl
411	58.8	2.6	3410	3	US-09-352-616A-110	Sequence 110, App	484	58.6	2.6	4880	3	US-09-392-277-1	Sequence 1, Appl
412	58.8	2.6	3410	3	US-09-602-877A-110	Sequence 110, App	485	58.6	2.6	4880	3	US-09-258-000-1	Sequence 1, Appl
413	58.8	2.6	3410	3	US-09-232-149A-110	Sequence 110, App	486	58.6	2.6	5125	3	US-09-031-563-4	Sequence 4, Appl
414	58.8	2.6	3410	4	US-09-159-812-110	Sequence 110, App	487	58.6	2.6	5125	3	US-09-392-277-4	Sequence 4, Appl
415	58.8	2.6	3410	4	US-09-636-215-110	Sequence 110, App	488	58.6	2.6	5125	3	US-09-258-000-4	Sequence 4, Appl
416	58.8	2.6	3410	4	US-09-685-166A-110	Sequence 110, App	489	58.6	2.6	6671	1	US-08-457-459-1	Sequence 1, Appl
417	58.8	2.6	3410	4	US-09-115-453-110	Sequence 110, App	490	58.6	2.6	6671	1	US-08-457-459-1	Sequence 1, Appl
418	58.8	2.6	3410	4	US-09-688-489-110	Sequence 110, App	491	58.6	2.6	6671	1	US-08-555-678-1	Sequence 1, Appl
419	58.8	2.6	3410	4	US-09-679-426-110	Sequence 110, App	492	58.6	2.6	6671	1	PCT-US95-02275-1	Sequence 1, Appl
420	58.8	2.6	3410	4	US-09-759-143-110	Sequence 110, App	493	58.4	2.6	75	4	US-09-621-976-12516	Sequence 25, Appl
421	58.8	2.6	3410	4	US-09-651-236-110	Sequence 110, App	494	58.4	2.6	80	3	US-07-920-281C-25	Sequence 25, Appl
422	58.6	2.6	300	4	US-09-621-976-16227	Sequence 16227, A	495	58.4	2.6	80	3	US-08-466-277-25	Sequence 25, Appl
423	58.6	2.6	443	4	US-09-936-885A-1	Sequence 1, Appl	496	58.4	2.6	80	4	US-09-688-842-25	Sequence 25, Appl
424	58.6	2.6	470	3	US-09-020-956-102	Sequence 102, App	497	58.4	2.6	127	4	US-09-621-976-13933	Sequence 13933, A
425	58.6	2.6	470	3	US-09-030-607-102	Sequence 102, App	498	58.4	2.6	159	4	US-09-621-976-17448	Sequence 17448, A
426	58.6	2.6	470	3	US-09-439-313-102	Sequence 102, App	499	58.4	2.6	176	4	US-09-621-976-13903	Sequence 13903, A
427	58.6	2.6	470	3	US-09-352-616A-102	Sequence 102, App	500	58.4	2.6	253	4	US-09-621-976-12799	Sequence 12799, A
428	58.6	2.6	470	3	US-09-232-149A-102	Sequence 102, App	501	58.4	2.6	587	4	US-09-205-258-64	Sequence 64, Appl
429	58.6	2.6	470	4	US-09-159-812-102	Sequence 102, App	502	58.4	2.6	687	4	US-09-774-639-106	Sequence 106, App
430	58.6	2.6	470	4	US-09-636-215-102	Sequence 102, App	503	58.4	2.6	759	4	US-09-465-559-5	Sequence 5, Appl
431	58.6	2.6	470	4	US-09-685-166A-102	Sequence 102, App	504	58.4	2.6	882	4	US-09-311-021-107	Sequence 107, App
432	58.6	2.6	470	4	US-09-115-453-102	Sequence 102, App	505	58.4	2.6	890	4	US-09-621-976-2725	Sequence 2725, Ap
433	58.6	2.6	470	4	US-09-688-489-102	Sequence 102, App	506	58.4	2.6	1052	4	US-09-489-847-23	Sequence 23, Appl
434	58.6	2.6	470	4	US-09-679-426-102	Sequence 102, App	507	58.4	2.6	1139	4	US-09-690-454-13	Sequence 13, Appl
435	58.6	2.6	470	4	US-09-759-143-102	Sequence 102, App	508	58.4	2.6	1405	4	US-09-244-111-9	Sequence 9, Appl
436	58.6	2.6	470	4	US-09-651-236-102	Sequence 102, App	509	58.4	2.6	1493	1	US-08-340-820-24	Sequence 24, Appl
437	58.6	2.6	509	3	US-09-030-607-202	Sequence 202, App	510	58.4	2.6	1493	1	US-08-593-535-24	Sequence 24, Appl
438	58.6	2.6	509	3	US-09-439-313-202	Sequence 202, App	511	58.4	2.6	1746	4	US-09-485-529-57	Sequence 57, Appl
439	58.6	2.6	509	3	US-09-352-616A-202	Sequence 202, App	512	58.4	2.6	1768	4	US-09-485-529-13	Sequence 13, Appl
440	58.6	2.6	509	3	US-09-232-149A-202	Sequence 202, App	513	58.4	2.6	2186	3	US-09-360-545-66	Sequence 66, Appl
441	58.6	2.6	509	4	US-09-159-812-202	Sequence 202, App	514	58.4	2.6	3047	4	US-09-873-737A-1	Sequence 1, Appl
442	58.6	2.6	509	4	US-09-636-215-202	Sequence 202, App	515	58.4	2.6	4064	4	US-09-873-737A-3	Sequence 3, Appl
443	58.6	2.6	509	4	US-09-685-166A-202	Sequence 202, App	516	58.4	2.6	5554	4	US-09-815-923-1	Sequence 1, Appl
444	58.6	2.6	509	4	US-09-115-453-202	Sequence 202, App	517	58.2	2.6	141	4	US-09-621-976-17446	Sequence 17446, A
445	58.6	2.6	509	4	US-09-688-489-202	Sequence 202, App	518	58.2	2.6	147	4	US-09-621-976-10383	Sequence 10383, A
446	58.6	2.6	509	4	US-09-679-426-202	Sequence 202, App	519	58.2	2.6	148	4	US-09-621-976-17447	Sequence 17447, A
447	58.6	2.6	509	4	US-09-759-143-202	Sequence 202, App	520	58.2	2.6	148	4	US-09-621-976-17450	Sequence 17450, A
448	58.6	2.6	509	4	US-09-651-236-202	Sequence 202, App	521	58.2	2.6	153	4	US-09-621-976-17451	Sequence 17451, A
449	58.6	2.6	711	4	US-09-621-976-17854	Sequence 17854, A	522	58.2	2.6	182	4	US-09-621-976-16234	Sequence 16234, A
450	58.6	2.6	730	4	US-09-270-767-14600	Sequence 14600, A	523	58.2	2.6	276	4	US-09-621-976-16611	Sequence 16611, A
451	58.6	2.6	760	4	US-09-205-258-232	Sequence 232, App	524	58.2	2.6	371	4	US-09-621-976-16048	Sequence 16048, A
452	58.6	2.6	931	4	US-08-482-273-31	Sequence 31, Appl	525	58.2	2.6	570	1	US-07-883-970A-10	Sequence 10, Appl
453	58.6	2.6	958	2	US-08-757-046A-5	Sequence 5, Appl	526	58.2	2.6	570	1	US-08-298-687A-10	Sequence 10, Appl
454	58.6	2.6	958	3	US-09-447-208-5	Sequence 5, Appl	527	58.2	2.6	609	1	US-08-298-829-10	Sequence 10, Appl
455	58.6	2.6	958	3	US-09-135-988-5	Sequence 5, Appl	528	58.2	2.6	609	2	US-08-530-797-9	Sequence 9, Appl
456	58.6	2.6	958	3	US-09-277-716-5	Sequence 5, Appl	529	58.2	2.6	609	2	US-08-787-335-9	Sequence 9, Appl
457	58.6	2.6	958	3	US-08-597-274A-5	Sequence 5, Appl	530	58.2	2.6	972	3	US-09-549-831-5	Sequence 5, Appl
458	58.6	2.6	958	3	US-08-908-909-5	Sequence 5, Appl	531	58.2	2.6	985	4	US-09-322-409-25	Sequence 25, Appl
459	58.6	2.6	958	3	US-09-609-161B-5	Sequence 5, Appl	532	58.2	2.6	985	4	US-09-322-409-27	Sequence 27, Appl
460	58.6	2.6	958	3	US-08-990-103-5	Sequence 5, Appl	533	58.2	2.6	985	4	US-09-451-527-25	Sequence 25, Appl
461	58.6	2.6	958	4	US-09-746-485A-5	Sequence 5, Appl	534	58.2	2.6	1214	4	US-09-451-527-27	Sequence 27, Appl
462	58.6	2.6	958	4	US-10-126-139-5	Sequence 5, Appl	535	58.2	2.6	1454	4	US-09-780-717-28	Sequence 28, Appl
463	58.6	2.6	958	4	US-10-126-798-5	Sequence 5, Appl	536	58.2	2.6	1454	4	US-09-614-912-63	Sequence 63, Appl
464	58.6	2.6	958	4	US-10-126-777-5	Sequence 5, Appl	537	58.2	2.6	1485	3	US-09-372-422A-39	Sequence 39, Appl
465	58.6	2.6	991	3	US-08-924-747-25	Sequence 25, Appl	538	58.2	2.6	1534	1	US-08-300-903A-6	Sequence 6, Appl

539	58.2	2.6	1534	4	US-08-988-197-6	Sequence 6, Appli	612	57.8	2.6	339	4	US-09-621-976-16015	Sequence 16015, A
540	58.2	2.6	1534	4	US-10-385-072-6	Sequence 6, Appli	613	57.8	2.6	491	3	US-09-311-021-191	Sequence 191, App
541	58.2	2.6	1578	3	US-09-416-050A-1	Sequence 1, Appli	614	57.8	2.6	1027	3	US-09-465-558-57	Sequence 57, Appl
542	58.2	2.6	1578	3	US-09-664-800-1	Sequence 1, Appli	615	57.8	2.6	1032	3	US-09-357-179-21	Sequence 21, Appl
543	58.2	2.6	1578	3	US-09-665-309-1	Sequence 1, Appli	616	57.8	2.6	1032	3	US-09-735-846-1	Sequence 1, Appli
544	58.2	2.6	1578	3	US-09-661-569-1	Sequence 1, Appli	617	57.8	2.6	1508	3	US-09-071-224-3	Sequence 3, Appli
545	58.2	2.6	1602	1	US-08-530-950-3	Sequence 3, Appli	618	57.8	2.6	1813	3	US-09-039-046-1	Sequence 8, Appli
546	58.2	2.6	1602	3	US-08-888-429A-3	Sequence 3, Appli	619	57.8	2.6	2301	3	US-09-232-191-8	Sequence 8, Appli
547	58.2	2.6	1602	3	US-09-149-879-3	Sequence 3, Appli	620	57.8	2.6	2301	3	US-09-232-200-8	Sequence 8, Appli
548	58.2	2.6	1602	4	US-09-057-009-3	Sequence 3, Appli	621	57.8	2.6	2301	3	US-09-232-197-8	Sequence 8, Appli
549	58.2	2.6	1602	4	US-09-593-653-3	Sequence 3, Appli	622	57.8	2.6	2301	3	US-09-232-201-8	Sequence 8, Appli
550	58.2	2.6	1736	3	US-09-182-816-22	Sequence 22, Appl	623	57.8	2.6	2301	3	US-09-232-195-8	Sequence 8, Appli
551	58.2	2.6	1736	3	US-09-182-816-24	Sequence 24, Appl	624	57.8	2.6	2381	1	US-08-021-608D-9	Sequence 9, Appli
552	58.2	2.6	1736	3	US-09-471-528-22	Sequence 22, Appl	625	57.8	2.6	2381	1	US-08-726-160-9	Sequence 9, Appli
553	58.2	2.6	1736	3	US-09-471-528-24	Sequence 24, Appl	626	57.8	2.6	2381	5	PCT-US94-01783-9	Sequence 9, Appli
554	58.2	2.6	1736	3	US-09-634-530-22	Sequence 22, Appl	627	57.8	2.6	2384	1	US-08-021-608D-1	Sequence 1, Appli
555	58.2	2.6	1736	3	US-09-634-530-24	Sequence 24, Appl	628	57.8	2.6	2384	1	US-08-726-160-1	Sequence 1, Appli
556	58.2	2.6	1882	4	US-09-419-679-3	Sequence 3, Appli	629	57.8	2.6	2384	5	PCT-US94-01783-1	Sequence 1, Appli
557	58.2	2.6	2203	4	US-09-801-861-1	Sequence 1, Appli	630	57.8	2.6	2625	4	US-09-270-767-10080	Sequence 10080, A
558	58.2	2.6	2203	4	US-10-224-562-1	Sequence 1, Appli	631	57.8	2.6	2625	4	US-09-232-200-44	Sequence 44, Appl
559	58.2	2.6	2431	1	US-07-847-743B-25	Sequence 25, Appl	632	57.8	2.6	2710	3	US-09-232-200-70	Sequence 70, Appl
560	58.2	2.6	2431	1	US-08-456-201-25	Sequence 25, Appl	633	57.8	2.6	2710	3	US-09-232-197-44	Sequence 44, Appl
561	58.2	2.6	2431	2	US-08-456-241-25	Sequence 25, Appl	634	57.8	2.6	2710	3	US-09-232-197-70	Sequence 70, Appl
562	58.2	2.6	2431	5	PCT-US92-04295A-25	Sequence 25, Appl	635	57.8	2.6	2710	3	US-09-232-201-44	Sequence 44, Appl
563	58.2	2.6	2718	4	US-09-667-135-1	Sequence 1, Appli	636	57.8	2.6	2710	3	US-09-232-201-70	Sequence 70, Appl
564	58.2	2.6	3238	3	US-08-123-934A-5	Sequence 5, Appli	637	57.8	2.6	2710	4	US-09-232-195-44	Sequence 44, Appl
565	58.2	2.6	3238	4	US-09-874-628-5	Sequence 5, Appli	638	57.8	2.6	2710	4	US-09-232-195-70	Sequence 70, Appl
566	58.2	2.6	3238	5	PCT-US94-10080-5	Sequence 5, Appli	639	57.8	2.6	2908	4	US-09-304-615-35	Sequence 35, Appl
567	58.2	2.6	3994	4	US-09-738-346-7	Sequence 7, Appli	640	57.6	2.6	137	4	US-09-621-976-18434	Sequence 18434, A
568	58	2.6	146	4	US-09-621-976-16115	Sequence 7, Appli	641	57.6	2.6	138	4	US-09-621-976-9595	Sequence 9595, Ap
569	58	2.6	351	4	US-09-621-976-15134	Sequence 15134, A	642	57.6	2.6	208	3	US-08-686-878A-37	Sequence 37, Appl
570	58	2.6	371	4	US-09-621-976-19223	Sequence 19223, A	643	57.6	2.6	208	3	US-09-175-928-37	Sequence 37, Appl
571	58	2.6	593	4	US-09-904-615-59	Sequence 59, Appl	644	57.6	2.6	266	4	US-09-621-976-16813	Sequence 16813, A
572	58	2.6	635	1	US-08-455-633A-35	Sequence 35, Appl	645	57.6	2.6	272	4	US-09-621-976-16932	Sequence 16932, A
573	58	2.6	635	1	US-08-416-336-5	Sequence 5, Appli	646	57.6	2.6	283	4	US-09-621-976-16989	Sequence 16989, A
574	58	2.6	635	5	US-08-456-460C-35	Sequence 35, Appl	647	57.6	2.6	316	4	US-09-513-999C-838	Sequence 838, App
575	58	2.6	635	5	PCT-US94-0535A-35	Sequence 35, Appl	648	57.6	2.6	550	4	US-09-010-147B-5	Sequence 5, Appli
576	58	2.6	664	4	US-09-904-615-66	Sequence 66, Appl	649	57.6	2.6	812	3	US-09-091-097-7	Sequence 7, Appli
577	58	2.6	1020	4	US-09-328-475C-43	Sequence 43, Appl	650	57.6	2.6	1075	3	US-08-400-006B-6	Sequence 6, Appli
578	58	2.6	1039	4	US-09-464-535-23	Sequence 23, Appl	651	57.6	2.6	1193	3	US-09-372-422A-23	Sequence 23, Appl
579	58	2.6	1069	3	US-09-205-258-74	Sequence 74, Appl	652	57.6	2.6	1201	4	US-09-461-325-36	Sequence 36, Appl
580	58	2.6	1206	3	US-09-465-558-53	Sequence 53, Appl	653	57.6	2.6	1201	4	US-10-012-542-36	Sequence 36, Appl
581	58	2.6	1325	1	US-08-306-691B-51	Sequence 51, Appl	654	57.6	2.6	1201	4	US-10-115-123-36	Sequence 36, Appl
582	58	2.6	1325	2	US-08-464-517-1	Sequence 1, Appli	655	57.6	2.6	1210	4	US-09-244-805-45	Sequence 45, Appl
583	58	2.6	1325	2	US-08-246-361A-1	Sequence 1, Appli	656	57.6	2.6	1230	4	US-09-244-805-6	Sequence 6, Appli
584	58	2.6	1325	3	US-08-463-722-1	Sequence 1, Appli	657	57.6	2.6	2184	3	US-08-355-918C-1	Sequence 1, Appli
585	58	2.6	1325	5	PCT-US93-05000-1	Sequence 1, Appli	658	57.6	2.6	2184	3	US-08-697-766A-1	Sequence 1, Appli
586	58	2.6	1412	4	US-09-614-912-197	Sequence 197, App	659	57.6	2.6	2311	4	US-09-720-317A-19	Sequence 19, Appl
587	58	2.6	1604	1	US-08-665-966-9	Sequence 9, Appli	660	57.6	2.6	2369	4	US-09-057-996-13	Sequence 13, Appl
588	58	2.6	1604	3	US-09-041-780-9	Sequence 9, Appli	661	57.6	2.6	3214	1	US-08-484-105-17	Sequence 17, Appl
589	58	2.6	1738	2	US-08-379-482A-2	Sequence 2, Appli	662	57.6	2.6	3214	1	US-08-484-106-17	Sequence 17, Appl
590	58	2.6	1738	4	US-09-918-909A-27	Sequence 27, Appl	663	57.6	2.6	4055	4	US-09-620-312D-706	Sequence 706, App
591	58	2.6	1740	4	US-09-709-103-45	Sequence 45, Appl	664	57.6	2.6	5503	2	US-08-726-012B-1	Sequence 1, Appli
592	58	2.6	1740	4	US-09-439-410A-45	Sequence 45, Appl	665	57.6	2.6	5503	4	US-09-023-655-989	Sequence 989, App
593	58	2.6	1798	3	US-09-797-906-1	Sequence 1, Appli	666	57.6	2.6	7859	2	US-07-854-596B-4	Sequence 4, Appli
594	58	2.6	1801	4	US-09-709-103-3	Sequence 3, Appli	667	57.6	2.6	7859	2	US-08-450-905B-15	Sequence 15, Appl
595	58	2.6	1801	4	US-09-439-410A-3	Sequence 3, Appli	668	57.6	2.6	7859	3	US-07-982-759P-15	Sequence 15, Appl
596	58	2.6	3124	3	US-09-734-030-1	Sequence 1, Appli	669	57.6	2.6	670889	4	US-09-949-016-12505	Sequence 12505, A
597	58	2.6	3124	4	US-10-153-921-1	Sequence 1, Appli	670	57.6	2.6	670890	4	US-09-949-016-14207	Sequence 14207, A
598	58	2.6	3124	4	US-10-669-689-1	Sequence 1, Appli	671	57.4	2.6	92	4	US-09-621-976-13620	Sequence 13620, A
599	58	2.6	3200	1	US-08-444-405-1	Sequence 1, Appli	672	57.4	2.6	102	4	US-09-621-976-11436	Sequence 11436, A
600	58	2.6	3200	1	US-08-384-850-1	Sequence 1, Appli	673	57.4	2.6	144	1	US-08-702-344-26	Sequence 26, Appl
601	58	2.6	3207	1	US-07-946-497-1	Sequence 1, Appli	674	57.4	2.6	144	4	US-09-621-976-17452	Sequence 17452, A
602	58	2.6	3207	1	US-08-483-322-1	Sequence 1, Appli	675	57.4	2.6	193	4	US-09-621-976-10543	Sequence 10543, A
603	58	2.6	3207	2	US-08-478-882-1	Sequence 1, Appli	676	57.4	2.6	304	4	US-09-621-976-16099	Sequence 16099, A
604	58	2.6	41736	2	US-09-949-016-17091	Sequence 17091, A	677	57.4	2.6	329	4	US-09-621-976-16012	Sequence 16012, A
605	57.8	2.6	140	4	US-09-621-976-17449	Sequence 17449, A	678	57.4	2.6	336	4	US-09-621-976-16051	Sequence 16051, A
606	57.8	2.6	195	4	US-09-621-976-18062	Sequence 18062, A	679	57.4	2.6	336	4	US-09-640-173-42	Sequence 42, Appl
607	57.8	2.6	213	3	US-08-481-190-15	Sequence 15, Appl	680	57.4	2.6	396	4	US-09-713-550-42	Sequence 42, Appl
608	57.8	2.6	222	3	PCT-US93-00869-15	Sequence 15, Appl	681	57.4	2.6	396	4	US-09-825-294-42	Sequence 42, Appl
609	57.8	2.6	222	5	US-09-621-976-13617	Sequence 13617, A	682	57.4	2.6	396	4	US-09-970-966-42	Sequence 42, Appl
610	57.8	2.6	246	4	US-09-621-976-16031	Sequence 16031, A	683	57.4	2.6	536	1	US-08-341-568-1	Sequence 1, Appli
611	57.8	2.6	332	4	US-09-621-976-16031	Sequence 16031, A	684	57.4	2.6	536	2	US-08-911-020-1	Sequence 1, Appli

685	57.4	2.6	742	1	US-07-847-010-12	Sequence 12, Appl	758	57	2.5	1696	4	US-09-835-811-1	Sequence 1, Appl
686	57.4	2.6	1034	4	US-09-311-021-105	Sequence 105, App	759	57	2.5	2158	1	US-07-602-608-1	Sequence 1, Appl
687	57.4	2.6	1273	4	US-09-270-767-14731	Sequence 14731, A	760	57	2.5	2158	1	US-08-261-578-1	Sequence 1, Appl
688	57.4	2.6	1708	4	US-09-859-053-31	Sequence 31, Appl	761	57	2.5	2187	3	US-09-127-219B-2	Sequence 2, Appl
689	57.4	2.6	2269	3	US-09-394-645-1	Sequence 1, Appl	762	57	2.5	2218	4	US-09-016-434-1157	Sequence 7, Appl
690	57.4	2.6	2269	3	US-09-243-560B-1	Sequence 1, Appl	763	57	2.5	2218	4	US-10-329-668-7	Sequence 7, Appl
691	57.4	2.6	2271	4	US-09-205-258-243	Sequence 243, App	764	57	2.5	2233	1	US-08-496-631-1	Sequence 1, Appl
692	57.4	2.6	2276	4	US-09-205-258-243	Sequence 183, App	765	57	2.5	2262	4	US-09-311-021-171	Sequence 171, App
693	57.4	2.6	2481	2	US-08-630-118A-1	Sequence 1, Appl	766	57	2.5	2516	4	US-09-949-016-766	Sequence 766, App
694	57.4	2.6	2481	2	US-08-838-399-1	Sequence 1, Appl	767	57	2.5	2882	4	US-09-949-016-724	Sequence 724, App
695	57.4	2.6	2481	3	US-09-235-839-1	Sequence 1, Appl	768	57	2.5	2964	4	US-09-578-063-25	Sequence 25, Appl
696	57.4	2.6	2481	3	US-09-327-035-1	Sequence 1, Appl	769	57	2.5	3300	3	US-09-336-643A-82	Sequence 82, Appl
697	57.4	2.6	2604	2	US-08-630-118A-3	Sequence 3, Appl	770	57	2.5	3300	3	US-09-112-096-28	Sequence 28, Appl
698	57.4	2.6	2604	2	US-08-838-393-3	Sequence 3, Appl	771	57	2.5	5668	3	US-09-112-096-14	Sequence 14, Appl
699	57.4	2.6	2604	3	US-09-235-839-3	Sequence 3, Appl	772	57	2.5	5668	4	US-09-636-215-777	Sequence 777, App
700	57.4	2.6	2604	3	US-09-327-035-3	Sequence 3, Appl	773	57	2.5	5668	4	US-09-685-166A-777	Sequence 777, App
701	57.4	2.6	2665	3	US-08-971-089-5	Sequence 5, Appl	774	57	2.5	5668	4	US-09-679-426-777	Sequence 777, App
702	57.4	2.6	4895	3	US-09-053-866-1	Sequence 1, Appl	775	57	2.5	5668	4	US-09-759-143-777	Sequence 777, App
703	57.4	2.6	4895	3	US-09-479-130-1	Sequence 1, Appl	776	57	2.5	5668	4	US-09-651-236-777	Sequence 777, App
704	57.4	2.6	4895	4	US-09-472-130A-1	Sequence 1, Appl	777	57	2.5	7286	3	US-09-331-581-3	Sequence 3, Appl
705	57.2	2.6	97	4	US-09-621-976-9086	Sequence 9086, App	778	57	2.5	7938	3	US-09-331-581-14	Sequence 14, Appl
706	57.2	2.6	105	4	US-09-621-976-13820	Sequence 13820, A	779	57	2.5	10660	3	US-08-267-803B-8	Sequence 8, Appl
707	57.2	2.6	153	4	US-09-621-976-18058	Sequence 18058, A	780	57	2.5	10660	3	US-09-041-886-16	Sequence 16, Appl
708	57.2	2.6	204	4	US-09-621-976-16458	Sequence 16458, A	c 781	57	2.5	192506	4	US-09-513-999C-36135	Sequence 36135, A
709	57.2	2.6	342	3	US-09-385-982-342	Sequence 342, App	782	56.8	2.5	184	4	US-09-513-999C-36135	Sequence 36135, A
710	57.2	2.6	508	4	US-09-621-976-17886	Sequence 17886, A	783	56.8	2.5	212	4	US-09-621-976-1325	Sequence 1325, App
711	57.2	2.6	790	3	US-09-363-970-4	Sequence 4, Appl	784	56.8	2.5	255	4	US-09-621-976-9406	Sequence 9406, App
712	57.2	2.6	844	4	US-09-690-942-3	Sequence 3, Appl	c 785	56.8	2.5	270	2	US-08-520-678A-30	Sequence 30, Appl
713	57.2	2.6	1023	4	US-09-229-947-38	Sequence 38, Appl	c 786	56.8	2.5	270	3	US-08-897-126-30	Sequence 30, Appl
714	57.2	2.6	1153	3	US-09-149-476-41	Sequence 41, Appl	c 787	56.8	2.5	554	4	US-09-696-169A-14	Sequence 14, Appl
715	57.2	2.6	1210	3	US-09-443-041A-29	Sequence 29, Appl	c 788	56.8	2.5	789	3	US-09-020-956-32	Sequence 32, Appl
716	57.2	2.6	1503	4	US-09-907-794A-220	Sequence 220, App	c 789	56.8	2.5	789	3	US-09-030-607-32	Sequence 32, Appl
717	57.2	2.6	1503	4	US-09-905-125A-220	Sequence 220, App	c 790	56.8	2.5	789	3	US-09-439-313-32	Sequence 32, Appl
718	57.2	2.6	1503	4	US-09-902-775A-220	Sequence 220, App	c 791	56.8	2.5	789	3	US-09-352-616A-32	Sequence 32, Appl
719	57.2	2.6	1503	4	US-09-906-700-220	Sequence 220, App	c 792	56.8	2.5	789	3	US-09-232-149A-32	Sequence 32, Appl
720	57.2	2.6	1503	4	US-09-903-603A-220	Sequence 220, App	c 793	56.8	2.5	789	4	US-09-159-812-32	Sequence 32, Appl
721	57.2	2.6	1503	4	US-09-904-920A-220	Sequence 220, App	c 794	56.8	2.5	789	4	US-09-636-215-32	Sequence 32, Appl
722	57.2	2.6	1503	4	US-09-909-064-220	Sequence 220, App	c 795	56.8	2.5	789	4	US-09-685-166A-32	Sequence 32, Appl
723	57.2	2.6	1503	4	US-09-905-381A-220	Sequence 220, App	c 796	56.8	2.5	789	4	US-09-115-453-32	Sequence 32, Appl
724	57.2	2.6	1503	4	US-09-906-618-220	Sequence 220, App	c 797	56.8	2.5	789	4	US-09-688-489-32	Sequence 32, Appl
725	57.2	2.6	2146	4	US-10-003-392-3	Sequence 3, Appl	c 798	56.8	2.5	789	4	US-09-673-426-32	Sequence 32, Appl
726	57.2	2.6	4419	4	US-09-620-312D-187	Sequence 187, App	c 799	56.8	2.5	789	4	US-09-759-143-32	Sequence 32, Appl
727	57.2	2.6	4874	4	US-09-187-330-2	Sequence 2, Appl	c 800	56.8	2.5	882	2	US-08-903-965C-9	Sequence 9, Appl
728	57.2	2.6	6065	4	US-09-800-729-35	Sequence 35, Appl	c 801	56.8	2.5	1051	3	US-09-245-041-10	Sequence 10, Appl
729	57.2	2.6	724	4	US-08-486-049-1	Sequence 1, Appl	c 802	56.8	2.5	1051	4	US-09-358-055B-10	Sequence 10, Appl
730	57	2.5	134	1	US-09-621-976-18433	Sequence 18433, A	c 803	56.8	2.5	1051	4	US-09-893-238-10	Sequence 23, Appl
731	57	2.5	140	1	US-08-628-417-5	Sequence 5, Appl	c 804	56.8	2.5	1074	3	US-09-357-251-23	Sequence 2, Appl
732	57	2.5	142	4	US-09-621-976-10801	Sequence 10801, A	c 805	56.8	2.5	1540	3	US-08-977-001-2	Sequence 2, Appl
733	57	2.5	169	4	US-09-621-976-11249	Sequence 11249, A	c 806	56.8	2.5	1653	3	US-09-345-469-2	Sequence 2, Appl
734	57	2.5	179	4	US-09-621-976-9575	Sequence 9575, App	c 807	56.8	2.5	1771	4	US-09-907-794A-158	Sequence 158, App
735	57	2.5	240	1	US-08-628-417-6	Sequence 6, Appl	c 808	56.8	2.5	1771	4	US-09-866-028-36	Sequence 36, Appl
736	57	2.5	249	4	US-09-621-976-19144	Sequence 19144, A	c 809	56.8	2.5	1771	4	US-09-905-125A-158	Sequence 158, App
737	57	2.5	258	4	US-09-621-976-15353	Sequence 15353, A	c 810	56.8	2.5	1771	4	US-09-902-775A-158	Sequence 158, App
738	57	2.5	271	4	US-09-621-976-10380	Sequence 10380, A	c 811	56.8	2.5	1771	4	US-09-902-775A-158	Sequence 158, App
739	57	2.5	336	4	US-09-621-976-16024	Sequence 16024, A	c 812	56.8	2.5	1771	4	US-09-906-700-158	Sequence 36, Appl
740	57	2.5	334	4	US-09-621-976-16434	Sequence 16434, A	c 813	56.8	2.5	1771	4	US-09-944-457-36	Sequence 158, App
741	57	2.5	350	4	US-09-621-976-15342	Sequence 15342, A	c 814	56.8	2.5	1771	4	US-09-903-603A-158	Sequence 158, App
742	57	2.5	674	4	US-09-620-405B-465	Sequence 465, App	c 815	56.8	2.5	1771	4	US-09-904-920A-158	Sequence 158, App
743	57	2.5	674	4	US-09-433-826B-465	Sequence 465, App	c 816	56.8	2.5	1771	4	US-09-909-064-158	Sequence 158, App
744	57	2.5	674	4	US-09-604-287A-465	Sequence 465, App	c 817	56.8	2.5	1771	4	US-09-903-381A-158	Sequence 158, App
745	57	2.5	674	4	US-09-834-759-465	Sequence 465, App	c 818	56.8	2.5	1771	4	US-09-906-618-158	Sequence 158, App
746	57	2.5	674	4	US-09-590-751A-465	Sequence 465, App	c 819	56.8	2.5	1835	3	US-09-485-549-1	Sequence 1, Appl
747	57	2.5	674	4	US-09-551-621-465	Sequence 465, App	c 820	56.8	2.5	2434	4	US-09-489-847-67	Sequence 67, Appl
748	57	2.5	1133	4	US-09-916-204-1	Sequence 1, Appl	c 821	56.8	2.5	2608	4	US-09-904-615-16	Sequence 16, Appl
749	57	2.5	1133	4	US-10-282-048-1	Sequence 1, Appl	c 822	56.8	2.5	3375	4	US-09-270-767-3	Sequence 3, Appl
750	57	2.5	1134	3	US-09-248-335-29	Sequence 29, Appl	c 823	56.8	2.5	139552	4	US-09-949-016-15300	Sequence 15300, A
751	57	2.5	1136	4	US-09-065-040-2	Sequence 2, Appl	c 824	56.6	2.5	87	4	US-09-621-976-14849	Sequence 14849, A
752	57	2.5	1158	4	US-09-949-016-463	Sequence 463, App	c 825	56.6	2.5	244	4	US-09-621-976-484	Sequence 16936, A
753	57	2.5	1507	3	US-08-453-223-1	Sequence 1, Appl	c 826	56.6	2.5	269	1	US-09-621-976-16936	Sequence 2, Appl
754	57	2.5	1538	4	US-09-205-258-193	Sequence 193, App	c 827	56.6	2.5	296	1	US-08-104-073-2	Sequence 7, Appl
755	57	2.5	1546	4	US-09-901-151-1	Sequence 1, Appl	c 828	56.6	2.5	966	1	US-08-514-014-7	Sequence 7, Appl
756	57	2.5	1559	4	US-09-489-847-42	Sequence 42, Appl	c 829	56.6	2.5	966	2	US-08-833-823-7	Sequence 38, Appl
757	57	2.5	1639	2	US-08-737-524B-1	Sequence 1, Appl	c 830	56.6	2.5	1048	4	US-09-489-847-38	Sequence 38, Appl

831	56.6	2.5	2065	3	US-09-370-473-5	Sequence 5, Appli	904	56	2.5	66	4	US-09-621-976-14819	Sequence 14819, A
832	56.6	2.5	2790	3	US-08-900-291B-1	Sequence 1, Appli	905	56	2.5	67	4	US-09-621-976-11909	Sequence 11909, A
833	56.4	2.5	132	4	US-09-621-976-13468	Sequence 13468, A	906	56	2.5	67	4	US-09-621-976-13917	Sequence 13917, A
834	56.4	2.5	145	4	US-09-621-976-16688	Sequence 16688, A	907	56	2.5	67	4	US-09-621-976-14753	Sequence 14753, A
835	56.4	2.5	145	4	US-09-621-976-16688	Sequence 16688, A	908	56	2.5	68	4	US-09-621-976-11613	Sequence 11613, A
836	56.4	2.5	146	4	US-09-621-976-16686	Sequence 16686, A	909	56	2.5	68	4	US-09-621-976-11912	Sequence 11912, A
837	56.4	2.5	146	4	US-09-621-976-16695	Sequence 16695, A	910	56	2.5	68	4	US-09-621-976-12005	Sequence 12005, A
838	56.4	2.5	552	4	US-09-461-325-111	Sequence 111, App	911	56	2.5	69	1	US-08-702-344-7	Sequence 7, Appli
839	56.4	2.5	552	4	US-10-112-542-111	Sequence 111, App	912	56	2.5	69	4	US-09-621-976-12006	Sequence 12006, A
840	56.4	2.5	552	4	US-10-115-123-111	Sequence 111, App	913	56	2.5	69	4	US-09-621-976-14105	Sequence 14105, A
841	56.4	2.5	612	4	US-09-902-540-1357	Sequence 1357, App	914	56	2.5	69	4	US-09-621-976-14869	Sequence 14869, A
842	56.4	2.5	1118	4	US-09-614-912-181	Sequence 181, App	915	56	2.5	69	4	US-09-573-080A-447	Sequence 447, App
843	56.4	2.5	1154	3	US-08-651-136C-7	Sequence 7, Appli	916	56	2.5	70	4	US-09-621-976-13579	Sequence 13579, A
844	56.4	2.5	1154	3	US-09-229-911A-7	Sequence 7, Appli	917	56	2.5	70	4	US-09-621-976-14750	Sequence 14750, A
845	56.4	2.5	1279	3	US-09-248-335-25	Sequence 25, Appli	918	56	2.5	71	4	US-09-621-976-14905	Sequence 14905, A
846	56.4	2.5	1296	4	US-09-461-325-29	Sequence 25, Appli	919	56	2.5	72	4	US-09-621-976-10445	Sequence 10445, A
847	56.4	2.5	1296	4	US-10-012-542-29	Sequence 29, Appli	920	56	2.5	72	4	US-09-621-976-14815	Sequence 14815, A
848	56.4	2.5	1296	4	US-10-115-123-29	Sequence 29, Appli	921	56	2.5	72	4	US-09-621-976-14842	Sequence 14842, A
849	56.4	2.5	1958	3	US-08-665-034A-3	Sequence 3, Appli	922	56	2.5	72	4	US-09-621-976-15064	Sequence 15064, A
850	56.4	2.5	2202	3	US-09-465-558-59	Sequence 59, Appli	923	56	2.5	73	4	US-09-621-976-14729	Sequence 14729, A
851	56.4	2.5	2320	3	US-09-202-904A-13	Sequence 13, Appli	924	56	2.5	73	4	US-09-621-976-14963	Sequence 14963, A
852	56.4	2.5	2485	4	US-09-889-463A-9	Sequence 9, Appli	925	56	2.5	74	4	US-09-621-976-14892	Sequence 14892, A
853	56.4	2.5	2744	3	US-09-071-101-1	Sequence 1, Appli	926	56	2.5	76	4	US-09-621-976-12446	Sequence 12446, A
854	56.4	2.5	2744	3	US-09-369-618-1	Sequence 1, Appli	927	56	2.5	76	4	US-09-621-976-14831	Sequence 14831, A
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861	56.2	2.5	166	4	US-09-621-976-18390	Sequence 18390, A	934	56	2.5	79	4	US-09-621-976-15090	Sequence 15090, A
862	56.2	2.5	194	4	US-09-621-976-15317	Sequence 15317, A	935	56	2.5	81	4	US-09-621-976-13152	Sequence 13152, A
863	56.2	2.5	195	4	US-09-621-976-15314	Sequence 15314, A	936	56	2.5	81	4	US-09-621-976-13152	Sequence 13152, A
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865	56.2	2.5	341	4	US-09-621-976-16135	Sequence 16135, A	938	56	2.5	83	4	US-09-621-976-14959	Sequence 14959, A
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867	56.2	2.5	941	4	US-09-205-258-186	Sequence 186, App	940	56	2.5	84	1	US-08-738-367-3	Sequence 3, Appli
868	56.2	2.5	981	4	US-09-780-717-4	Sequence 4, Appli	941	56	2.5	84	4	US-09-621-976-14571	Sequence 14571, A
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876	56	2.5	56	4	US-09-621-976-12139	Sequence 12139, A	949	56	2.5	91	4	US-09-338-933-201	Sequence 201, App
877	56	2.5	56	4	US-09-621-976-14556	Sequence 14556, A	950	56	2.5	91	4	US-09-216-681-201	Sequence 201, App
878	56	2.5	57	4	US-09-621-976-11970	Sequence 11970, A	951	56	2.5	91	4	US-09-216-003A-201	Sequence 201, App
879	56	2.5	57	4	US-09-621-976-13937	Sequence 13937, A	952	56	2.5	91	4	US-09-667-857-201	Sequence 201, App
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882	56	2.5	59	4	US-09-621-976-13752	Sequence 13752, A	955	56	2.5	94	4	US-09-338-933-261	Sequence 261, App
883	56	2.5	60	3	US-09-457-959-8	Sequence 8, Appli	956	56	2.5	94	4	US-09-216-003A-261	Sequence 261, App
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885	56	2.5	60	4	US-09-621-976-13761	Sequence 13761, A	958	56	2.5	97	4	US-09-621-976-12430	Sequence 12430, A
886	56	2.5	60	4	US-09-621-976-14742	Sequence 14742, A	959	56	2.5	98	1	US-08-088-658-42	Sequence 42, Appli
887	56	2.5	60	4	US-09-621-976-14884	Sequence 14884, A	960	56	2.5	98	2	US-08-471-907A-42	Sequence 42, Appli
888	56	2.5	60	4	US-10-079-178-8	Sequence 8, Appli	961	56	2.5	98	4	US-09-621-976-11744	Sequence 11744, A
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891	56	2.5	61	4	US-09-621-976-14799	Sequence 14799, A	964	56	2.5	101	3	US-09-404-879A-293	Sequence 293, App
892	56	2.5	61	4	US-09-621-976-14834	Sequence 14834, A	965	56	2.5	101	4	US-09-338-933-293	Sequence 293, App
893	56	2.5	61	4	US-09-621-976-14948	Sequence 14948, A	966	56	2.5	101	4	US-09-216-003A-293	Sequence 293, App
894	56	2.5	62	4	US-09-621-976-11091	Sequence 11091, A	967	56	2.5	101	4	US-09-667-857-293	Sequence 293, App
895	56	2.5	62	4	US-09-621-976-14130	Sequence 14130, A	968	56	2.5	102	4	US-09-621-976-14804	Sequence 14804, A
896	56	2.5	62	4	US-09-621-976-14936	Sequence 14936, A	969	56	2.5	105	3	US-09-284-627-23	Sequence 23, Appli
897	56	2.5	63	4	US-09-621-976-13480	Sequence 13480, A	970	56	2.5	111	3	US-09-297-535-23	Sequence 23, Appli
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c 978	56	2.5	141	5	PCT-US94-04706-1	Sequence 1, Appl	1051	55.8	2.5	1249	4	US-10-012-542-128	Sequence 128, App
c 979	56	2.5	173	4	US-09-621-976-9851	Sequence 9851, Ap	1052	55.8	2.5	1249	4	US-10-115-123-128	Sequence 93, Appl
	56	2.5	188	4	US-09-621-976-10364	Sequence 10364, A	c1052	55.8	2.5	1260	4	US-03-461-325-93	Sequence 93, Appl
	56	2.5	196	4	US-09-442-054A-42	Sequence 42, Appl	c1054	55.8	2.5	1260	4	US-10-012-542-93	Sequence 93, Appl
c 981	56	2.5	196	4	US-09-442-054A-42	Sequence 42, Appl	c1055	55.8	2.5	1260	4	US-10-115-123-93	Sequence 93, Appl
c 983	56	2.5	253	2	US-08-520-678A-25	Sequence 25, Appl	1056	55.8	2.5	1529	4	US-09-523-263B-7	Sequence 7, Appl
c 984	56	2.5	253	2	US-08-897-126-25	Sequence 25, Appl	1057	55.8	2.5	1705	4	US-09-205-258-216	Sequence 216, App
c 985	56	2.5	260	2	US-08-520-678A-29	Sequence 29, Appl	1058	55.8	2.5	2296	3	US-08-496-841C-137	Sequence 137, App
c 986	56	2.5	260	3	US-08-897-126-29	Sequence 29, Appl	1059	55.8	2.5	2695	4	US-09-706-197-3	Sequence 3, Appl
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	56	2.5	347	4	US-09-621-976-16136	Sequence 16136, A	1064	55.6	2.5	177	4	US-09-621-976-8073	Sequence 8073, Ap
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	56	2.5	530	4	US-10-012-542-28	Sequence 28, Appl	c1068	55.6	2.5	612	3	US-09-385-982-280	Sequence 280, App
	56	2.5	530	4	US-10-115-123-28	Sequence 28, Appl	1069	55.6	2.5	1951	3	US-09-465-558-35	Sequence 35, Appl
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	56	2.5	1174	2	US-08-872-437-1	Sequence 1, Appl	1075	55.4	2.5	474	3	US-09-528-706-97	Sequence 97, Appl
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	56	2.5	1315	3	US-09-221-448A-1	Sequence 1, Appl	1079	55.4	2.5	1375	4	US-09-489-847-120	Sequence 120, App
	56	2.5	1361	4	US-09-489-847-64	Sequence 64, Appl	1080	55.4	2.5	1376	4	US-09-489-847-66	Sequence 66, Appl
	56	2.5	1447	3	US-09-443-041A-27	Sequence 27, Appl	1081	55.4	2.5	2331	4	US-09-866-028-54	Sequence 54, Appl
	56	2.5	1618	4	US-09-800-729-29	Sequence 29, Appl	1082	55.4	2.5	2331	4	US-09-944-457-54	Sequence 54, Appl
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	56	2.5	2389	4	US-09-800-729-33	Sequence 33, Appl	1093	55.2	2.5	959	4	US-09-721-822A-10	Sequence 10, Appl
	56	2.5	2394	4	US-09-455-486-5	Sequence 5, Appl	1094	55.2	2.5	1445	3	US-09-697-367-19	Sequence 19, Appl
	56	2.5	2527	4	US-09-244-805-29	Sequence 29, Appl	1095	55.2	2.5	1445	3	US-09-918-909A-19	Sequence 19, Appl
	56	2.5	2527	4	US-09-917-254-27	Sequence 27, Appl	1096	55.2	2.5	1933	4	US-09-920-759-3	Sequence 3, Appl
	56	2.5	2808	4	US-09-917-254-27	Sequence 27, Appl	1097	55.2	2.5	118143	4	US-09-949-016-17196	Sequence 17196, A
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	56	2.5	3871	3	US-09-094-410-3	Sequence 3, Appl	1102	55	2.5	150	4	US-09-621-976-13989	Sequence 13989, A
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	56	2.5	3871	4	US-08-570-142D-3	Sequence 3, Appl	1104	55	2.5	487	3	US-09-257-179-22	Sequence 22, Appl
	56	2.5	3871	4	US-08-708-123D-3	Sequence 3, Appl	1105	55	2.5	563	4	US-09-621-976-19183	Sequence 19183, A
	56	2.5	3871	4	US-08-583-153A-3	Sequence 3, Appl	1106	55	2.5	605	4	US-09-943-016-145251	Sequence 145251
	56	2.5	3871	4	US-08-570-142D-3	Sequence 3, Appl	c1107	55	2.5	681	3	US-09-227-357-66	Sequence 66, Appl
	56	2.5	3871	4	US-08-638-524B-3	Sequence 3, Appl	c1108	55	2.5	685	3	US-09-621-976-1878	Sequence 1878, Ap
	56	2.5	6200	3	US-09-439-923-1	Sequence 1, Appl	1109	55	2.5	787	4	US-09-270-767-12633	Sequence 12633, A
	56	2.5	6200	4	US-09-711-202A-1	Sequence 1, Appl	1110	55	2.5	1151	4	US-09-621-976-12633	Sequence 7, Appl
	56	2.5	6200	4	US-10-029-907-6	Sequence 6, Appl	1111	55	2.5	1558	1	US-08-455-550-7	Sequence 10, Appl
	56	2.5	8638	4	US-10-029-907-4	Sequence 4, Appl	1112	55	2.5	1776	3	US-08-655-352-10	Sequence 10, Appl
	56	2.5	8643	4	US-10-029-907-4	Sequence 4, Appl	1113	55	2.5	1776	3	US-09-258-016-10	Sequence 10, Appl
	56	2.5	9472	4	US-08-150-204E-96	Sequence 96, Appl	1114	55	2.5	1776	3	US-09-257-825B-10	Sequence 10, Appl
	56	2.5	9589	1	US-07-925-695-1	Sequence 1, Appl	1115	55	2.5	1886	4	US-09-594-506-31	Sequence 31, Appl
	56	2.5	9589	1	US-07-925-695-2	Sequence 2, Appl	1116	55	2.5	1934	3	US-08-776-844-1	Sequence 1, Appl
	56	2.5	235	4	US-09-621-976-9455	Sequence 9455, Ap	1117	55	2.5	1934	3	US-09-909-325-1	Sequence 1, Appl
	56	2.5	250	4	US-09-621-976-18363	Sequence 18363, A	1118	55	2.5	1934	3	US-09-909-326-1	Sequence 1, Appl
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	55.8	2.5	1013	1	US-07-920-519-30	Sequence 30, Appl	1120	55	2.5	2028	3	US-09-340-993-12	Sequence 12, Appl
	55.8	2.5	1013	1	US-08-086-410-23	Sequence 23, Appl	1121	55	2.5	2349	3	US-09-468-442-12	Sequence 12, Appl
	55.8	2.5	1013	1	US-08-314-586-30	Sequence 30, Appl	1122	55	2.5	2349	4	US-09-805-455-1	Sequence 1, Appl

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1125	55	2.5	2821	4	US-09-671-325-1669	Sequence 1669, Ap	US-09-034-756-5	3	12980	2.4	54.4	cl198	Sequence 5, Appl
1126	55	2.5	2821	4	US-09-658-824-1669	Sequence 1669, Ap	US-09-284-627-15	3	80	2.4	54.2	cl199	Sequence 15142, A
1127	54.8	2.4	250	4	US-09-621-976-17371	Sequence 17371, A	US-09-621-976-15142	4	289	2.4	54.2	1200	Sequence 15142, A
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c1335	53.2	2.4	314	4	US-09-621-976-16347	Sequence 16347, A	c1408	52.4	2.3	830	3	US-08-688-609-1	Sequence 1, Appl
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c1483 51.8 2.3 48018 4 US-09-949-016-17573 Sequence 17573, A
1484 51.8 2.3 119801 4 US-09-949-016-13453 Sequence 13453, A
c1485 51.6 2.3 71 4 US-09-816-089A-5 Sequence 5, Appli
c1486 51.6 2.3 90 3 US-09-254-048A-1 Sequence 1, Appli
c1487 51.6 2.3 90 3 US-09-921-203-1 Sequence 1, Appli
c1488 51.6 2.3 90 4 US-10-106-832-1 Sequence 1, Appli
1489 51.6 2.3 208 4 US-09-621-976-15504 Sequence 15504, A
c1490 51.6 2.3 601 4 US-09-949-016-31132 Sequence 31132, A
c1491 51.6 2.3 601 4 US-09-949-016-47199 Sequence 47199, A
c1492 51.6 2.3 601 4 US-09-949-016-80023 Sequence 80023, A
1493 51.6 2.3 601 4 US-09-949-016-86544 Sequence 86544, A
1494 51.6 2.3 601 4 US-09-949-016-193087 Sequence 193087,
1495 51.6 2.3 601 4 US-09-949-016-193088 Sequence 193088,
1496 51.6 2.3 601 4 US-09-949-016-193180 Sequence 193180,
1497 51.6 2.3 601 4 US-09-949-016-193181 Sequence 193181,
1498 51.6 2.3 601 4 US-09-949-016-193273 Sequence 193273,
1499 51.6 2.3 601 4 US-09-949-016-193274 Sequence 193274,
1500 51.6 2.3 601 4 US-09-949-016-193366 Sequence 193366,
ALIGNMENTS
RESULT 1
US-09-621-976-97 90 4 US-10-106-832-1
; Sequence 97, Application US/09621976
; Patent No. 6635063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 97
; LENGTH: 672
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 227..670
; NAME/KEY: sig_peptide
; LOCATION: 227..307
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 7.0999990463257
; OTHER INFORMATION: seq VLLLLLLRGMFS/SP
; NAME/KEY: misc feature
; LOCATION: 586,602..603
; OTHER INFORMATION: n=a, g, c or t
US-09-621-976-97
Query Match 27.3%; Score 612.8; DB 4; Length 672;
Best Local Similarity 98.1%; Pred. No. 7.2e-146;
Matches 635; Conservative 5; Mismatches 3; Indels 4; Gaps 2;
QY 1 GAATGAATACCTCCGAAGCGCTTTGTTCTCCAGATGTGAATAGTCCACTATACCAGCC 60
Db 27 GAATGAATACCTCCGAAGCGCTTTGTTCTCCAGATGTGAATAGTCCACTATACCAGCC 86
QY 61 TCGTCTTCTTCGGGGGACACGTTGGGTTCAGGGCAGAGAGATATTTAATGTACCCT 120
Db 87 TCGTCTTCTTCGGGGGACACGTTGGGTTCAGGGCAGAGAGATATTTAATGTACCCT 146
QY 121 CTTCGGGCTTTCATGGGACTCCCTCTGCCACATTTTTCGAGGTTCGGAAAGTTGCTAGA 180
Db 147 CTTCGGGCTTTCATGGGACTCCCTCTGCCACATTTTTCGAGGTTCGGAAAGTTGCTAGA 206
QY 181 GCGTTTCAGAACTCCAGCCTTAATGGATCCCAAACTCGGAGAAATGGTGGTCCCTGCTGG 240
Db 207 GCGTTTCAGAACTCCAGCCTTAATGGATCCCAAACTCGGAGAAATGGTGGTCCCTGCTGG 266
QY 241 CTG---TGTGCTGCTGCTGGAGCGGGCATGTTCTCTCACCTCCCGCCCCCGG 297
Db 267 CTGTCGTGCTGCTGCTGCTGGAGCGGGCATGTTCTCTCACCTCCCGCCCCCGG 326
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QY 1453 GGATTGCAAAATTTGATGACACCCAGTATCTCGACGAAAAAGAGCGATCAGAACAGTGT 1512
Db |||||
QY 1371 GGGTCTCGACTTCAGTCAACCTCATTTACCTGGCTGGGAGAGAGCCATGAAGACAGTTT 1430
Db |||||
QY 1513 TTGGAACAGAACACAGATATGATCCGGATGATCCACCATTCCTAAATGCGCAATGTTCC 1572
Db |||||
QY 1431 TTGGTGTGAGCCAGACTTGACCAAGGAGCGCGAGTATTTCCCGTGACCTTGACCTTTC 1490
QY 1573 AGGAGATCGTCCACAGAGCGTGTGCTAATTCCTGGGAGCTGTTGATGATCGGAGAC 1632
Db |||||
QY 1491 AGGAGGCCACGGGCAAGAACGTCAATGCTGCTGCTGCTGGGTACGGATGACGGAGCCC 1550
QY 1633 ATTCGCAAGATGAGAAAAATCAACAGGTGGAATCATAGAGGGGAACCAAAATTTATTTCTG 1692
Db |||||
QY 1551 ACTCCAGAAATGAAAGCTCAACAGGTATTAACATACATAGAGGGAACCAAGATGCTGCGCG 1610
QY 1693 CCTTTTCTTAGAGATGCGCCAGCTCCATTAATCAACAAGAACCTTCT 1739
Db |||||
QY 1611 CGTACCTGTATGAGGTCTCCAGCTGAAGGACTAGGCCAAGCCCTCT 1657

RESULT 3
US-09-270-767-14369/C
; Sequence 14369, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
; FILE REFERENCE: File Reference: 7326-094
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14369
; LENGTH: 1489
; TYPE: DNA
; ORGANISM: *Drosophila melanogaster*
US-09-270-767-14369

Query Match 16.68; Score 373.2; DB 4; Length 1489;
Best Local Similarity 56.44; Pred. No. 1e-84;
Matches 718; Conservative 0; Mismatches 553; Indels 3; Gaps 1;

QY 440 GCGTCGGGACACGCTGCGAGCGCTGGGGGCCCGTGTGGCTCGTGACATGGTCTCTCA 499
Db |||||
QY 1484 GACCGGGATCGGTGAGTCTCTGGGCGCGGAGACGAGCTGGAGATGGGTGAGCA 1425
Db |||||
QY 500 GCAGCTGCCGATGGTCAGAGTCTTCCATACCTCCCGTCATCTGCGCGAACTGGGGAG 559
Db |||||
QY 1424 GACTTTGCCGAAACGGCCAGATTAACCTCTACCAAGGTTCTGCTGGAACTTTGGGCA 1365
QY 560 CGATCCCAAGGACCGTGTCTCTAGGCGACCTGGAGCTGGAGCTGCTGACCG 619
Db |||||
QY 1364 AGACCCCTTAAGAAGACCGTGTGGTCTATGCTATGCTGATGTCAGCCCGCCCTGAA 1305
QY 620 GGGCGATGGTGGCTCAGCGACCCCTATGCTGACGAGGTAGCGGGAACCTTTATGG 679
Db |||||
QY 1304 GGAAGATGGATGGAACACCAATCCCTTGGAGCTTACAGAGTGGATGGAACCTGTTGG 1245
QY 680 ACAGGAGCGACCGACACAAAGGCCCTGTCTGGCTGGATCAATGCTGTGAGCGCCTT 739
Db |||||
QY 1244 ACAGGAGCGATCCGACGACAAAGGACCTGTCTGTGCTGGATCCAGCTATCGAAGCTTA 1185
QY 740 CAGAGCCCTGGACAGATCTTCTGTGAATATCAAAATTCATCATTTAGGGGATGGAAGA 799
Db |||||
QY 1184 TCAGAAGCTCAACATTTGCACTGCTGTGATGTTAAATTCGTATTTGAGGGAATGGAGGA 1125
QY 800 GGCTGCTCTGTTGCCCTGAGGAACTTGTGGAAAGAAAGAACCGGATTTCTTCTCTGG 859
Db |||||
QY 1124 AAGCGGAGGAGGCGCTCGATGACTGTTATTTGGAAACGTAAGATAAATTTCTTAGCGGA 1065
QY 860 TGTGGACTACATTTGTAATTTTCAAGATAACCTGTGGATCAGCGCAAGGAAGCAACATCAC 919

Db |||||
QY 1064 TGTGATTTTGTGTCATATCCGATAACTACTGGCTTGGAAAAAAGCGCCCTTCCCTCAC 1005
QY 920 TTATGGAAACCGGGGAAACAGCTACTTCTATGTTGGAGTGAATGACAGACAGGATTT 979
Db |||||
QY 1004 ATATGGGCTTTCGGGTTTGGCATACTTTCAAGTGGAGGTGGAATGCTCCAGCAAGACTT 945
QY 980 TCACTCAGGAACCTTTGGTGGCATCCTTTCATGAACCAATGCTGATCTGGTGTGCTCTCT 1039
Db |||||
QY 944 GCATAGTGGAGTTTGGGGGTACAGTTTCAAGCAANTGCCGANTCTGTGTCATTTGCT 885
QY 1040 CGGTAGCCTGGTAGACTCTGCTGCTCATATCTCTGGTCCCTGGATCTATGATGAAGTGT 1099
Db |||||
QY 884 GAGCATTTCTTGTGTAAGATACAAATATCTAGTCCCTGGTGGATCGCAGCTGCG 825
QY 1100 TCCTCTTACAGAGAGGAAATTAATACATACAAAGCATCCATCTAGACCTAGAGATA 1159
Db |||||
QY 824 ACCACAGATTAGAACGAGCAATCTATATATGAAACATAGACTTTTGAAGTTTCTGAGTA 765
QY 1160 CCGGAATAGCAGCGCGGTTGAGAAATTTCTGTTTCGATACCTAAGGAGGAGATTTCTAATGCA 1219
Db |||||
QY 764 CAAGAAAGACATTTGGTTTGAACAGCTGCCGATATGGCGATAAAACAGGTACTTCA 705
QY 1220 ---CCTCTGGAGTACCCATCTCTTCTATTCATGGGATCGAGGCGCGTTTGTATGACC 1276
Db |||||
QY 704 AGCCAGGTGGCGCTATCCCACTCTTCTGTTTCAAGGATTTGAAGTGCATTTTATGAGCC 645
QY 1277 TGGAACTTAACAGTCTATCTGCGCGAGTTATAGGAAATTTTCAATCGCTAGTCCC 1336
Db |||||
QY 644 AGCGCAAAACATGTCATTCGGAAGAGTTATTTGTAAGTTCTCTATTCGCTTGTCCC 585
QY 1337 TCACATGAATGTCTGCGGTGAAAAACAGGTGACACGACATCTTGAAGATGTGTTCTC 1396
Db |||||
QY 584 CAACCAAGATCCAAAGCATATTGAGGAGTGTGTTGTAATACCTTAATGATAAATGGGC 525
QY 1397 CAAAGAAATAGTTTCCAAAGATGTTGTTTCCATGACTCTAGGACTCACCCGTTGGAT 1456
Db |||||
QY 524 CGAGCGAGGATCTCTTAAACAAATGAAGTTTCAATGCTCTCAGTGGCAAGCCCTGAC 465
QY 1457 TGCAAATATGATGACACCCAGTATCTCGCAGCAAAAGAGCGATCAGACAGTGTGG 1516
Db |||||
QY 464 TGAGGACCCCTAACCATCTCTTATGAGGCTGCAAAAGAGCCATAAGCATGTTTTCAA 405
QY 1517 AACAGAACAGATATGATCGGATGATCCACATTTCCAAATTTGCCAAATGTTCCAGGA 1576
Db |||||
QY 404 TGTGGAAACAGATATGACCGGAGAGGGATCTATTCAGTAACGTTAATTCATTTGAGGA 345
QY 1577 GATCGTCCAAAGAGCGTGTGCTAATTCGCTGGGAGCTGTTGATGATGGAGAACATTC 1636
Db |||||
QY 344 AGCCACTGGTAAAAACGTTATCTTCTGCGAGTGGTGATGTGACGAGCGTGGCCATTC 285
QY 1637 GCAGATGAGAAATCAACAGGTGGAATCTACATAGAGGGAACCAAAATTTTGTGCTTC 1696
Db |||||
QY 284 TCAAAATGAAATCGATATTTACAAATACATCGAAGGCACATAAACTTCTTGGCGCTA 225
QY 1697 TTTCTTAGAGATGG 1710
Db |||||
QY 224 TCTGCAGAGTGG 211

RESULT 4

US-09-513-999C-13950
; Sequence 13950, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24

Db 1231 GATAGTTTCACTGCTGCTGCCAAGGCAACTCAAGATGTTTGGATGTTGTTCTGATTTT 1290
QY 1533 ATCCGGATGGATCCACATTTCCAAATGTCCAAATGTTCCAGGAGATCGTCCACAAGGC 1592
Db 1291 ACTAGAGAGGTGGTTCAATTCATTTGACTTTTGAAGAAGAAATGGGTGTTGAT 1350
QY 1593 GTGGTGCTAATTCGGCTGGGAGCTGTTGATGATGAGAGAAATTCGACAGAAATGAGAAATC 1652
Db 1351 GTTTTACTTTTCCAAATGGGTAGAGGTGATGATGCTCATTCATCAATCAATGAAATTA 1410
QY 1653 AACAGTGGAACTACATAGAGGAGGACCAATATTTCCTGCTTTT 1699
Db 1411 GATGTAAGTAACATATATCAATGTTGTAAGGATTTGGGTGGGTATNT 1457

RESULT 6

US-08-204-740-5
; Sequence 5, Application US/08204740
; Patent No. 5753432
; GENERAL INFORMATION:
; APPLICANT: Gudkov, Andrei
; APPLICANT: Kazarov, Alexander
; APPLICANT: Mazo, Ilya
; APPLICANT: Robinson, Igor B
; TITLE OF INVENTION: Methods for Identifying Genetic
; TITLE OF INVENTION: Suppressor Elements and Genes Associated with Malignant
; TITLE OF INVENTION: Growth in Cancer Cells
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Alligretti & Witcoff, Ltd.
; STREET: 10 S. Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/204,740
; FILING DATE: 04-MAR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5753432nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 93,354-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-204-740-5

Query Match 4.3%; Score 96.4; DB 1; Length 273;
Best Local Similarity 64.1%; Pred. No. 1.2e-14;
Matches 177; Conservative 0; Mismatches 96; Indels 3; Gaps 2;
QY 427 GAATGATGCGCGTGGTGGGACACGCTGCAGCGCTCGGGGGCCCGTGTGGCTCGGTGG 486
Db 1 GGATGATGAGGTGGCGAGCTGCCGATGTCCAGAGGCTGGGGGGCTCCGTGGAACTGGTGG 60
QY 487 ACATGGGTCTTCAGCAGCTGCCCGATGGTCAGAGTCTTCCAAATACCTCCCGTCATCCTGG 546
Db 61 ATATCGGGAAGCAGAAGCTCCAGATGGCTCGGAGATACCACTTCTCCCATC--TGCTGG 118

QY 547 CCGAACCTGGGAGCGATCCCAAGAGGACCGTGTGCTTTCTACGGCACTTGGACGTGC 606
Db 119 GCAAGCTAGCAGCGGACCCCAAGAGAAACCGTGTGCATTTACGGGCACTGGACGTGC 178
QY 607 AGCCTGCTGACCGGGGGGATGGGTGCTCAGGACCCCTATGTGCTACGGAGGTAGACG 666
Db 179 AGCCTGC-GCCCTGGAGGACGGTGGGACAGCGAGCCCTTACCTTGGTGGAGCGGAAG 237
QY 667 GGAACCTTTTACGAGGAGCGGACCGACCAACAAG 702
Db 238 GCAAGCTGTATGGAGAGGCTCCACGAGCATAGG 273

RESULT 7

US-09-081-167A-5
; Sequence 5, Application US/09081167A
; Patent No. 6083745
; GENERAL INFORMATION:
; APPLICANT: Gudkov, Andrei
; APPLICANT: Kazarov, Alexander
; APPLICANT: Mazo, Ilya
; APPLICANT: Robinson, Igor B
; TITLE OF INVENTION: Methods for Identifying Genetic
; TITLE OF INVENTION: Suppressor Elements and Genes Associated with Malignant
; TITLE OF INVENTION: Growth in Cancer Cells
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 S. Wacker Drive, 32nd Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/081,167A
; FILING DATE: 18-MAY-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6083745nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 93,354-KK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-081-167A-5

Query Match 4.3%; Score 96.4; DB 3; Length 273;
Best Local Similarity 64.1%; Pred. No. 1.2e-14;
Matches 177; Conservative 0; Mismatches 96; Indels 3; Gaps 2;
QY 427 GAATGATGCGCGTGGTGGGACACGCTGCAGCGCTCGGGGGCCCGTGTGGCTCGGTGG 486
Db 1 GGATGATGAGGTGGCGAGCTGCCGATGTCCAGAGGCTGGGGGGCTCCGTGGAACTGGTGG 60
QY 487 ACATGGGTCTTCAGCAGCTGCCCGATGGTCAGAGTCTTCCAAATACCTCCCGTCATCCTGG 546
Db 61 ATATCGGGAAGCAGAAGCTCCAGATGGCTCGGAGATACCACTTCTCCCATC--TGCTGG 118
QY 547 CCGAACCTGGGAGCGCATCCCAAGAGGACCGTGTGCTTTCTACGGCCACTTGGACGTGC 606

Wed Feb 16 11:38:00 2005

Db 119 GCAAGCTAGGACGACCCAGAAACCGTGTGCAATTTAGGGACCTGACGTC 178
 QY 607 AGCTGCTGACCGGGCGATGGTGGCTCAGGACCCCTATGTGCTGACGAGGTAGACG 666
 Db 179 AGCTGTC-GCCCTGGAGACGGGTGGGACAGCGAGCCCTTCACCTTGGTGGAGCGGGAAG 237
 QY 667 GGAACCTTTATGGACGAGGAGCGACCGACAAACAAAG 702
 Db 238 GCAAGCTGTATGGAGAGGCTCCACGACGATAAGG 273

RESULT 8
 US-09-081-395-5
 ; Sequence 5, Application US/09081395
 ; Patent No. 6083746
 ; GENERAL INFORMATION:
 ; APPLICANT: Gudkov, Andrei
 ; APPLICANT: Kazarov, Alexander
 ; APPLICANT: Mazo, Ilya
 ; APPLICANT: Roninson, Igor B
 ; TITLE OF INVENTION: Methods for Identifying Genetic
 ; TITLE OF INVENTION: Suppressor Elements and Genes Associated with Malignant
 ; TITLE OF INVENTION: Growth in Cancer Cells
 ; NUMBER OF SEQUENCES: 15
 ; CORRESPONDENCE ADDRESS:
 ; STREET: 300 S. Wacker Drive, 32nd Floor
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/081,395
 ; FILING DATE: 18-MAY-1998
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: No. 6083746nan, Kevin E
 ; REGISTRATION NUMBER: 35,303
 ; REFERENCE/DOCKET NUMBER: 93,354-KK
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312-913-0001
 ; TELEFAX: 312-913-0002
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 273 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; US-09-081-395-5

Query Match 4.3%; Score 96.4; DB 3; Length 273;
 Best Local Similarity 64.1%; Pred. No. 1.2e-14;
 Matches 177; Conservative 0; Mismatches 96; Indels 3; Gaps 2;

QY 427 GAATGATGGCGGTGGCGGACAGCTGCGAGCGCTGGGGGCGGCTGGGCTCGGTGG 486
 Db 1 GGATGATGGAGGTGGCGAGTGTCCAGAGGCTGGGGGCTCGGTGAACTGGTGG 60
 QY 487 ACATGGGTCTCTCAGCAGCTGCCGAGTCTTCCAAATACCTCCCGTCATCCTGG 546
 Db 61 ATATCGGGAAGCAGAGCTCCAGATGGCTCGGAGATACCACTTCTCCCATC--TGCTGG 118
 QY 547 CCGAAGCTGGGGAGCGATCCACGAAAGGCGCCGCTGCTTCTACGGGCACTTGGAGCTGC 606
 Db 119 GCAAGCTAGGACGACCCAGAAACCGTGTGCAATTTAGGGACCTGACGTC 178

QY 607 AGCTGCTGACCGGGCGATGGTGGCTCAGGACCCCTATGTGCTGACGAGGTAGACG 666
 Db 179 AGCTGTC-GCCCTGGAGACGGGTGGGACAGCGAGCCCTTCACCTTGGTGGAGCGGGAAG 237
 QY 667 GGAACCTTTATGGACGAGGAGCGACCGACAAACAAAG 702
 Db 238 GCAAGCTGTATGGAGAGGCTCCACGACGATAAGG 273

RESULT 9
 US-09-416-833-5
 ; Sequence 5, Application US/09416833
 ; Patent No. 6197521
 ; GENERAL INFORMATION:
 ; APPLICANT: Gudkov, Andrei
 ; APPLICANT: Kazarov, Alexander
 ; APPLICANT: Mazo, Ilya
 ; APPLICANT: Roninson, Igor B
 ; TITLE OF INVENTION: Methods for Identifying Genetic
 ; TITLE OF INVENTION: Suppressor Elements and Genes Associated with Malignant
 ; TITLE OF INVENTION: Growth in Cancer Cells
 ; NUMBER OF SEQUENCES: 13
 ; CORRESPONDENCE ADDRESS:
 ; STREET: 10 S. Wacker Drive, Suite 3000
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/416,833
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/204,740
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: No. 6197521nan, Kevin E
 ; REGISTRATION NUMBER: 35,303
 ; REFERENCE/DOCKET NUMBER: 93,354-C
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312-715-1000
 ; TELEFAX: 312-715-1234
 ; TELEX: 910-221-5317
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 273 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; US-09-416-833-5

Query Match 4.3%; Score 96.4; DB 3; Length 273;
 Best Local Similarity 64.1%; Pred. No. 1.2e-14;
 Matches 177; Conservative 0; Mismatches 96; Indels 3; Gaps 2;

QY 427 GAATGATGGCGGTGGCGGACAGCTGCGAGCGCTGGGGGCGGCTGGGCTCGGTGG 486
 Db 1 GGATGATGGAGGTGGCGAGTGTCCAGAGGCTGGGGGCTCGGTGAACTGGTGG 60
 QY 487 ACATGGGTCTCTCAGCAGCTGCCGAGTCTTCCAAATACCTCCCGTCATCCTGG 546
 Db 61 ATATCGGGAAGCAGAGCTCCAGATGGCTCGGAGATACCACTTCTCCCATC--TGCTGG 118
 QY 547 CCGAAGCTGGGGAGCGATCCACGAAAGGCGCCGCTGCTTCTACGGGCACTTGGAGCTGC 606

Db 119 GCAAGCTAGGACGACCCCGAGAAACCGTGTGCAATTTACGGGACCTGGACGTGC 178
QY 607 AGCCTGCTGACCGGGGCGATGGGTGGCTCAGGACCCCTATGTCTGACGAGGTAGACG 666
Db 179 AGCCTGC-GCCCTGGAGGACGGGTGGGACAGCGCCCTTACCTTGGTGGAGCGGAAG 237
QY 667 GGAACCTTTATGACGAGGAGCGACCGACACAAAG 702
Db 238 GCAAGCTGTATGGGAGAGGCTCCACGGACGATAAGG 273

RESULT 10

PCT-US95-02521-5
; Sequence 5, Application PC/TUS9502521
; GENERAL INFORMATION:
; APPLICANT: Methods for Identifying Genetic
; TITLE OF INVENTION: Suppressor Elements and Genes Associated with Malignant
; TITLE OF INVENTION: Growth in Cancer Cells
; NUMBER OF SEQUENCES: 13
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION NUMBER: PCT/US95/02521
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
PCT-US95-02521-5

Query Match 4.3%; Score 96.4; DB 5; Length 273;
Best Local Similarity 64.1%; Pred. No. 1.2e-14;
Matches 177; Conservative 0; Mismatches 96; Indels 3; Gaps 2;
QY 427 GAATGATGGCGGTGGCTGGGACACGCTGAGCGCCCTGGGGGCCGTGTGGCTCGGTGG 486
Db 1 GGATGATGGAGGTGGGAGCTGCCGATGCCAGAGGCTGGGGGCTCCGTGGAACCTGGTG 60
QY 487 ACATGGGTCTCAGCAGCTGCCGATGCTCAGAGTCTTCCAATACCTCCCGTCATCTGG 546
Db 61 ATATCGGGAAGCAGAACTCCAGATGGCTCGGAGATACCACCTTCTCCCATC--TGCTGG 118
QY 547 CCGAACTGGGGAGCGATCCACGAAAGCGCACCGTGTCTTCTACGGCCACTTGGACGTGC 606
Db 119 GCAAGCTAGGACGACCCCGAGAAACCGTGTGCAATTTACGGGACCTGGACGTGC 178
QY 607 AGCCTGCTGACCGGGGCGATGGGTGGCTCAGGACCCCTATGTCTGACGAGGTAGACG 666
Db 179 AGCCTGC-GCCCTGGAGGAGGGTGGGACAGCGAGCCCTTACCTTGGTGGAGCGGAAG 237
QY 667 GGAACCTTTATGACGAGGAGCGACCGACACAAAG 702
Db 238 GCAAGCTGTATGGGAGAGGCTCCACGGACGATAAGG 273

RESULT 11

US-09-513-999C-22131
; Sequence 22131, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG

; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 22131
; LENGTH: 334
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 277
; OTHER INFORMATION: y=c or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 303
; OTHER INFORMATION: y=c or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 334
; OTHER INFORMATION: s=g or c
US-09-513-999C-22131

Query Match 4.1%; Score 92.2; DB 4; Length 334;
Best Local Similarity 95.9%; Pred. No. 1.6e-13;
Matches 94; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2090 CGTGACACATAATCATTCATCCATCAATGATCGCTTGTACCACTCTTCTTTATC 2149
Db 1 CGTGACACATAATCATTCATCCATCAATGATCGCTTGTACCACTCTTCTTTATC 60
QY 2150 TTATTATAAAATGTTGGTCTCCACCACCTGCTCCCA 2187
Db 61 TTATTATAAAATGTTGGTCTCCACCACCTGACTACAA 98

RESULT 12

US-09-583-110-2168
; Sequence 2168, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 2168
; LENGTH: 1374
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-2168

Query Match 3.8%; Score 85.8; DB 4; Length 1374;
Best Local Similarity 46.7%; Pred. No. 1.4e-11;
Matches 381; Conservative 0; Mismatches 422; Indels 12; Gaps 3;

QY 576 ACCGTGTGCTTCTACGGCCACTTGGACGCTGACGCTGCTGACCGGGCGATGGGTGGCTC 635
Db 250 ACCTTGATTTCTATAACCACTATGACACTGTCCAGCGGATGGGGATCAGGTCTGGACA 309
QY 636 ACCGACCCCTATGTCTGCTGACGGAGGTAGACGGGAACTTTATGACGAGGAGCGAC 695
Db 310 GAGGATCCTTTTACGCTTTCGGTCCGCAATGGCTTCATGTATGGCGTGGGTGTGATGAC 369

QY 696 AACAAAGCCCTGCTTGGCTTGGATCAATGCTGTGAGCGCTTCAGAGCCCTGGAGCAA 755
Db 370 GACAAGGGTCATATCACAGCTCGCTTGGATGCTTTTGAGAAAATATATGACGACCATGAT 429
QY 756 GATCTTCCTGTAATATCAAAATTCATCATTTAGGGGATGGAAGGCTGGCTCTGTGCC 815
Db 430 GATTTACCTGTCAATATCAGCTTTATCATTTAGGGAGCGGAGGATCGCTTCAACAGAC 489
QY 816 CTGGAGGAACTTGTGGAAAAGAAAGGACCGAATTTCTCTCTGCTGTGCTGACTACATTTGA 875
Db 490 CTAGATAAGTATTGGAAGGATGACGACAAA---CTCCATGGGGCGAATTTGTTGCTC 546
QY 876 ATTTGAGATACTGCTGGATCAGCAAGGAGGACCAATCATTATGGAACCGCGGG 935
Db 547 TGGGAACCAAGGACCAAAATGCTTGGAAACATCGGAAATTTCTGGTGGCAATTAAGGG 606
QY 936 RACAGCTACTTCAATGCTGAGGTGAAATGACAGACCAAGATTTTCACTCAGGAACCTTT 995
Db 607 ATTTGACCTTTGATGCCAGGTAAGGATTAAGCGCTGATGGATATCCACTCGAG---TTAT 663
QY 996 GGTGGCATCTTTCATGAACCAATGCTGATCTGCTGCTTCTCTCGGTAGCTGTGAGAC 1055
Db 664 GGTGGCTTGTGGAATCAGCTCCTTGGTATCTCTCCCAAGCCTTACAGTCTCTCTGCTGCT 723
QY 1056 TGTCTGCTCATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1115
Db 724 GCGGATGCGCGTATCTTGGTGAAGCTTGTACGAAGAGTACATGAGCCCAATGAACGA 783
QY 1116 GAAATAAATACATACAAAGCCATCCATCTAGACCTAGAAAGATACCGGAATAGAGCCGG 1175
Db 784 GAAATGCGCTTGTGTAAGAACTTATGCTCAACGAAACCCAGAGGAGTTAGTCGGATTTAT 843
QY 1176 GTTGAGAAATTTCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1229
Db 844 GGAATGAGTGTGCTCTCTTACAGGAGGAGCGGATGGCCCTTTCTAAAGCTTTCTTTTC 903
QY 1230 TACCATCTCTTCTTATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1289
Db 904 GAGCCAGCGCTTAATATCAAGGAATCCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 963
QY 1290 GTCATACCTGGCGAGTTATAGAAAATTTTCAATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1349
Db 964 ATTTTCCCTGCAAGCCAGTGCAGCTAGAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1023
QY 1350 TCTGCGGTGAAAACAGGTGACACGATCTTGA 1384
Db 1024 CATGATGTTCTGGAATAAATTCGGAACACGCTAGA 1058

RESULT 13
US-08-961-527-225
; Sequence 225, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESS: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER:

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 225:
SEQUENCE CHARACTERISTICS:
LENGTH: 3766 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

Query Match 3.8%; Score 85.8; DB 3; Length 3766;
Best Local Similarity 46.7%; Pred. No. 2.3e-11;
Matches 381; Conservative 0; Mismatches 422; Indels 12; Gaps 3;

QY 576 ACCGTGTCTTCTACGGCCACTTGGACGTGCGAGCTGTCACCGGGCGATGGGTGGTCTC 635
Db 1233 ACCTTGATTTTCTATAACCACTATGACACTGTGCCAGCGGATCGGTCCTTGGACA 1292
QY 636 ACGGACCCCTATGCTGACCGAGGTACACGGGAACTTTATGACGAGGAGCGACCGAC 695
Db 1293 GAGGATCCTTTACGCTTTCGCTCGCAATGCTTCATGATGGCGTGGGGTTCATGAC 1352
QY 696 AACAAAGCCCTGCTTGGCTTGGATCAATGCTGTGAGCGCTTCAGAGCCCTGGAGCAA 755
Db 1353 GACAAGGTCATATCACAGCTCGCTTGGATGCTTTTGAGAAAATATATGACGACCATGAT 1412
QY 756 GATCTTCCTGTAATATCAAAATTCATCATTTAGGGGATGGAAGGCTGGCTCTGTTGCC 815
Db 1413 GATTTACCTGTCAATATCAGCTTTATCATGAGGAGCGGAGGAATTCGCTTCAACAGAC 1472
QY 816 CTGGAGGAACTTGTGAAAAGAAAGAACGACCGATTTCTCTCTGCTGTGAGACTACATTTGA 875
Db 1473 CTAGATAAGTATTGGAAGGATGCAACAAA---CTCCGTGGGGCGGATTTGTTGCTC 1529
QY 876 ATTTGAGATACTGCTGGATCAGCAAGGAGGACCAATCACTTATGGAACCGCGGG 935
Db 1530 TGGGAACCAAGGACCAAAATGCTTGGAAACAGCTGGAATTTCTGCTGGCAATAAGGGG 1589
QY 936 AACAGCTACTTTCATGCTGGAGGTGAATGACAGAGCAGGATTTTCACTCAGGAACCTTT 995
Db 1590 ATTTGACCTTTGATGCCAAGGTAAAAGCGCTGATGTGGATATCCACTCGAGTTATGCT 1649
QY 996 GGTGGCATCTTTCATGAACCAATGCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1055
Db 1650 GGTGTTGGGATCAGCTCTTGGTATCTCTCCAGGCTTACAGTCTCTCTGCTGCTG-- 1707
QY 1056 TCGTCTGCTCATATCTGCT 1115
Db 1708 -CGGATGGCGGTATCTTGGTTCGAAGCTTGTACGAAGAGTACGAAGAGCCCAATGAACGA 1766
QY 1116 GAAATAAATACATACAAAGCCATCCATCTAGACCTAGAAAGATACCGGAATAGAGCCCGG 1175
Db 1767 GAAATGCGCTTGTAGAAACTTATGCTCAACGAAACCCAGAGGAGTTAGTCGGATTTAT 1826
QY 1176 GTTGAGAAATTTCTGTTCTGATATCAAGGAGGAGA-----TTCTAATGACCTCTGGAGG 1229
Db 1827 GGAATGGAGTTGCTCTCTTACAGGAGGAGCGGATGGCCCTTTCTAAAGCTTTCTTTTTC 1886
QY 1230 TACCAATCTCTTCTTATTCATGCGATCGAGGGCGGTTTGTAGAGCTCGAGCTGGAATAAACA 1289
Db 1887 GATCCAGCGCTTAATATCAAGGAATCCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1946
QY 1290 GTCATACCTGGCGGAGTTATAGAAAATTTTCAATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1349
Db 1947 ATTTTACCTGCAAGACCCAGTGCACAGCTAGAGGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2006

Qy 1350 TCTCGGTGAAACACAGGTGACACGACATCTTGA 1384
Db 2007 CATGATGTTCTGGAAAAATTCGGAACAGCTAGA 2041

RESULT 14

US-09-198-452A-1/c
; Sequence 1, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griflais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1
; LENGTH: 1230025
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
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OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature

Query Match 3.6%; Score 80; DB 4; Length 1230025;

Best Local Similarity 48.5%; Pred. No. 1.3e-08;

Matches 255; Conservative 0; Mismatches 265; Indels 6; Gaps 1;

QY 586 TCTACGCGCACTTGGAGTGCAGCTCTGACCGGGCGGATGGTGGCTCACGGACCCCT 645
|||||
Db 1136774 TCTATACCACTATGATGTGACCGACAGCTATCTGATGTGGAGGGAGATCCCT 1136715

QY 646 ATGTGCTGACGAGGTAGACGGGAACTTTATGACGAGGAGCGACCAAGGCC 705
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Db 1136714 TTATCCTTAGAAGAGATGGCAATCTCTATGCCGAGGAGCCTCTGTATAACAAAGGAC 1136655
QY 706 CTGCTTGGCTTGGATCAATGCTGTGAGCGCTTCAGAGCCCTGGAGCAAGATCTTCTG 765
Db 1136654 AATGTTTTTACACCTTAAAGGCATTACAGCACTATTACGAATCTCAAGGAAACTTCCCTC 1136595
QY 766 TGAATATCAAAATTCATATTGAGGGGATGGAAGAGGTGGCTCTGTGTGCCCTGGAGGAAC 825
Db 1136594 TAAATATATTGTTGTTAAATTGAGGGTGAAGAGAGAGTGGGAGTCTCGCATTTATTACTT 1136535
QY 826 TTGTGAAAAAGAAAAGGACCGATTCTCTCTGTGTGGACTACATTGTATTTTCAGATA 885
Db 1136534 GGTTAGAAAAAGAAAAGAGCTTT-----ACGCGGGGACTATCTTCTGTATCGTAGATG 1136481
QY 886 ACCTGTGATCAGCCAAAGGAAGCCAGCAATCACTTATGAACCCGCGGGGAACAGCTACT 945
Db 1136480 GGGGTTTCTCTTCTGAAAAACACCCCTACGTAACATTTGAGCTCGGGGTATTGTTCCA 1136421
QY 946 TCATGTTGGAGGTGAAATGCAAGACCAAGGATTTTCACTCAGGAACCTTTGGTGGCATCC 1005
Db 1136420 TGAANAATCTCCCTTGAAGAGGGGAACAAGGACATGCCTCAGGAGTTTTAGGAGGAATTG 1136361
QY 1006 TTCATGAACCAATGGCTGATCTGTTGCTCTTCTCGGTAGCTGGTAGACTCTCTGGTC 1065
Db 1136360 CCTACAATACGAATCGTCTTTATCAGAAATTTCTGAGCTCTCTGCATCACCCCTGACAATT 1136301
QY 1066 ATATCCTGTCCTCGGAATCTATGATGAAGTGTTCCTCTTACAGA 1111
Db 1136300 CTATAGCTATTGAAGGATTTTATGATGATCTCTCTCCCCCTCGGA 1136255

RESULT 15

US-09-438-185A-1/c

; Sequence 1, Application US/09438185A

; Patent No. 6822071

; GENERAL INFORMATION:

; APPLICANT: Stephens, Richard

; APPLICANT: Mitchell, Wayne

; APPLICANT: Kalman, Sue

; APPLICANT: Davis, Ronald

; APPLICANT: The Regents of the University of California

; TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence

; FILE REFERENCE: 018941-000411US

; CURRENT APPLICATION NUMBER: US/09/438,185A

; CURRENT FILING DATE: 2002-03-13

; PRIOR APPLICATION NUMBER: US 60/108,279

; PRIOR FILING DATE: 1998-11-12

; PRIOR APPLICATION NUMBER: US 60/128,606

; PRIOR FILING DATE: 1999-04-08

; NUMBER OF SEQ ID NOS: 1074

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 1

; LENGTH: 1230230

; TYPE: DNA

; ORGANISM: Chlamydia pneumoniae

US-09-438-185A-1

Query Match 3.6%; Score 80; DB 4; Length 1230230;

Best Local Similarity 48.5%; Pred. No. 1.3e-08;

Matches 255; Conservative 0; Mismatches 265; Indels 6; Gaps 1;

QY 586 TCTACGCGCACTTGGAGTGCAGCTCTGACCGGGCGGATGGTGGCTCACGGACCCCT 645
|||||
Db 1126624 TCTATAACCACCTATGATGTGACCGACGACAGCTATCTGATGTGGAGGGAGATCCCT 1126565

QY 646 ATGTGCTGACGAGGTAGACGGGAACTTTATGACGAGGAGCGACCAAGGCC 705

Db 1126564 TTATCCTTAGAAGAGAGATGGCAATCTCTATGCCGAGAGGCTCTGTATACAAAGGAC 1126505

QY 706 CTGCTTGTGGCTTGGATCAATGTGTGAGCGCTTTCAGAGCCCTGGAGCAAGATCTTCTG 765

Db 1126504 AATGTTTTTACACCTTAAAGGCATTACAGCACTATTACGAATCTCAAGGAAACTTCCCTC 1126445

Qy 766 TGAATATCAAAATTCATATTGAGGGATGGAAGGCTGGCTCTGTGGCCCTGGAGGAAC 825
Db 1126444 TAAATATTTATTGGTTAATTGAGGGTGAAGAAGAGAGTGGGAGTCTCGCATTTATTACTT 1126385
Qy 826 TTGTGGAAGAAAGAACCGATTCTTCTCTGGTGTGGACTACATTCTTAATTTTCAGATA 885
Db 1126384 GGTAGAAAAGAAAAGAAAGCTTT-----ACGGCGGACTATCTTCTGATCGTAGATG 1126331
Qy 886 ACCTGTGGATCAGCCAAAGCAAGCCAGCAATCATTATGAAACCCGGGGAAACAGCTACT 945
Db 1126330 GGGGTTTCCTTTCTGAAAAACACCCCTACGTAAGCATTGGAGCTCGGGTATTGTTCCA 1126271
Qy 946 TCATGGTGGAGGTGAATGCGAGACACCGAGATTTTCACTCAGGAACCTTTGGTGGCATCC 1005
Db 1126270 TGAATACTCCCTTTGAAGAGGGGAACAAGGACATGCATCAGGAGTTTTTAGGAGGAATTG 1126211
Qy 1006 TTCATGAACCAATGGCTGATCTGGTTGCTCTTCTCGGTAGCCTGTAGACTCGTCTGGTC 1065
Db 1126210 CCTACAATACGAATCGTGCTTTATCAGAAATTCGAGCTCTCTGCATCACCCCTGACAAT 1126151
Qy 1066 ATATCCTGGTCCCTGGAAATCTATGATGAAGTGGTTCTCTTTACAGA 1111
Db 1126150 CTATAGCTATTGAAGGATTTTATGATGATCTTGCTCTCCCTCCGGA 1126105

Search completed: February 13, 2005, 23:21:02
Job time : 318 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 13, 2005, 12:41:51 ; Search time 6549 Seconds
(without alignments)
16588.272 Million cell updates/sec

Title: US-10-036-342-56

Perfect score: 2242

Sequence: 1 gaatgaataacctccgaagcc.....aaaaaaaaaaaaaaaaaaaaa 2242

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_ats.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2241	100.0	2242	9	AX358756 Homo sapi
2	2182.8	97.4	2784	6	AX527744 Sequence
3	2147.4	95.8	2235	6	AX059560 Sequence
4	2135.6	95.3	2152	6	BD205653 97 human
5	1877.6	83.7	1970	9	AX098369 Homo sapi
6	1616	72.1	1640	9	AXA417564 Homo sapi
7	1531.6	68.3	1587	6	AX231101 Sequence
8	1531.6	68.3	1587	6	AX231560 Sequence
9	1531.6	68.3	1587	6	AX232218 Sequence
10	1531.6	68.3	1587	6	AX233356 Sequence
11	1524	68.0	1524	6	AX138669 Sequence
12	1521	67.8	1521	6	AX527746 Sequence
13	1506.4	67.2	1524	6	AX139747 Sequence
14	1031.2	46.0	2675	10	BC081877 Rattus no
15	1006.2	44.9	2774	10	BC043305 Mus muscu.
16	672.6	30.0	1692	5	BC043305 Mus muscu.
17	612.8	27.3	672	6	AX931960 Gallus ga
18	612.8	27.3	672	6	AX931960 Gallus ga
19	612.8	27.3	672	6	AX969294 Sequence
					BD108013 EST and e

BC060450 Xenopus l	5	BC060450	3060	25.6	575	20
AC127485 Homo sapi	2	AC127485	175905	23.5	527.8	21
AC116904 Homo sapi	2	AC116904	164394	23.4	524.6	22
CQ845803 Sequence	6	CQ845803	3755	23.1	518	23
AK131263 Homo sapi	9	AK131263	3755	24	518	24
AY166869 Xenopus l	5	AY166869	1574	22.5	504.4	25
AY18285 Xenopus l	5	AY18285	1593	22.5	504.4	26
BC055979 Xenopus l	5	BC055979	1652	22.5	504.4	27
BC045077 Xenopus l	5	BC045077	1567	22.4	502.8	28
BC075171 Xenopus l	5	BC075171	1592	22.3	500.4	29
BC064197 Xenopus t	5	BC064197	1616	22.2	498	30
BC056069 Xenopus t	5	BC056069	1615	22.1	495.6	31
BC064175 Xenopus t	5	BC064175	1629	21.7	485.4	32
BC076079 Dario rer	5	BC076079	2076	21.6	484.4	33
BC005532 Mus muscu	10	BC005532	2152	21.6	484.4	34
AB046738 Mus muscu	10	AB046738	2050	21.5	482.8	35
AK131124 Mus muscu	10	AK131124	2033	21.3	477.2	36
AY391414 Dario rer	5	AY391414	2056	21.0	470.4	37
AX427498 Sequence	6	AX427498	1879	20.9	469.4	38
AJ347717 Homo sapi	6	AJ347717	1527	20.9	469	39
AX235623 Sequence	6	AX235623	2221	20.9	469	40
BC003176 Homo sapi	9	BC003176	2565	20.9	469	41
BC001375 Homo sapi	9	BC001375	2635	20.9	469	42
BD156591 Primer fo	6	BD156591	2643	20.9	469	43
AX398119 Sequence	6	AX398119	2643	20.9	469	44
AX877308 Sequence	6	AX877308	2643	20.9	469	45
AX001692 Homo sapi	6	AX001692	2643	20.9	469	46
AX319871 Sequence	6	AX319871	1428	20.9	467.8	47
AX398114 Sequence	6	AX398114	1428	20.9	467.8	48
AX523938 Sequence	6	AX523938	1428	20.9	467.8	49
AR339440 Sequence	6	AR339440	2710	20.8	466.4	50
AK097155 Homo sapi	9	AK097155	2749	20.8	466.2	51
AJ719629 Gallus ga	3	AJ719629	2090	20.5	460.4	52
AY118368 Drosophil	3	AY118368	1703	16.9	378.8	53
CQ715173 Sequence	6	CQ715173	1365	16.9	378.2	54
AR509409 Sequence	6	AR509409	1489	16.6	373.2	55
CQ597783 Sequence	6	CQ597783	1347	15.5	348.2	56
CQ597789 Sequence	6	CQ597789	1389	15.5	348.2	57
AF258592 Homo sapi	9	AF258592	2364	14.9	334.8	58
BD156089 Primer fo	6	BD156089	2005	14.5	325.6	59
AX876362 Sequence	6	AX876362	2005	14.5	325.6	60
AK001262 Homo sapi	9	AK001262	2005	14.5	325.6	61
AX595118 Sequence	6	AX595118	1446	13.6	304.2	62
AX819122 Sequence	6	AX819122	1446	13.6	304.2	63
AX830152 Sequence	6	AX830152	1446	13.6	304.2	64
AY692702 Saccharom	8	AY692702	1446	13.6	304.2	65
DS0617 Saccharomyc	8	YSCCHRVIN	270148	13.6	304.2	66
AX294028 Neurospor	8	NC103E1	87435	13.1	293.2	67
AX898087 Sequence	6	AX898087	300	13.1	292.8	68
BD033620 Sequence	6	BD033620	300	13.1	292.8	69
Continuation (9 of	8	AE016819_08	110000	12.6	281.8	70
BD156936 Primer fo	6	BD156936	1920	12.5	281	71
AX877943 Sequence	6	AX877943	1920	12.5	281	72
AX001983 Homo sapi	9	AX001983	1920	12.5	281	73
Continuation (24 o	8	CR382132_23	110000	12.5	280.4	74
CQ715367 Sequence	6	CQ715367	279	12.4	279	75
CR382121 Klyuverom	8	CR382121_00	279	12.4	268.4	76
AL355921 Schizosac	8	SPBC1198	26756	11.2	252	77
U33008 Schizosacch	8	SPU33008	37596	11.2	252	78
U33010 Schizosacch	8	SPU33010	85837	11.2	252	79
Continuation (17 o	8	CR382139_16	110000	10.8	241.4	80
Continuation (3 of	8	CR380949_2	4519	10.3	234.4	81
AK024471 Homo sapi	9	AK024471	1162	10.2	231.4	82
D89150 Schizosacch	8	D89150	178631	10.0	227.5	83
AC009704 Homo sapi	9	AC009704	1479	10.0	225	84
AK545521 Sequence	6	AK545521	3538	10.0	224.8	85
CQ597788 Sequence	6	CQ597788	4027	10.0	224.2	86
AC018050 Drosophil	3	AC018050	26596	10.0	224.2	87
AC007477 Drosophil	3	AC007477	171334	10.0	224.2	88
AC007054 Drosophil	3	AC007054	176510	10.0	224.2	89
AE003785 Drosophil	3	AE003785	301129	10.0	224.2	90
BD147408 Primer fo	6	BD147408	774	9.9	222	91
					222	92

93	222	9.9	774	6	AX867346	Sequence	166	96.4	4.3	273	6	AR137594	AR137594 Sequence
94	208.4	9.3	40487	3	AY190950	Drosophila	167	96	4.3	110000	1	AP006841_43	Continuation (44 o
95	205.4	9.2	568	6	AX398096	Sequence	168	95.4	4.3	299050	1	AX398096	Continuation (44 o
96	205.4	9.2	594	6	AX398095	Sequence	169	93.8	4.2	168128	5	AX398095	Continuation (44 o
97	204.8	9.1	701	6	AX398092	Sequence	170	93.8	4.2	176850	2	AX398092	Continuation (44 o
98	204.2	9.1	83253	3	AY186999	Drosophila	171	93.8	4.2	215910	2	AX398099	Continuation (44 o
99	203.4	9.1	64201	2	AC117833	Homo sapi	172	93.2	4.2	136886	2	AC117833	Continuation (44 o
100	203.4	9.1	64201	2	AC117833	Homo sapi	173	92.2	4.1	334	6	AX906268	Continuation (44 o
101	191.8	8.6	699	6	AX398102	Sequence	174	92.2	4.1	334	6	BD041801	Continuation (44 o
102	188.2	8.4	514	6	AX398099	Sequence	175	91.4	4.1	134405	2	AC113582	Continuation (44 o
103	186.8	8.3	554	5	AY260749	Oreochrom	176	91.2	4.1	206423	2	AC113582	Continuation (44 o
104	181.6	8.1	606	6	AX398093	Sequence	177	89.6	4.0	110000	1	AX908798_15	Continuation (44 o
105	180.8	8.1	623	6	AX398094	Sequence	178	88.8	4.0	11431	1	AX908798_15	Continuation (44 o
106	178.4	8.0	640	6	AX398097	Sequence	179	88.8	4.0	15085	1	AE002038	Continuation (44 o
107	174.4	7.8	704	6	BD149742	Primer fo	180	88.4	3.9	87166	2	AC098644	Continuation (44 o
108	174.4	7.8	704	6	AX869680	Sequence	181	88.4	3.9	97166	2	AC098644	Continuation (44 o
109	172.6	7.7	613	6	AX398098	Sequence	182	86.6	3.9	301731	1	AE016934	Continuation (44 o
110	169.4	7.6	73476	2	AC123772	Homo sapi	183	85.8	3.8	1371	6	AX566904	Continuation (44 o
111	165.6	7.4	19383	3	CER11H6	Sequence	184	85.8	3.8	1374	6	AX566904	Continuation (44 o
112	165.2	7.4	149982	2	AC148745	Sequence	185	85.8	3.8	3766	6	AX481264	Continuation (44 o
113	165.2	7.4	162565	2	AC148810	Bos tauru	186	85.8	3.8	3766	6	AX481264	Continuation (44 o
114	158	7.0	249832	2	AC096927	Sequence	187	85.8	3.8	3766	6	AX481264	Continuation (44 o
115	158	7.0	255946	2	AC126480	Rattus no	188	85.8	3.8	3766	6	AX481264	Continuation (44 o
116	157.4	7.0	754	6	BD148888	Primer fo	189	85.8	3.8	10146	1	AE007331	Continuation (44 o
117	157.4	7.0	754	6	AX868826	Sequence	190	85.8	3.8	175936	2	SPNEU1908	Continuation (44 o
118	154.8	6.9	148033	2	AC121513	Mus muscu	191	85.8	3.8	349980	6	AX571760	Continuation (44 o
119	154.4	6.9	20066	9	BC047599	Homo sapi	192	84.8	3.8	52514	2	AC149165	Continuation (44 o
120	153.2	6.8	218336	2	AC094007	Rattus no	193	84.8	3.8	53496	2	AC149150	Continuation (44 o
121	153	6.8	73476	2	AC123772	Homo sapi	194	84.2	3.8	11612	1	AE008398	Continuation (44 o
122	152.8	6.8	1467	9	BC065925	Homo sapi	195	81.8	3.7	320150	1	AP005033	Continuation (44 o
123	150.2	6.7	558	6	AX398100	Sequence	196	81	3.6	311000	1	SC093122	Continuation (44 o
124	150	6.7	179254	2	AC149168	Sequence	197	81	3.6	110000	1	AP006840_14	Continuation (44 o
125	146.4	6.5	128095	2	AC148812	Sequence	198	80	3.6	10968	1	AE002246	Continuation (44 o
126	145.2	6.5	43541	3	CBR002A05	Sequence	199	80	3.6	13485	1	AE001678	Continuation (44 o
127	143	6.4	665	6	AX398101	Sequence	200	80	3.6	110000	6	AR310754_11	Continuation (44 o
128	140	6.2	495	6	AX398103	Sequence	201	80	3.6	324746	1	AE017160	Continuation (44 o
129	134.2	6.0	305153	1	AP001520	Bacillus	202	80	3.6	325665	1	AP002548	Continuation (44 o
130	132.2	5.9	561	11	BV063773	S212P6035	203	79.8	3.6	3820	6	AR227379	Continuation (44 o
131	130.6	5.8	172828	10	AC124187	Mus muscu	204	79.8	3.6	26309	6	CQ363747	Continuation (44 o
132	129.6	5.8	886	6	BD134445	Human nuc	205	79.8	3.6	110000	1	AE017283_21	Continuation (44 o
133	129.6	5.8	886	6	AX017274	Sequence	206	78.8	3.5	110000	8	AE016818_03	Continuation (44 o
134	129.6	5.8	886	6	AX524978	Sequence	207	78.2	3.5	110000	8	CR382137_05	Continuation (44 o
135	129.6	5.8	1638	6	BD134485	Human nuc	208	78	3.5	2138	10	BC039782	Continuation (44 o
136	129.6	5.8	1638	6	AX017395	Sequence	209	77.8	3.5	474	6	AR412920	Continuation (44 o
137	129.6	5.8	1638	6	AX525089	Sequence	210	77.8	3.5	474	6	AX969754	Continuation (44 o
138	128.4	5.7	518	6	AX398108	Sequence	211	77.8	3.5	474	6	BD108473	Continuation (44 o
139	128.2	5.7	464	6	AX398104	Sequence	212	77.2	3.4	3348	10	BC066211	Continuation (44 o
140	126	5.6	127	11	G42956	WRAF-817-ST	213	76.8	3.4	409	6	AX885762	Continuation (44 o
141	125.2	5.6	536	6	AX398112	Sequence	214	76.8	3.4	409	6	BD025372	Continuation (44 o
142	124.4	5.5	366	6	AX398109	Sequence	215	76.8	3.4	464	6	AX885761	Continuation (44 o
143	121.8	5.4	512	6	AX398113	Sequence	216	76.8	3.4	464	6	BD025371	Continuation (44 o
144	120.2	5.4	402	6	AX398107	Sequence	217	75.8	3.4	110000	8	CR382128_12	Continuation (44 o
145	119.6	5.3	345	6	AX398111	Sequence	218	74.2	3.3	1739	8	PCU42442	Continuation (44 o
146	119.6	5.3	380	6	AX398110	Sequence	219	74.2	3.3	1826	8	AF196975	Continuation (44 o
147	119.6	5.3	143786	3	AC024859	Caenorhab	220	73.8	3.3	171260	2	CR812474	Continuation (44 o
148	119.6	5.3	298960	2	AC006896	Caenorhab	221	73.6	3.3	110000	2	AC119727_0	Continuation (44 o
149	118.2	5.3	386	6	AX398106	Sequence	222	73.4	3.3	2382	9	BC050393	Continuation (44 o
150	118	5.3	110000	1	AP006840_13	Continuation (14 o	223	72.6	3.2	75284	2	AX927314	Continuation (44 o
151	116.2	5.2	12249	1	AE002039	Deinococc	224	72	3.2	467	6	CQ397777	Continuation (44 o
152	112.6	5.0	387	6	AX398105	Sequence	225	72	3.2	467	6	CQ404074	Continuation (44 o
153	108.6	4.8	654	6	CQ411141	Sequence	226	72	3.2	1178	10	BC048734	Continuation (44 o
154	108.2	4.8	259335	2	AC126194	Rattus no	227	72	3.2	2550	9	HSMB01250	Continuation (44 o
155	103.6	4.6	465	6	CQ398470	Sequence	228	72	3.2	2852	6	AX868768	Continuation (44 o
156	103.6	4.6	465	6	CQ404757	Sequence	229	71.8	3.2	1135	4	AF119337	Continuation (44 o
157	103.6	4.6	301933	1	AE017174	Sequence	230	71.8	3.2	1993	9	BC063485	Continuation (44 o
158	103	4.6	255446	2	AC095420	Rattus no	231	71.8	3.2	4396	10	BC058991	Continuation (44 o
159	100.4	4.5	52514	2	AC149165	Xenopus t	232	71.8	3.2	254733	3	AC117075	Continuation (44 o
160	100.4	4.5	70137	2	AC149160	Xenopus t	233	71.6	3.2	1625	9	BC072433	Continuation (44 o
161	100.4	4.5	90513	2	AC149162	Xenopus t	234	71.4	3.2	760	11	G09488	Continuation (44 o
162	97.6	4.4	110000	8	CR382132_09	Continuation (10 o	235	71.4	3.2	110000	8	CR382139_15	Continuation (44 o
163	96.4	4.3	273	6	AR008079	Sequence	236	71.2	3.2	861	9	BC009550	Continuation (44 o
164	96.4	4.3	273	6	AR102193	Sequence	237	71.2	3.2	2580	9	BC062567	Continuation (44 o
165	96.4	4.3	273	6	AR102204	Sequence	238	71	3.2	2087	10	BC054081	Continuation (44 o

c 239	70.8	3.2	535	6	CQ524536	CQ524536 Sequence	312	68.2	3.0	2417	9	BC050684	Homo sapi
240	70.6	3.2	1461	5	BC064230	BC064230 Xenopus t	313	68.2	3.0	3396	10	BC030323	Mus muscu
c 241	70.6	3.1	110000	15	Continuation (16 o	Continuation (16 o	314	68.2	3.0	4402	10	BC058080	Mus muscu
242	70.4	3.1	580	6	CQ526169	CQ526169 Sequence	315	68.2	3.0	85165	8	NCB18D24	Neurospor
243	70.4	3.1	2228	10	BC023765	BC023765 Mus muscu	c 316	68.2	3.0	157180	8	NCB18D24	Neurospor
244	70.4	3.1	300050	1	AP004596	AP004596 Oceanobac	c 317	68.2	3.0	157180	8	NCB18D24	Neurospor
245	70.2	3.1	725	5	BC049478	BC049478 Danio rer	c 318	68	3.0	636	6	CQ566958	Sequence
246	70.2	3.1	790	10	BC038163	BC038163 Mus muscu	c 319	68	3.0	850	6	CQ566958	Sequence
247	70.2	3.1	1527	6	BD227255	BD227255 Secreted	320	68	3.0	850	6	CQ566958	Sequence
248	70.2	3.1	1580	6	BD231696	BD231696 31 human	321	68	3.0	867	9	BC042105	Homo sapi
c 249	70	3.1	381	6	CQ472479	CQ472479 Sequence	322	68	3.0	1009	9	BC065500	Homo sapi
250	69.8	3.1	2690	10	BC058562	BC058562 Mus muscu	323	68	3.0	1240	9	BC073164	Homo sapi
c 251	69.8	3.1	425	6	CQ408472	CQ408472 Sequence	324	68	3.0	1690	6	E32442	Mammal-deri
c 252	69.8	3.1	491	6	CQ397758	CQ397758 Sequence	325	68	3.0	1800	5	BC066699	Danio rer
c 253	69.8	3.1	491	6	CQ404055	CQ404055 Sequence	326	68	3.0	2184	5	BC068356	Danio rer
254	69.8	3.1	1056	3	AY069036	AY069036 Drosophil	c 327	67.8	3.0	309	6	CQ511416	Sequence
255	69.8	3.1	2005	9	BSM803426	BSM803426 Homo sapi	328	67.8	3.0	429	6	CQ525026	Sequence
c 256	69.8	3.1	331039	3	AC116979	AC116979 Dictyoste	329	67.8	3.0	556	6	CQ508215	Sequence
257	69.6	3.1	908	5	BC084191	BC084191 Xenopus t	330	67.8	3.0	556	6	CQ508315	Sequence
258	69.6	3.1	1242	10	BC062228	BC062228 Rattus no	331	67.8	3.0	556	6	CQ510257	Sequence
259	69.6	3.1	1880	9	AB060863	AB060863 Macaca fa	332	67.8	3.0	556	6	CQ511753	Sequence
c 260	69.4	3.1	287	6	CQ422263	CQ422263 Sequence	333	67.8	3.0	809	9	BC063537	Homo sapi
261	69.4	3.1	2279	10	BC025490	BC025490 Mus muscu	334	67.8	3.0	834	9	BC063494	Homo sapi
262	69.4	3.1	142668	2	CR407568	CR407568 Danio rer	335	67.8	3.0	1018	3	BT003804	Drosophil
c 263	69.4	3.1	164335	2	BX950865	BX950865 Danio rer	336	67.8	3.0	1061	8	BT009502	Triticum
c 264	69.2	3.1	621	6	AX187131	AX187131 Sequence	337	67.8	3.0	1230	5	BC071358	Danio rer
c 265	69.2	3.1	1374	5	BC053159	BC053159 Danio rer	338	67.8	3.0	1568	10	BC048399	Mus muscu
266	69.2	3.1	1946	5	BC077411	BC077411 Xenopus t	339	67.8	3.0	1607	3	AK174679	Ciona int
267	69.2	3.1	2534	10	BC066224	BC066224 Mus muscu	340	67.8	3.0	2117	9	BC016320	Homo sapi
268	69.2	3.1	4250	5	BSM803434	BSM803434 Homo sapi	341	67.8	3.0	5770	5	BC059180	Danio rer
269	69	3.1	1095	5	BC066469	BC066469 Danio rer	c 342	67.8	3.0	216474	2	AC139414	Rattus no
270	69	3.1	1490	9	BC001236	BC001236 Homo sapi	343	67.6	3.0	575	6	BD269743	50 human
271	69	3.1	1619	9	BC032001	BC032001 Homo sapi	344	67.6	3.0	1194	9	BC016139	Homo sapi
272	69	3.1	1684	9	BC064148	BC064148 Homo sapi	345	67.6	3.0	1227	10	BC049617	Mus muscu
273	69	3.1	2247	8	VFA011303	VFA011303 Vicia fab	346	67.6	3.0	1271	9	BC029647	Homo sapi
c 274	69	3.1	2466	9	BSM802197	BSM802197 Homo sapi	347	67.6	3.0	1461	9	BC063130	Homo sapi
c 275	68.8	3.1	392	6	CQ395758	CQ395758 Sequence	348	67.6	3.0	1478	5	BC067687	Danio rer
c 276	68.8	3.1	392	6	CQ402088	CQ402088 Sequence	349	67.6	3.0	1497	9	AB048888	Macaca fa
c 277	68.8	3.1	708	5	AY190729	AY190729 Pagrus ma	350	67.6	3.0	1638	9	BC034291	Homo sapi
278	68.8	3.1	1051	9	AK026408	AK026408 Homo sapi	351	67.6	3.0	1661	9	BC025755	Homo sapi
279	68.8	3.1	2325	5	BC065681	BC065681 Danio rer	352	67.6	3.0	1912	10	BC027060	Mus muscu
280	68.8	3.1	2369	9	AK026627	AK026627 Homo sapi	c 353	67.6	3.0	1932	6	AK026947	Homo sapi
c 281	68.6	3.1	492	6	CQ410352	CQ410352 Sequence	354	67.6	3.0	3899	6	BD191414	Secreted
c 282	68.6	3.1	550	6	AX185654	AX185654 Sequence	355	67.6	3.0	4116	5	BC075557	Xenopus t
c 283	68.6	3.1	2055	9	BC008485	BC008485 Homo sapi	356	67.6	3.0	4493	9	BC064843	Homo sapi
284	68.6	3.1	2675	9	BC033734	BC033734 Homo sapi	357	67.6	3.0	4519	9	BC055007	Homo sapi
c 285	68.4	3.1	396	6	AK391193	AK391193 Sequence	358	67.6	3.0	9330	3	AF466305	Dictyoste
c 286	68.4	3.1	396	6	AR392898	AR392898 Sequence	c 359	67.6	3.0	110000	3	AC116957_2	Continuation (3 of
c 287	68.4	3.1	396	6	AR489628	AR489628 Sequence	360	67.4	3.0	453	6	CQ524875	Sequence
c 288	68.4	3.1	396	6	AR493869	AR493869 Sequence	c 361	67.4	3.0	545	6	AX185705	Xenopus t
c 289	68.4	3.1	396	6	AX093198	AX093198 Sequence	362	67.4	3.0	1951	5	BC084252	Xenopus t
290	68.4	3.1	615	10	BC043668	BC043668 Mus muscu	363	67.4	3.0	2607	9	BC024261	Homo sapi
291	68.4	3.1	627	9	BC023973	BC023973 Homo sapi	364	67.4	3.0	4176	9	BSM807871	Sequence
c 292	68.4	3.1	647	6	CQ397898	CQ397898 Sequence	365	67.4	3.0	4397	6	CQ498439	Sequence
c 293	68.4	3.1	647	6	CQ404191	CQ404191 Sequence	366	67.4	3.0	4485	10	BC052459	Mus muscu
294	68.4	3.1	1323	6	BD180179	BD180179 Highly th	367	67.4	3.0	4655	10	BC064463	Mus muscu
295	68.4	3.1	1993	9	BC013377	BC013377 Homo sapi	c 368	67.4	3.0	300955	1	AE016996	Chlamydo
296	68.4	3.1	2055	8	TAU48227	TAU48227 Triticum ae	c 369	67.2	3.0	234	6	CQ481603	Sequence
297	68.4	3.1	2161	9	BC034395	BC034395 Homo sapi	c 370	67.2	3.0	376	6	CQ524552	Sequence
c 298	68.4	3.1	2239	6	AR174875	AR174875 Sequence	371	67.2	3.0	916	5	BC082880	Xenopus t
299	68.4	3.1	2239	6	AR174875	AR174875 Sequence	372	67.2	3.0	1043	6	AX188197	Sequence
300	68.4	3.1	2239	6	BD008446	BD008446 Nucleic a	373	67.2	3.0	1091	6	AR271010	Sequence
301	68.4	3.1	2239	6	BD008446	BD008446 Nucleic a	374	67.2	3.0	1091	6	AX053122	Sequence
302	68.4	3.1	2771	6	BD209997	BD209997 Nucleic a	375	67.2	3.0	1101	9	BC050400	Homo sapi
303	68.4	3.1	2771	6	AX010492	AX010492 Sequence	376	67.2	3.0	1343	5	BC057508	Danio rer
304	68.4	3.1	3232	9	AF090901	AF090901 Homo sapi	377	67.2	3.0	1720	5	BC056713	Danio rer
c 305	68.4	3.1	110000	3	AC116984	AC116984 Dictyoste	378	67.2	3.0	1820	9	BC035606	Homo sapi
306	68.4	3.1	202089	2	CR382364	CR382364 Danio rer	379	67.2	3.0	1893	10	BC022165	Mus muscu
c 307	68.2	3.0	327	6	CQ395651	CQ395651 Sequence	380	67.2	3.0	2207	10	BC066857	Mus muscu
c 308	68.2	3.0	327	6	CQ401984	CQ401984 Sequence	381	67.2	3.0	2356	10	BC061208	Mus muscu
309	68.2	3.0	420	8	CNS01B5E	CU113802 Botrytis	382	67.2	3.0	2465	9	BC040164	Homo sapi
310	68.2	3.0	1069	10	BC008653	BC008653 Mus muscu	383	67.2	3.0	2672	9	BC035512	Homo sapi
311	68.2	3.0	2258	5	BC054598	BC054598 Danio rer	384	67.2	3.0	2684	9	BSM805935	Homo sapi

385	67.2	3.0	2923	8	ATHSP91	Z70314 A.thaliana	458	66.4	3.0	1906	10	BC007169	BC007169 Mus muscu
386	67.2	3.0	3047	5	BC056574	BC056574 Danio rer	459	66.4	3.0	1927	6	AR214141	AR214141 Sequence
387	67.2	3.0	3585	10	BC063072	BC063072 Mus muscu	460	66.4	3.0	1960	9	BC064376	BC064376 Homo sapi
388	67.2	3.0	4041	5	BC080392	BC080392 Xenopus l	461	66.4	3.0	2034	9	BC037974	BC037974 Homo sapi
389	67	3.0	346	6	BC039807	BC039807 Sequence	462	66.4	3.0	2438	10	BC075617	BC075617 Mus muscu
390	67	3.0	346	6	CQ404361	CQ404361 Sequence	463	66.4	3.0	2703	5	BC084491	BC084491 Xenopus t
391	67	3.0	404	6	CQ245456	CQ245456 Sequence	464	66.4	3.0	3183	9	BC037327	BC037327 Homo sapi
392	67	3.0	461	6	CQ410708	CQ410708 Sequence	465	66.4	3.0	4515	5	AB047853	AB047853 Gallus ga
393	67	3.0	768	6	CQ415516	CQ415516 Sequence	466	66.4	3.0	4587	5	AB047852	AB047852 Gallus ga
394	67	3.0	1006	9	AF111112	AF111112 Homo sapi	467	66.4	3.0	8177	9	BSM805964	BSM805964 Homo sapi
395	67	3.0	1169	10	BC055454	BC055454 Mus muscu	468	66.2	3.0	379	6	CQ427910	CQ427910 Sequence
396	67	3.0	1309	9	BC009884	BC009884 Homo sapi	469	66.2	3.0	470	6	CQ523311	CQ523311 Sequence
397	67	3.0	1674	9	BC050418	BC050418 Homo sapi	470	66.2	3.0	476	6	CQ397629	CQ397629 Sequence
398	67	3.0	1709	3	AK174332	AK174332 Clona int	471	66.2	3.0	476	6	CQ403928	CQ403928 Sequence
399	67	3.0	1709	9	BC032784	BC032784 Homo sapi	472	66.2	3.0	476	6	CQ422235	CQ422235 Sequence
400	67	3.0	1925	6	BD195666	BD195666 70 human	473	66.2	3.0	723	6	CQ397655	CQ397655 Sequence
401	67	3.0	1925	6	CQ775711	CQ775711 Sequence	474	66.2	3.0	723	6	CQ403953	CQ403953 Sequence
402	67	3.0	1925	6	AR352721	AR352721 Sequence	475	66.2	3.0	724	5	BC082953	BC082953 Xenopus l
403	67	3.0	2554	10	BC022172	BC022172 Mus muscu	476	66.2	3.0	810	6	CQ398775	CQ398775 Sequence
404	67	3.0	2635	10	BC032204	BC032204 Mus muscu	477	66.2	3.0	810	6	CQ405056	CQ405056 Sequence
405	67	3.0	3447	9	BC052983	BC052983 Homo sapi	478	66.2	3.0	1152	9	BC015991	BC015991 Homo sapi
406	67	3.0	3700	5	BC084282	BC084282 Xenopus l	479	66.2	3.0	1152	9	BC021621	BC021621 Homo sapi
407	67	3.0	3964	5	BC077739	BC077739 Xenopus l	480	66.2	3.0	1378	6	BD191241	BD191241 186 human
408	67	3.0	5441	3	AC115584	AC115584 Dictyoste	481	66.2	3.0	1378	6	AX924751	AX924751 Sequence
409	66.8	3.0	330	6	CQ410575	CQ410575 Sequence	482	66.2	3.0	1487	5	BC079692	BC079692 Xenopus l
410	66.8	3.0	445	6	CQ395672	CQ395672 Sequence	483	66.2	3.0	1674	3	AY070845	AY070845 Drosophil
411	66.8	3.0	445	6	CQ402005	CQ402005 Sequence	484	66.2	3.0	1674	3	BC028200	BC028200 Homo sapi
412	66.8	3.0	610	6	CQ398031	CQ398031 Sequence	485	66.2	3.0	2323	6	BD191059	BD191059 186 human
413	66.8	3.0	610	6	CQ404323	CQ404323 Sequence	486	66.2	3.0	2323	6	AX924569	AX924569 Sequence
414	66.8	3.0	693	9	BC042451	BC042451 Homo sapi	487	66.2	3.0	2335	6	BC045171	BC045171 Homo sapi
415	66.8	3.0	1564	9	AB125186	AB125186 Macaca fa	488	66.2	3.0	2411	5	BC071111	BC071111 Xenopus l
416	66.8	3.0	1689	5	BC044066	BC044066 Xenopus l	489	66.2	3.0	2505	10	BC061964	BC061964 Rattus no
417	66.8	3.0	1689	5	BC044066	BC044066 Xenopus l	490	66.2	3.0	2800	9	BC014632	BC014632 Homo sapi
418	66.8	3.0	1693	10	BC051454	BC051454 Mus muscu	491	66.2	3.0	2800	9	BC074650	BC074650 Xenopus t
419	66.8	3.0	1742	5	BC074598	BC074598 Xenopus t	492	66.2	3.0	3507	9	BC047450	BC047450 Homo sapi
420	66.8	3.0	1844	9	BC007718	BC007718 Homo sapi	493	66.2	3.0	4146	10	BC058389	BC058389 Mus muscu
421	66.8	3.0	4438	10	BC067016	BC067016 Mus muscu	494	66.2	3.0	4336	10	BC079878	BC079878 Mus muscu
422	66.8	3.0	6155	5	AX323748	AX323748 Sequence	495	66.2	3.0	4372	10	BC054749	BC054749 Mus muscu
423	66.8	3.0	183648	3	AC117081	AC117081 Dictyoste	496	66.2	3.0	6742	5	BC081543	BC081543 Xenopus t
424	66.8	3.0	196	9	IROEST145	AL839939 Homo sapi	497	66.2	3.0	146570	3	AC117076	AC117076 Dictyoste
425	66.6	3.0	291	6	CQ399019	CQ399019 Sequence	498	66.2	3.0	164335	2	AX950865	AX950865 Danio rer
426	66.6	3.0	291	6	CQ405298	CQ405298 Sequence	499	66.2	3.0	309267	1	AE017235	AE017235 Mycobacte
427	66.6	3.0	310	6	AX440309	AX440309 Sequence	500	66	2.9	375	6	CQ513063	CQ513063 Sequence
428	66.6	3.0	390	6	CQ410737	CQ410737 Sequence	501	66	2.9	384	6	CQ395463	CQ395463 Sequence
429	66.6	3.0	445	6	CQ410337	CQ410337 Sequence	502	66	2.9	384	6	CQ401799	CQ401799 Sequence
430	66.6	3.0	601	8	ATH245866	AX245866 Arabidops	503	66	2.9	464	6	CQ471935	CQ471935 Sequence
431	66.6	3.0	688	6	CQ422987	CQ422987 Sequence	504	66	2.9	656	5	BC081675	BC081675 Danio rer
432	66.6	3.0	936	6	BD107846	BD107846 36 human	505	66	2.9	656	5	BSM805497	BSM805497 Homo sapi
433	66.6	3.0	2150	10	BC080776	BC080776 Mus muscu	506	66	2.9	706	9	BC054047	BC054047 Homo sapi
434	66.6	3.0	2326	5	BC073076	BC073076 Xenopus l	507	66	2.9	830	9	BC041445	BC041445 Homo sapi
435	66.6	3.0	2350	9	BC038457	BC038457 Homo sapi	508	66	2.9	890	9	BC014163	BC014163 Homo sapi
436	66.6	3.0	2768	9	BSM803699	AL833291 Homo sapi	509	66	2.9	1181	6	BD191338	BD191338 186 human
437	66.6	3.0	2826	6	BC040919	BC040919 Homo sapi	510	66	2.9	1181	6	AX924848	AX924848 Sequence
438	66.6	3.0	2846	6	AR252533	AR252533 Sequence	511	66	2.9	1195	9	BSM802132	BSM802132 Homo sapi
439	66.6	3.0	2846	6	AX092306	AX092306 Sequence	512	66	2.9	1212	6	BD191221	BD191221 186 human
440	66.6	3.0	2846	6	AX376102	AX376102 Sequence	513	66	2.9	1212	6	AX924731	AX924731 Sequence
441	66.6	3.0	2846	6	AX403343	AX403343 Sequence	514	66	2.9	1370	9	BC073975	BC073975 Homo sapi
442	66.6	3.0	2846	6	AX353346	AX353346 Homo sapi	515	66	2.9	1445	9	BC040875	BC040875 Homo sapi
443	66.6	3.0	2933	10	BC063258	BC063258 Mus muscu	516	66	2.9	1447	6	AX086256	AX086256 Sequence
444	66.6	3.0	3666	9	BSM805090	AL833816 Homo sapi	517	66	2.9	1464	9	BC021958	BC021958 Homo sapi
445	66.6	3.0	5149	10	BC050918	BC050918 Mus muscu	518	66	2.9	1539	9	BC002373	BC002373 Homo sapi
446	66.4	3.0	228	6	CQ410517	CQ410517 Sequence	519	66	2.9	1556	9	BC064397	BC064397 Homo sapi
447	66.4	3.0	255	6	AX211073	AX211073 Sequence	520	66	2.9	1739	9	AK026045	AK026045 Homo sapi
448	66.4	3.0	266	6	CQ475720	CQ475720 Sequence	521	66	2.9	1785	5	BC067644	BC067644 Danio rer
449	66.4	3.0	300	6	CQ472434	CQ472434 Sequence	522	66	2.9	1906	10	BC063161	BC063161 Rattus no
450	66.4	3.0	522	6	CQ0507363	BC0507363 Sequence	523	66	2.9	1933	3	SMF86674	SMF86674 Schistosoma
451	66.4	3.0	556	9	BC027917	BC027917 Homo sapi	524	66	2.9	2033	10	BC021915	BC021915 Mus muscu
452	66.4	3.0	728	10	BC032976	BC032976 Mus muscu	525	66	2.9	2095	9	BC073888	BC073888 Homo sapi
453	66.4	3.0	1059	10	BC039808	BC039808 Mus muscu	526	66	2.9	2166	9	AK025798	AK025798 Homo sapi
454	66.4	3.0	1139	9	AK074398	AK074398 Homo sapi	527	66	2.9	2176	9	BC040224	BC040224 Homo sapi
455	66.4	3.0	1359	9	BC030149	BC030149 Homo sapi	528	66	2.9	2188	9	BC031566	BC031566 Homo sapi
456	66.4	3.0	1781	6	AK300434	AK300434 Sequence	529	66	2.9	2291	9	AK000753	AK000753 Homo sapi
457	66.4	3.0	1874	6	CQ769657	CQ769657 Sequence	530	66	2.9	2360	9	BC063595	BC063595 Homo sapi

531	66	2.9	2410	9	BC036849	Homo sapi	604	65.6	2.9	1342	6	AR243851	Sequence
532	66	2.9	2769	10	BC058616	Mus muscu	605	65.6	2.9	1538	5	BC051777	Danio rer
533	66	2.9	2833	9	BSM803718	Al832410	606	65.6	2.9	1584	5	BC042270	Xenopus l
534	66	2.9	2979	9	BC031084	BC031084	607	65.6	2.9	1619	10	BC057862	Mus muscu
535	66	2.9	3012	9	BSM808446	AX648298	608	65.6	2.9	1720	10	BC058559	Mus muscu
536	66	2.9	3116	6	AR487919	AX487919	609	65.6	2.9	1737	10	BC081887	Rattus no
537	66	2.9	3610	10	BC055012	BC055012	610	65.6	2.9	1745	9	BC043567	Homo sapi
538	66	2.9	3962	9	BSM807528	AX647383	611	65.6	2.9	1989	10	BC047157	Mus muscu
539	66	2.9	4154	9	BSM803629	AL832322	612	65.6	2.9	2038	9	BC043591	Homo sapi
540	66	2.9	4454	9	BSM806344	AX5338143	613	65.6	2.9	2039	9	BSM806781	Homo sapi
541	66	2.9	110000	3	AC116984_1	Continuation (2 of	614	65.6	2.9	2041	9	BSM806781	Homo sapi
c 542	65.8	2.9	216	6	CO397929	Sequence	615	65.6	2.9	2068	10	BC064122	Mus muscu
c 543	65.8	2.9	216	6	CO404221	Sequence	616	65.6	2.9	2352	9	S69510	cytokeatin
c 544	65.8	2.9	425	6	AX284646	AX284646	617	65.6	2.9	3004	9	BC064983	Homo sapi
545	65.8	2.9	522	4	AB063246	AB063246	618	65.6	2.9	3110	10	BC057617	Mus muscu
546	65.8	2.9	522	6	BD142629	BD142629	c 619	65.6	2.9	3527	8	SCYBR281C	S. cerevisia
547	65.8	2.9	522	6	BD181690	BD181690	620	65.6	2.9	4082	9	BSM805880	AX537790
548	65.8	2.9	522	6	E49223	E49223	c 621	65.6	2.9	5216	6	AX281348	Sequence
549	65.8	2.9	525	9	BC034020	BC034020	c 622	65.6	2.9	5216	6	AX345249	Sequence
c 550	65.8	2.9	608	6	CO398119	Sequence	c 623	65.6	2.9	32421	8	SCDPB3	X76053 S. cerevisia
c 551	65.8	2.9	608	6	CO404407	Sequence	c 624	65.6	2.9	81975	2	AP000450	AP000450
552	65.8	2.9	617	9	IR0EST087	AL357195	625	65.6	2.9	184182	2	CR352221	Danio rer
553	65.8	2.9	638	4	AB063244	AB063244	626	65.6	2.9	203687	2	EX957279	CR352221
554	65.8	2.9	638	6	BD142627	BD142627	627	65.6	2.9	217000	2	AC114158	Danio rer
555	65.8	2.9	638	6	BD181688	BD181688	628	65.6	2.9	225294	2	AC105897	AC114158
556	65.8	2.9	638	6	E49221	E49221	c 629	65.4	2.9	330	6	AX185119	Rattus no
557	65.8	2.9	1065	10	BC026521	BC026521	c 630	65.4	2.9	413	6	CO427117	Sequence
558	65.8	2.9	1139	9	BSM807844	AX647698	c 631	65.4	2.9	578	6	AX282981	Sequence
559	65.8	2.9	1474	9	BC039576	BC039576	632	65.4	2.9	578	6	AX282981	Sequence
560	65.8	2.9	1883	6	AR528702	AR528702	633	65.4	2.9	690	8	ATH245631	AX245631
561	65.8	2.9	1883	6	AX464368	AX464368	c 634	65.4	2.9	752	6	CO430891	Sequence
562	65.8	2.9	1883	6	AX697077	AX697077	635	65.4	2.9	753	10	BC049652	Mus muscu
563	65.8	2.9	1883	9	AY358954	AY358954	636	65.4	2.9	905	3	AF081800	Dictyoste
564	65.8	2.9	1903	9	BC031676	BC031676	637	65.4	2.9	1119	9	BC071717	Homo sapi
565	65.8	2.9	1966	9	BSM808089	AX647923	638	65.4	2.9	1311	3	BT011164	Drosophil
566	65.8	2.9	2073	9	BSM802983	AL713655	639	65.4	2.9	1312	6	AX306543	Sequence
567	65.8	2.9	2172	9	AB096991	AB096991	640	65.4	2.9	1340	9	BC064379	Sequence
568	65.8	2.9	2195	5	BC079680	BC079680	641	65.4	2.9	1426	3	AX069730	Drosophil
569	65.8	2.9	2440	8	AB021862	AB021862	642	65.4	2.9	1493	9	BSM805897	AX538346
570	65.8	2.9	2529	10	BC054360	BC054360	643	65.4	2.9	1567	9	BC058074	Homo sapi
571	65.8	2.9	2647	9	BC043484	BC043484	644	65.4	2.9	1619	10	RATWHCMRA	Rattus norv
572	65.8	2.9	2938	5	BC057479	BC057479	645	65.4	2.9	1636	6	AX090420	Sequence
573	65.8	2.9	2940	6	BC037172	BC037172	646	65.4	2.9	1626	8	AY150283	Eucalyptu
574	65.8	2.9	3145	6	CO870633	CO870633	647	65.4	2.9	1663	6	BD260635	49 human
575	65.8	2.9	3345	9	BC041132	BC041132	648	65.4	2.9	1801	9	BSM807650	Homo sapi
576	65.8	2.9	3380	9	AB062978	AB062978	649	65.4	2.9	1848	9	BC053543	Homo sapi
577	65.8	2.9	6347	10	AY035343	AY035343	650	65.4	2.9	1974	10	BC064004	Homo sapi
c 578	65.8	2.9	17534	6	AX348413	AX348413	651	65.4	2.9	2059	6	CO845785	Sequence
c 579	65.8	2.9	25136	2	AC099801	AC099801	652	65.4	2.9	2069	9	AK131389	Homo sapi
c 580	65.8	2.9	219941	2	AC099717	AC099717	653	65.4	2.9	2115	5	BC051611	Danio rer
581	65.6	2.9	249	6	AR424795	AR424795	654	65.4	2.9	2533	9	BSM803787	Homo sapi
582	65.6	2.9	249	6	AX985489	AX985489	655	65.4	2.9	2608	6	BD250066	48 human
583	65.6	2.9	249	6	BD120348	BD120348	656	65.4	2.9	2735	9	BC046366	Homo sapi
c 584	65.6	2.9	319	6	CO399044	CO399044	657	65.4	2.9	2817	9	BC000556	Homo sapi
c 585	65.6	2.9	319	6	CO405323	CO405323	658	65.4	2.9	3200	10	BC049178	Mus muscu
c 586	65.6	2.9	372	6	CO0505680	CO0505680	659	65.4	2.9	3295	10	BC005469	Mus muscu
c 587	65.6	2.9	394	6	CO410884	CO410884	660	65.4	2.9	3301	10	BC029098	Mus muscu
c 588	65.6	2.9	429	6	CO526617	CO526617	661	65.4	2.9	3490	10	BC028819	Mus muscu
589	65.6	2.9	442	6	CO522574	CO522574	662	65.4	2.9	3682	10	BC052169	Mus muscu
590	65.6	2.9	572	5	AY612425	AY612425	663	65.4	2.9	3826	5	BC060479	Xenopus l
591	65.6	2.9	599	9	BC035333	BC035333	664	65.4	2.9	3826	5	BC051756	Homo sapi
592	65.6	2.9	604	6	BD270370	BD270370	665	65.4	2.9	4726	9	BSM808819	Homo sapi
593	65.6	2.9	673	5	BC055524	BC055524	666	65.4	2.9	5143	10	BC035523	Mus muscu
594	65.6	2.9	720	10	BC030308	BC030308	667	65.4	2.9	145032	2	AX890579	Danio rer
595	65.6	2.9	942	5	BC057474	BC057474	c 668	65.4	2.9	158504	2	AC107810	Mus muscu
596	65.6	2.9	961	9	AK000718	AK000718	c 669	65.2	2.9	318	6	CO399318	Sequence
597	65.6	2.9	989	5	BC083533	BC083533	c 670	65.2	2.9	318	6	CO405595	Sequence
598	65.6	2.9	1084	9	BC026265	BC026265	c 671	65.2	2.9	327	6	CO474244	Sequence
599	65.6	2.9	1180	6	BD132791	BD132791	c 672	65.2	2.9	337	6	CO529058	Sequence
600	65.6	2.9	1180	6	BD132792	BD132792	c 673	65.2	2.9	368	6	CO422024	Sequence
601	65.6	2.9	1180	6	AF012536	AF012536	c 674	65.2	2.9	566	6	CO410439	Sequence
602	65.6	2.9	1330	10	BC064023	BC064023	c 675	65.2	2.9	643	6	AX186197	Sequence
603	65.6	2.9	1342	6	BD223153	BD223153	676	65.2	2.9	773	6	BD072968	70 human

677	65.2	2.9	776	8	AB007819	AB007819 Citrus un	750	2.9	2924	9	BC063554	BC063554 Homo sapi
678	65.2	2.9	931	9	BC010286	BC010286 Homo sapi	751	2.9	2970	9	BC064624	BC064624 Homo sapi
679	65.2	2.9	933	10	BC048388	BC048388 Mus muscu	752	2.9	3124	10	BC052923	BC052923 Mus muscu
680	65.2	2.9	937	8	CLJACO1V	X57832 C.lacryma-j	753	2.9	3250	5	BC068779	BC068779 Xenopus l
681	65.2	2.9	1064	9	BC047708	BC047708 Homo sapi	754	2.9	3250	9	BC063474	BC063474 Homo sapi
682	65.2	2.9	1250	9	BC033385	BC033385 Homo sapi	755	2.9	3660	10	BC051069	BC051069 Mus muscu
683	65.2	2.9	1344	8	BT009299	BT009299 Triticum	756	2.9	3916	10	BC018439	BC018439 Mus muscu
684	65.2	2.9	1360	10	BC010258	BC010258 Mus muscu	757	2.9	4223	10	BC058958	BC058958 Mus muscu
685	65.2	2.9	1375	3	AK115965	AK115965 Ciona int	758	2.9	4236	5	BC071048	BC071048 Xenopus l
686	65.2	2.9	1480	9	BC032007	BC032007 Homo sapi	759	2.9	4260	9	BC033735	BC033735 Homo sapi
687	65.2	2.9	1513	6	AX320874	AX320874 Sequence	760	2.9	4990	6	CQ493127	CQ493127 Sequence
688	65.2	2.9	1600	10	BC042579	BC042579 Mus muscu	761	2.9	4990	6	CQ493522	CQ493522 Sequence
689	65.2	2.9	1720	9	BC053999	BC053999 Homo sapi	762	2.9	201	11	BV200403	BV200403 sgrm20407
690	65.2	2.9	1734	6	AX092320	AX092320 Sequence	763	2.9	214	6	CQ487824	CQ487824 Sequence
691	65.2	2.9	1734	6	AX358902	AX358902 Sequence	764	2.9	247	6	CQ524135	CQ524135 Sequence
692	65.2	2.9	1734	6	AX362395	AX362395 Sequence	765	2.9	249	6	AR424794	AR424794 Sequence
693	65.2	2.9	1734	6	AX376134	AX376134 Sequence	766	2.9	249	6	AX985488	AX985488 Sequence
694	65.2	2.9	1734	6	AX403750	AX403750 Sequence	767	2.9	249	6	BD120347	BD120347 EST and e
695	65.2	2.9	1734	6	AX454564	AX454564 Sequence	768	2.9	278	6	CQ517619	CQ517619 Sequence
696	65.2	2.9	1734	6	AX491042	AX491042 Sequence	769	2.9	296	6	CQ466754	CQ466754 Sequence
697	65.2	2.9	1734	6	AX696983	AX696983 Sequence	770	2.9	474	6	AX284811	AX284811 Sequence
698	65.2	2.9	1734	9	AY358412	AY358412 Homo sapi	771	2.9	533	6	AX284811	AX284811 Sequence
699	65.2	2.9	1821	9	BC004951	BC004951 Homo sapi	772	2.9	538	9	BC071930	BC071930 Homo sapi
700	65.2	2.9	1845	9	HSM800467	AL050172 Homo sapi	773	2.9	539	6	CQ398781	CQ398781 Sequence
701	65.2	2.9	2208	5	BC088212	BC088212 Xenopus t	774	2.9	539	6	CQ405062	CQ405062 Sequence
702	65.2	2.9	2208	9	BC016137	BC016137 Homo sapi	775	2.9	539	6	CQ410791	CQ410791 Sequence
703	65.2	2.9	2347	10	BC055476	BC055476 Mus muscu	776	2.9	703	6	BD276320	BD276320 MOLECULES
704	65.2	2.9	2469	3	AK116766	AK116766 Ciona int	777	2.9	703	6	AX049467	AX049467 Sequence
705	65.2	2.9	2489	5	BC068397	BC068397 Danio rer	778	2.9	770	3	AX174296	AX174296 Ciona int
706	65.2	2.9	2490	5	BC066711	BC066711 Danio rer	779	2.9	836	5	BC075785	BC075785 Danio rer
707	65.2	2.9	2846	9	HSM802834	AL442082 Homo sapi	780	2.9	918	10	BC049727	BC049727 Mus muscu
708	65.2	2.9	2930	9	BC037961	BC037961 Homo sapi	781	2.9	935	10	BC049693	BC049693 Mus muscu
709	65.2	2.9	3000	9	BC040558	BC040558 Homo sapi	782	2.9	946	3	AY089358	AY089358 Drosophill
710	65.2	2.9	3340	5	AF364811	AF364811 Danio rer	783	2.9	998	8	AB079024	AB079024 Nicotiana
711	65.2	2.9	3399	9	BC063840	BC063840 Homo sapi	784	2.9	1374	3	AX173685	AX173685 Ciona int
712	65.2	2.9	3796	5	BC066783	BC066783 Xenopus t	785	2.9	1479	9	BC036767	BC036767 Homo sapi
713	65.2	2.9	4091	9	HSM803794	AL832486 Homo sapi	786	2.9	1500	9	AK027104	AK027104 Homo sapi
714	65.2	2.9	4504	9	HSM803661	AL832353 Homo sapi	787	2.9	1551	9	BC055126	BC055126 Danio rer
715	65.2	2.9	5929	9	HSM806922	EX640814 Homo sapi	788	2.9	1597	5	BC006103	BC006103 Homo sapi
716	65	2.9	281	6	CQ410312	EX640814 Homo sapi	789	2.9	1761	9	BC028038	BC028038 Homo sapi
717	65	2.9	298	6	CQ527058	CQ527058 Sequence	790	2.9	1815	9	BC026103	BC026103 Homo sapi
718	65	2.9	336	6	CQ397671	CQ397671 Sequence	791	2.9	1836	5	BC054588	BC054588 Danio rer
719	65	2.9	336	6	CQ403968	CQ403968 Sequence	792	2.9	1839	8	DI4059	DI4059 Ananas como
720	65	2.9	346	6	CQ410605	CQ410605 Sequence	793	2.9	2156	6	AX098198	AX098198 Sequence
721	65	2.9	388	6	AX070834	AX070834 Sequence	794	2.9	2170	10	BC052486	BC052486 Mus muscu
722	65	2.9	514	6	AK000450	AK000450 Homo sapi	795	2.9	2181	9	BC037561	BC037561 Homo sapi
723	65	2.9	565	6	CQ410458	CQ410458 Sequence	796	2.9	2190	9	BC063454	BC063454 Homo sapi
724	65	2.9	599	6	BD210257	BD210257 Human gen	797	2.9	2190	5	BC072042	BC072042 Xenopus l
725	65	2.9	749	9	BC008417	BC008417 Homo sapi	798	2.9	2203	9	BC020540	BC020540 Homo sapi
726	65	2.9	762	5	BC062844	BC062844 Danio rer	799	2.9	2305	10	BC005428	BC005428 Mus muscu
727	65	2.9	828	10	BC049756	BC049756 Mus muscu	800	2.9	2332	6	CQ414481	CQ414481 Sequence
728	65	2.9	912	10	RNY17327	Y17327 Rattus norv	801	2.9	2370	10	BC029024	BC029024 Mus muscu
729	65	2.9	1037	8	AY046929	AY046929 Oryza sat	802	2.9	2407	10	BC058192	BC058192 Mus muscu
730	65	2.9	1095	9	HSM801185	AL117648 Homo sapi	803	2.9	2410	5	BC077410	BC077410 Xenopus l
731	65	2.9	1154	9	HSM808002	EX647856 Homo sapi	804	2.9	2590	9	BC073988	BC073988 Homo sapi
732	65	2.9	1290	5	BC065608	BC065608 Danio rer	805	2.9	2658	9	BC027867	BC027867 Homo sapi
733	65	2.9	1308	9	BC021569	BC021569 Homo sapi	806	2.9	2870	9	HSM800882	AL110225 Homo sapi
734	65	2.9	1316	10	BC018263	BC018263 Mus muscu	807	2.9	2888	3	DMGELS	X75630 D.melanogae
735	65	2.9	1366	9	BC043379	BC043379 Homo sapi	808	2.9	3061	9	BC008751	BC008751 Homo sapi
736	65	2.9	1383	5	BC053308	BC053308 Danio rer	809	2.9	3080	10	BC052728	BC052728 Mus muscu
737	65	2.9	1403	9	BC005858	BC005858 Homo sapi	810	2.9	3080	10	BC064444	BC064444 Mus muscu
738	65	2.9	1447	5	BC020589	BC020589 Homo sapi	811	2.9	3114	5	BC080333	BC080333 Xenopus t
739	65	2.9	1455	5	BC053247	BC053247 Danio rer	812	2.9	3129	5	BC073066	BC073066 Xenopus l
740	65	2.9	1500	5	BC065586	BC065586 Danio rer	813	2.9	3309	10	BC051423	BC051423 Mus muscu
741	65	2.9	1560	8	BT009323	BT009323 Triticum	814	2.9	3473	9	BC030601	BC030601 Homo sapi
742	65	2.9	1605	9	BC065230	BC065230 Homo sapi	815	2.9	3513	6	AX277590	AX277590 Sequence
743	65	2.9	1637	5	BC067576	BC067576 Danio rer	816	2.9	4265	9	HSM806990	HSM806990
744	65	2.9	1695	3	AK112719	AK112719 Ciona int	817	2.9	4710	10	BC060613	BC060613 Mus muscu
745	65	2.9	1748	9	BC027853	BC027853 Homo sapi	818	2.9	302156	3	AC116977	AC116977 Dictyoste
746	65	2.9	2101	5	BC067661	BC067661 Danio rer	819	2.9	198	6	CQ487384	CQ487384 Sequence
747	65	2.9	2231	5	BC081288	UC3810288 Xenopus t	820	2.9	201	11	BV207631	BV207631 sgrm22410
748	65	2.9	2486	3	CRU23830	UP3830 Caenorhabdi	821	2.9	212	6	CQ677317	CQ677317 Sequence
749	65	2.9	2833	9	HSM802926	AL512765 Homo sapi	822	2.9	267	6	CQ410745	CQ410745 Sequence

823	64.6	2.9	285	6	AX284863	Sequence	896	64.6	2.9	33899	2	AC149412	Phakopsor
c 824	64.6	2.9	309	6	CQ398213	Sequence	c 897	64.6	2.9	36188	3	AC116922	AC116922 Dictyoste
c 825	64.6	2.9	309	6	CQ404500	Sequence	c 898	64.6	2.9	194593	2	AC139989	AC139989 Rattus no
826	64.6	2.9	358	6	CQ671266	Sequence	899	64.6	2.9	271546	3	AE014843	AE014843 Plasmodiu
827	64.6	2.9	384	6	BD275366	Sequence	c 900	64.6	2.9	349980	6	AX344558	AX344558 Sequence
828	64.6	2.9	414	9	BC061644	Homo sapi	901	64.4	2.9	177	6	AR413410	AR413410 Sequence
829	64.6	2.9	550	6	CQ525224	Sequence	902	64.4	2.9	177	6	BD108963	BD108963 EST and e
c 830	64.6	2.9	556	6	CQ508215	Sequence	903	64.4	2.9	177	6	AX970244	AX970244 Sequence
c 831	64.6	2.9	556	6	CQ508315	Sequence	904	64.4	2.9	268	6	AR412436	AR412436 Sequence
c 832	64.6	2.9	556	6	CQ510257	Sequence	905	64.4	2.9	268	6	AX969270	AX969270 Sequence
c 833	64.6	2.9	556	6	CQ511753	Sequence	906	64.4	2.9	268	6	BD107989	BD107989 EST and e
c 834	64.6	2.9	695	6	CQ423017	Sequence	907	64.4	2.9	300	3	AF153692	AF153692 Mesobuthu
835	64.6	2.9	794	9	BC058920	Homo sapi	c 908	64.4	2.9	393	6	CQ408183	CQ408183 Sequence
836	64.6	2.9	860	6	BD260192	50 human	909	64.4	2.9	395	3	AF151795	AF151795 Butrus ma
837	64.6	2.9	913	5	BC041718	Sequence	c 910	64.4	2.9	402	6	CQ411023	CQ411023 Sequence
838	64.6	2.9	920	10	BC047780	Xenopus l	911	64.4	2.9	444	6	CQ524602	CQ524602 Sequence
839	64.6	2.9	931	10	BC049725	Mus muscu	c 912	64.4	2.9	673	6	CQ397868	CQ397868 Sequence
840	64.6	2.9	935	5	BC071066	Sequence	c 913	64.4	2.9	673	6	CQ404162	CQ404162 Sequence
841	64.6	2.9	1024	3	AK174562	Ciona int	914	64.4	2.9	691	5	BC071138	BC071138 Xenopus l
842	64.6	2.9	1032	10	BC002285	Sequence	915	64.4	2.9	738	9	BSM806309	BSM806309 Homo sapi
843	64.6	2.9	1044	10	BC049565	Mus muscu	916	64.4	2.9	805	10	BC063183	BC063183 Rattus no
844	64.6	2.9	1058	9	BC053997	Homo sapi	917	64.4	2.9	916	3	RP061144	RP061144 Rhodnius pr
845	64.6	2.9	1108	8	AF378131	Zantedesc	918	64.4	2.9	916	6	E12747	E12747 Rhodnius pr
846	64.6	2.9	1118	9	AK000652	Homo sapi	919	64.4	2.9	916	6	E17385	E17385 cDNA encodi
847	64.6	2.9	1162	8	AF275315	Lotus jap	920	64.4	2.9	1022	8	AY044236	AY044236 Lycopersi
848	64.6	2.9	1180	5	BC066714	Danio rer	921	64.4	2.9	1138	9	HSM802391	HSM802391 Homo sapi
849	64.6	2.9	1254	6	BD276346	143 Human	922	64.4	2.9	1372	8	ATCOQ3	ATCOQ3 Arabidopsis
850	64.6	2.9	1260	9	BC042335	Homo sapi	923	64.4	2.9	1410	10	BC061781	BC061781 Rattus no
851	64.6	2.9	1341	9	BC043518	Homo sapi	924	64.4	2.9	1436	5	BC074511	BC074511 Xenopus t
852	64.6	2.9	1359	5	BC053194	Danio rer	925	64.4	2.9	1500	9	BC056861	BC056861 Homo sapi
853	64.6	2.9	1457	9	BC056863	Homo sapi	926	64.4	2.9	1560	3	AF061281	AF061281 Dictyoste
854	64.6	2.9	1521	10	BC083563	Rattus no	927	64.4	2.9	1567	9	AB047887	AB047887 Macaca fa
855	64.6	2.9	1545	10	BC067396	Mus muscu	928	64.4	2.9	1616	10	BC010209	BC010209 Mus muscu
856	64.6	2.9	1569	10	BC083659	Rattus no	929	64.4	2.9	1700	9	BC072389	BC072389 Homo sapi
857	64.6	2.9	1572	9	HSM808149	Sequence	930	64.4	2.9	1731	9	BC012800	BC012800 Homo sapi
858	64.6	2.9	1706	5	BC082351	Xenopus l	931	64.4	2.9	1775	9	BC039831	BC039831 Homo sapi
859	64.6	2.9	1769	9	BC025749	Homo sapi	932	64.4	2.9	1776	10	BC024054	BC024054 Mus muscu
860	64.6	2.9	1793	3	AK112657	Ciona int	933	64.4	2.9	1780	3	AX151519	AX151519 Ciona int
861	64.6	2.9	1903	10	BC023012	Mus muscu	934	64.4	2.9	1808	6	AX535019	AX535019 Sequence
862	64.6	2.9	1925	9	BC050524	Homo sapi	935	64.4	2.9	1865	10	BC054438	BC054438 Mus muscu
863	64.6	2.9	1950	9	BC028206	Homo sapi	936	64.4	2.9	1899	6	AX055388	AX055388 Sequence
864	64.6	2.9	2079	5	BC084664	Xenopus l	937	64.4	2.9	1899	6	AX077025	AX077025 Sequence
865	64.6	2.9	2122	9	BC037277	Homo sapi	938	64.4	2.9	1899	6	AX080781	AX080781 Sequence
866	64.6	2.9	2131	5	BC047846	Danio rer	939	64.4	2.9	1899	6	AX574484	AX574484 Sequence
867	64.6	2.9	2207	9	BC043549	Homo sapi	940	64.4	2.9	1899	9	AY358921	AY358921 Homo sapi
868	64.6	2.9	2234	5	BC053153	Danio rer	941	64.4	2.9	1920	10	BC061765	BC061765 Rattus no
869	64.6	2.9	2246	6	AR212256	Sequence	c 942	64.4	2.9	1946	3	DDIRRS	DDIRRS Dictyostell
870	64.6	2.9	2246	6	AR265251	Sequence	943	64.4	2.9	1982	3	CEL427855	CEL427855 Caenorhab
871	64.6	2.9	2246	10	AF017152	Mus muscu	944	64.4	2.9	2062	8	WHTEFLX	WHTEFLX Wheat trans
872	64.6	2.9	2307	5	BC070730	Xenopus l	945	64.4	2.9	2085	5	BC077186	BC077186 Xenopus l
873	64.6	2.9	2330	5	BC064863	Xenopus t	946	64.4	2.9	2085	9	BC029120	BC029120 Homo sapi
874	64.6	2.9	2330	5	BC064863	Xenopus t	947	64.4	2.9	2106	9	BC027948	BC027948 Homo sapi
875	64.6	2.9	2390	9	AF090900	Sequence	948	64.4	2.9	2143	9	BC023558	BC023558 Homo sapi
876	64.6	2.9	2445	10	BC050514	Mus muscu	949	64.4	2.9	2219	4	AB044390	AB044390 Sus scrofa
877	64.6	2.9	2524	5	BC045217	Xenopus l	950	64.4	2.9	2291	6	AR274977	AR274977 Sequence
878	64.6	2.9	2576	5	BC057416	Danio rer	951	64.4	2.9	2291	6	AR559328	AR559328 Sequence
879	64.6	2.9	2677	9	BC050385	Homo sapi	952	64.4	2.9	2291	9	HSU42031	HSU42031 Human 54 kD
880	64.6	2.9	2730	9	BC053349	Homo sapi	953	64.4	2.9	2363	9	AB056372	AB056372 Macaca fa
881	64.6	2.9	2754	10	BC066817	Mus muscu	954	64.4	2.9	2371	9	HSM605927	HSM605927 Homo sapi
882	64.6	2.9	3092	9	BC043441	Homo sapi	955	64.4	2.9	2604	9	BC032396	BC032396 Homo sapi
883	64.6	2.9	3413	9	BC064848	Homo sapi	956	64.4	2.9	2621	10	BC052772	BC052772 Mus muscu
884	64.6	2.9	4299	9	HSM807262	Sequence	957	64.4	2.9	2626	9	BC036765	BC036765 Homo sapi
885	64.6	2.9	4362	9	HSM805498	Sequence	958	64.4	2.9	2703	9	BC063394	BC063394 Homo sapi
886	64.6	2.9	4438	9	HSM807504	Sequence	959	64.4	2.9	2832	9	BC041896	BC041896 Homo sapi
887	64.6	2.9	4508	10	BC053013	Mus muscu	960	64.4	2.9	2875	9	HSM808745	HSM808745 Homo sapi
888	64.6	2.9	4640	6	AX376008	Sequence	961	64.4	2.9	2914	10	BC050274	BC050274 Mus muscu
889	64.6	2.9	4649	6	CQ767646	Sequence	962	64.4	2.9	3095	9	HSM804691	HSM804691 Homo sapi
890	64.6	2.9	4649	6	AY358647	Sequence	963	64.4	2.9	3218	9	BC050412	BC050412 Homo sapi
891	64.6	2.9	4669	5	BC048022	Xenopus l	964	64.4	2.9	3300	9	BC011656	BC011656 Homo sapi
892	64.6	2.9	4727	5	BC070018	Danio rer	965	64.4	2.9	3724	5	BC068927	BC068927 Xenopus l
893	64.6	2.9	5000	10	BC058783	Mus muscu	966	64.4	2.9	3763	9	BC025767	BC025767 Homo sapi
894	64.6	2.9	12178	10	AF466694	Rattus no	967	64.4	2.9	3782	9	HSM804515	HSM804515 Homo sapi
c 895	64.6	2.9	23499	2	AC149322	Phakopsor	968	64.4	2.9	3894	10	BC053925	BC053925 Mus muscu

969	64.4	2.9	4381	9	HSMB080410	1042	64	2.9	240	6	AX284880	AX284880 Sequence
970	64.4	2.9	4454	3	AY070553	1043	64	2.9	281	6	CQ529993	CQ529993 Sequence
971	64.4	2.9	4753	10	BC058514	1044	64	2.9	299	6	CQ397773	CQ397773 Sequence
972	64.4	2.9	4981	9	HSMB05684	1045	64	2.9	299	6	CQ404070	CQ404070 Sequence
973	64.4	2.9	105320	3	AC116920	1046	64	2.9	311	3	AF159977	AF159977 Butus ma
974	64.4	2.9	110000	3	AC116305	1047	64	2.9	314	6	CQ472429	CQ472429 Sequence
975	64.4	2.9	111079	9	HS116305	1048	64	2.9	337	6	CQ527057	CQ527057 Sequence
976	64.4	2.9	155657	10	AC124454	1049	64	2.9	388	6	CQ410454	CQ410454 Sequence
977	64.4	2.9	200578	2	AC147296	1050	64	2.9	398	8	BT008934	BT008934 Trilicium
978	64.4	2.9	270418	1	AE017303	1051	64	2.9	416	6	CQ484252	CQ484252 Sequence
979	64.4	2.9	349980	6	CQ870473	1052	64	2.9	507	6	CQ397890	CQ397890 Sequence
980	64.2	2.9	373	6	CQ526228	1053	64	2.9	533	6	CQ404183	CQ404183 Sequence
981	64.2	2.9	381	3	AF159974	1054	64	2.9	507	6	AX184534	AX184534 Sequence
982	64.2	2.9	523	6	CQ522700	1055	64	2.9	709	8	AB053296	AB053296 Oryza sat
983	64.2	2.9	844	5	BC009571	1056	64	2.9	790	3	AF040384	AF040384 Schistos
984	64.2	2.9	923	5	BC084674	1057	64	2.9	845	9	BC044653	BC044653 Homo sapi
985	64.2	2.9	942	5	BC049498	1058	64	2.9	896	3	AY055470	AY055470 Lucilia c
986	64.2	2.9	989	8	CPCRM7	1059	64	2.9	935	10	BC061157	BC061157 Mus muscu
987	64.2	2.9	1108	9	BC018104	1060	64	2.9	1023	9	BC063642	BC063642 Homo sapi
988	64.2	2.9	1174	9	AF094850	1061	64	2.9	1098	6	AR105082	AR105082 Sequence
989	64.2	2.9	1267	3	AY122138	1062	64	2.9	1098	8	AF244681	AF244681 Zea mays
990	64.2	2.9	1343	10	S63521	1063	64	2.9	1129	10	BC060535	BC060535 Rattus no
991	64.2	2.9	1349	9	BC065039	1064	64	2.9	1162	8	AF117707	AF117707 Lycopersi
992	64.2	2.9	1390	3	AK174654	1065	64	2.9	1164	6	AX098194	AX098194 Sequence
993	64.2	2.9	1432	10	BC026548	1066	64	2.9	1178	10	BC012273	BC012273 Mus muscu
994	64.2	2.9	1441	6	A65340	1067	64	2.9	1221	5	BC082954	BC082954 Xenopus l
995	64.2	2.9	1441	6	AR150478	1068	64	2.9	1260	5	BC065590	BC065590 Danio rer
996	64.2	2.9	1451	9	AF028823	1069	64	2.9	1314	9	BC012733	BC012733 Homo sapi
997	64.2	2.9	1547	10	BC058197	1070	64	2.9	1319	9	BC002359	BC002359 Homo sapi
998	64.2	2.9	1553	9	BC017440	1071	64	2.9	1331	6	BC015490	BC015490 Homo sapi
999	64.2	2.9	1673	10	BC010324	1072	64	2.9	1331	6	CQ776637	CQ776637 Sequence
1000	64.2	2.9	1860	9	BC063016	1073	64	2.9	1338	5	BC064198	BC064198 Xenopus t
1001	64.2	2.9	1960	10	BC061459	1074	64	2.9	1387	3	AY069134	AY069134 Drosophi
1002	64.2	2.9	1985	6	BD172402	1075	64	2.9	1422	5	BC080890	BC080890 Xenopus t
1003	64.2	2.9	1985	6	BD172721	1076	64	2.9	1544	6	AR255999	AR255999 Sequence
1004	64.2	2.9	1985	6	BD173040	1077	64	2.9	1555	9	AB063070	AB063070 Macaca fa
1005	64.2	2.9	1985	6	BD173359	1078	64	2.9	1568	10	BC003796	BC003796 Mus muscu
1006	64.2	2.9	1985	6	BD175393	1079	64	2.9	1570	5	BC074376	BC074376 Xenopus l
1007	64.2	2.9	1985	6	CQ881212	1080	64	2.9	1592	5	BC074590	BC074590 Xenopus t
1008	64.2	2.9	1985	6	AR410771	1081	64	2.9	1593	5	BC080114	BC080114 Xenopus l
1009	64.2	2.9	1985	6	AR439135	1082	64	2.9	1616	10	BC026899	BC026899 Mus muscu
1010	64.2	2.9	1985	6	AR473155	1083	64	2.9	1645	10	BC039761	BC039761 Mus muscu
1011	64.2	2.9	1985	6	AR527141	1084	64	2.9	1827	5	AB105880	AB105880 Oryzias l
1012	64.2	2.9	1985	6	AR566174	1085	64	2.9	1865	9	BC047609	BC047609 Homo sapi
1013	64.2	2.9	1985	6	AX375960	1086	64	2.9	1952	9	BC002343	BC002343 Homo sapi
1014	64.2	2.9	1985	6	AX375960	1087	64	2.9	1957	9	BC006494	BC006494 Homo sapi
1015	64.2	2.9	1985	6	BD075542	1088	64	2.9	1957	9	BC006516	BC006516 Homo sapi
1016	64.2	2.9	1985	6	AY358500	1089	64	2.9	1981	9	BC037532	BC037532 Homo sapi
1017	64.2	2.9	2023	9	BC025685	1090	64	2.9	2066	10	BC046399	BC046399 Mus muscu
1018	64.2	2.9	2138	10	BC035945	1091	64	2.9	2116	10	BC030862	BC030862 Mus muscu
1019	64.2	2.9	2186	10	BC079471	1092	64	2.9	2137	9	BC033678	BC033678 Homo sapi
1020	64.2	2.9	2348	10	BC057177	1093	64	2.9	2145	9	BC037968	BC037968 Homo sapi
1021	64.2	2.9	2360	9	BC065193	1094	64	2.9	2167	10	BC028325	BC028325 Mus muscu
1022	64.2	2.9	2385	6	BD186882	1095	64	2.9	2223	5	BC067619	BC067619 Panio rer
1023	64.2	2.9	2426	6	BC004874	1096	64	2.9	2245	9	BC028076	BC028076 Homo sapi
1024	64.2	2.9	2487	6	BD074862	1097	64	2.9	2312	9	AK000250	AK000250 Homo sapi
1025	64.2	2.9	2975	9	BC012172	1098	64	2.9	2420	9	BC072670	BC072670 Homo sapi
1026	64.2	2.9	3309	9	BC017311	1099	64	2.9	2439	10	BC017643	BC017643 Mus muscu
1027	64.2	2.9	3399	5	HSMB06327	1100	64	2.9	2489	10	BC055307	BC055307 Mus muscu
1028	64.2	2.9	3505	9	BC053544	1101	64	2.9	2517	5	BC063218	BC063218 Xenopus t
1029	64.2	2.9	3520	9	BC0492521	1102	64	2.9	2533	8	AY161310	AY161310 Pisum sat
1030	64.2	2.9	3544	10	BC058943	1103	64	2.9	2656	9	BC071753	BC071753 Homo sapi
1031	64.2	2.9	3674	10	BC062650	1104	64	2.9	2698	5	BC053122	BC053122 Danio rer
1032	64.2	2.9	3992	10	BC062650	1105	64	2.9	2890	10	BC036168	BC036168 Mus muscu
1033	64.2	2.9	4069	9	BC054003	1106	64	2.9	3010	9	BC075802	BC075802 Homo sapi
1034	64.2	2.9	4500	9	BC035514	1107	64	2.9	3024	9	AB047609	AB047609 Macaca fa
1035	64.2	2.9	14006	6	AX346860	1108	64	2.9	3209	9	BC064576	BC064576 Homo sapi
1036	64.2	2.9	161200	3	AC116957	1109	64	2.9	3315	9	BC037319	BC037319 Homo sapi
1037	64.2	2.9	182870	2	AC109190	1110	64	2.9	3399	9	BC045453	BC045453 Homo sapi
1038	64.2	2.9	193047	9	AC147069	1111	64	2.9	4356	9	BC022792	BC022792 Homo sapi
1039	64.2	2.9	201	6	CQ526416	1112	64	2.9	4496	9	BC058918	BC058918 Homo sapi
1040	64.2	2.9	221	6	CQ663915	1113	64	2.9	5739	6	AX345621	AX345621 Sequence
1041	64.2	2.9	221	6	CQ663915	1114	64	2.9	7240	9	HSMB08174	HSMB08174 Homo sapi

c1115	64	2.9	8305	6	AX346470	Sequence	1188	63.8	2.8	2312	6	AR478071	Sequence
c1116	64	2.9	9699	9	BC066363	Homo sapi	1189	63.8	2.8	2312	6	AR535342	Sequence
c1117	64	2.9	40611	3	AC116987	Dictyoste	1190	63.8	2.8	2312	6	AX045159	Sequence
c1118	64	2.9	19187	3	AC117072	Dictyoste	1191	63.8	2.8	2317	9	BC027906	Homo sapi
c1119	63.8	2.8	198	6	C0488001	Sequence	1192	63.8	2.8	2342	10	BC069844	Mus muscu
c1120	63.8	2.8	202	6	C0486699	Sequence	1193	63.8	2.8	2359	9	BSM808756	Homo sapi
c1121	63.8	2.8	218	6	C0517186	Sequence	1194	63.8	2.8	2368	3	AK112620	Ciona int
c1122	63.8	2.8	241	6	C0525610	Sequence	1195	63.8	2.8	2442	10	BC020028	Mus muscu
c1123	63.8	2.8	244	6	AX408053	Sequence	1196	63.8	2.8	2610	9	BC038448	Homo sapi
c1124	63.8	2.8	301	6	C0516510	Sequence	1197	63.8	2.8	2675	10	BC023831	Mus muscu
c1125	63.8	2.8	321	6	C0671494	Sequence	1198	63.8	2.8	2792	10	AF177401	Spermophi
c1126	63.8	2.8	338	3	AF156596	Buthus ma	1199	63.8	2.8	2856	9	HSAS08777	Homo sapi
c1127	63.8	2.8	359	9	AK026647	Homo sapi	1200	63.8	2.8	3040	5	BC056332	Danio rer
c1128	63.8	2.8	381	6	C0526814	Sequence	1201	63.8	2.8	3101	10	BC059280	Mus muscu
c1129	63.8	2.8	405	6	C0411907	Sequence	1202	63.8	2.8	3326	9	BSM808512	Homo sapi
c1130	63.8	2.8	419	9	BC021680	Homo sapi	1203	63.8	2.8	3591	9	BC037320	Homo sapi
c1131	63.8	2.8	436	6	AX284728	Sequence	1204	63.8	2.8	3715	9	BC054004	Homo sapi
c1132	63.8	2.8	445	6	C0473555	Sequence	1205	63.8	2.8	3884	9	BSM806337	Homo sapi
c1133	63.8	2.8	496	6	C0397791	Sequence	1206	63.8	2.8	4016	9	BC042556	Homo sapi
c1134	63.8	2.8	496	6	C0404088	Sequence	1207	63.8	2.8	4246	9	BC037888	Homo sapi
c1135	63.8	2.8	500	6	C0408389	Sequence	1208	63.8	2.8	4297	10	BC063098	Mus muscu
c1136	63.8	2.8	521	6	C0419873	Sequence	1209	63.8	2.8	6262	9	BSM807046	Homo sapi
c1137	63.8	2.8	559	6	C0517792	Sequence	1210	63.8	2.8	78402	8	NCB16M17	Neurospor
c1138	63.8	2.8	585	6	C0467430	Sequence	1211	63.8	2.8	90373	3	AC115680	Dictyoste
c1139	63.8	2.8	618	6	BD191023	Secreted	1212	63.8	2.8	182871	3	AC117176	Dictyoste
c1140	63.8	2.8	667	9	BC041440	Homo sapi	c1213	63.8	2.8	183648	3	AC117081	Dictyoste
c1141	63.8	2.8	710	10	BC049608	Mus muscu	1214	63.8	2.8	191949	2	AC109158	Mus muscu
c1142	63.8	2.8	711	6	C0422915	Sequence	1215	63.6	2.8	201	11	BV202821	sqnm20999
c1143	63.8	2.8	741	6	AX414257	Sequence	1216	63.6	2.8	255	6	C0521197	Sequence
c1144	63.8	2.8	741	6	AX971091	Sequence	c1217	63.6	2.8	289	6	C0423504	Sequence
c1145	63.8	2.8	741	6	BD109810	EST and e	c1218	63.6	2.8	302	6	CQ398264	Sequence
c1146	63.8	2.8	883	9	BC015164	Homo sapi	c1219	63.6	2.8	302	6	CQ404551	Sequence
c1147	63.8	2.8	891	5	BC079953	Xenopus t	c1220	63.6	2.8	356	6	CQ471948	Sequence
c1148	63.8	2.8	921	5	BC081142	Xenopus l	c1221	63.6	2.8	383	6	CQ502211	Sequence
c1149	63.8	2.8	972	6	I22272	Sequence 1	c1222	63.6	2.8	383	6	CQ511079	Sequence
c1150	63.8	2.8	1058	5	BC064179	Xenopus t	c1223	63.6	2.8	463	6	CQ526887	Sequence
c1151	63.8	2.8	1071	9	AF078844	Homo sapi	c1224	63.6	2.8	498	6	CQ481059	Sequence
c1152	63.8	2.8	1108	10	BC032259	Mus muscu	c1225	63.6	2.8	596	6	CQ477183	Sequence
c1153	63.8	2.8	1129	9	BC013587	Homo sapi	1226	63.6	2.8	642	10	MMU95114	Mus musculu
c1154	63.8	2.8	1217	9	AK026533	Homo sapi	1227	63.6	2.8	659	9	AF151109	Homo sapi
c1155	63.8	2.8	1247	6	BD271574	49 human	c1228	63.6	2.8	738	6	CQ431080	Sequence
c1156	63.8	2.8	1400	9	BC035287	Homo sapi	1229	63.6	2.8	762	9	BC047115	Homo sapi
c1157	63.8	2.8	1408	10	BC048693	Mus muscu	1230	63.6	2.8	871	5	BC061446	Xenopus t
c1158	63.8	2.8	1414	10	BC049767	Mus muscu	1231	63.6	2.8	958	9	BC034296	Homo sapi
c1159	63.8	2.8	1447	9	BC044232	Homo sapi	1232	63.6	2.8	1013	3	AK174215	Ciona int
c1160	63.8	2.8	1495	5	BC074583	Xenopus t	1233	63.6	2.8	1015	5	BC080081	Xenopus l
c1161	63.8	2.8	1580	10	BC072688	Rattus no	1234	63.6	2.8	1073	6	BD190930	Secreted
c1162	63.8	2.8	1595	9	BC043553	Homo sapi	1235	63.6	2.8	1079	5	BC060411	Xenopus l
c1163	63.8	2.8	1602	5	BC074589	Xenopus t	1236	63.6	2.8	1087	5	BC083541	Danio rer
c1164	63.8	2.8	1610	5	AB075198	Oryzias l	1237	63.6	2.8	1130	10	BC061770	Rattus no
c1165	63.8	2.8	1611	5	BC077257	Xenopus l	1238	63.6	2.8	1243	8	AB093028	Pyrrus com
c1166	63.8	2.8	1619	9	BC043510	Homo sapi	1239	63.6	2.8	1319	9	BC034528	Homo sapi
c1167	63.8	2.8	1634	9	BC040915	Homo sapi	1240	63.6	2.8	1378	9	BC040939	Homo sapi
c1168	63.8	2.8	1669	10	BC064715	Mus muscu	1241	63.6	2.8	1381	5	BC063358	Xenopus t
c1169	63.8	2.8	1710	5	BC053110	Danio rer	1242	63.6	2.8	1420	5	BC074693	Xenopus t
c1170	63.8	2.8	1744	9	AB070194	Macaca fa	1243	63.6	2.8	1425	3	AK114531	Ciona int
c1171	63.8	2.8	1785	5	BC055495	Danio rer	1244	63.6	2.8	1439	10	BC058686	Mus muscu
c1172	63.8	2.8	1930	5	BC054953	Xenopus l	1245	63.6	2.8	1545	6	AR307542	Sequence
c1173	63.8	2.8	1946	9	BSM808123	Sequence	1246	63.6	2.8	1545	6	AX401915	Sequence
c1174	63.8	2.8	1995	5	BC082524	Xenopus t	1247	63.6	2.8	1571	10	RNU67958	Rattus norv
c1175	63.8	2.8	2012	10	BC048918	Mus muscu	1248	63.6	2.8	1571	10	BC072658	Mus muscu
c1176	63.8	2.8	2024	9	BC025694	Homo sapi	1249	63.6	2.8	1590	9	BC008284	Homo sapi
c1177	63.8	2.8	2042	9	BC044947	Homo sapi	1250	63.6	2.8	1603	6	CQ490224	Sequence
c1178	63.8	2.8	2047	10	BC051189	Mus muscu	1251	63.6	2.8	1603	6	CQ491236	Sequence
c1179	63.8	2.8	2085	10	BC067207	Mus muscu	1252	63.6	2.8	1603	6	CQ496086	Sequence
c1180	63.8	2.8	2091	6	AR228745	Sequence	1253	63.6	2.8	1603	6	CQ497104	Sequence
c1181	63.8	2.8	2094	5	BC044310	Homo sapi	1254	63.6	2.8	1628	10	BSM801754	Homo sapi
c1182	63.8	2.8	2095	5	BC084410	Xenopus l	1255	63.6	2.8	1648	10	BC052159	Mus muscu
c1183	63.8	2.8	2106	9	BC015775	Homo sapi	1256	63.6	2.8	1687	9	BC041166	Homo sapi
c1184	63.8	2.8	2152	5	BC077173	Xenopus l	1257	63.6	2.8	1696	5	BC067590	Danio rer
c1185	63.8	2.8	2280	10	BC055379	Mus muscu	1258	63.6	2.8	1798	9	AB060834	Macaca fa
c1186	63.8	2.8	2298	6	BD192299	Secreted	1259	63.6	2.8	1815	5	BC044453	Danio rer
c1187	63.8	2.8	2312	3	TG093689	Toxoplasma	1260	63.6	2.8	1850	10	BC016432	Mus muscu

1261 63.6 2.8 1865 9 BC016153 Homo sapi 1334
 1262 63.6 2.8 1884 10 BC036992 Mus muscu 1335
 1263 63.6 2.8 1933 6 BD270058 Secreted 1336
 1264 63.6 2.8 1975 5 BC057415 Danilo rer 1337
 1265 63.6 2.8 1988 3 AY069585 Drosophi 1338
 1266 63.6 2.8 2068 9 BC016791 Homo sapi 1339
 1267 63.6 2.8 2090 9 BC071171 Homo sapi 1340
 1268 63.6 2.8 2118 9 BC073946 Homo sapi 1341
 1269 63.6 2.8 2176 9 BC051801 Homo sapi 1342
 1270 63.6 2.8 2214 9 HSM807772 Homo sapi 1343
 1271 63.6 2.8 2350 5 BC078091 Xenopus 1 1344
 1272 63.6 2.8 2380 9 HSM808648 Homo sapi 1345
 1273 63.6 2.8 2394 9 AF061795 Homo sapi 1346
 1274 63.6 2.8 2417 10 BC026514 Mus muscu 1347
 1275 63.6 2.8 2465 5 BC070798 Xenopus 1 1348
 1276 63.6 2.8 2723 5 BC077764 Homo sapi 1349
 1277 63.6 2.8 2869 9 AF151685 Homo sapi 1350
 1278 63.6 2.8 2874 9 BC037236 Homo sapi 1351
 1279 63.6 2.8 2993 10 BC050858 Mus muscu 1352
 1280 63.6 2.8 3484 9 BC018919 Homo sapi 1353
 1281 63.6 2.8 3556 9 BC033587 Homo sapi 1354
 1282 63.6 2.8 3676 9 HSM801343 Homo sapi 1355
 1283 63.6 2.8 3773 5 BC077375 Xenopus 1 1356
 1284 63.6 2.8 4420 10 BC036971 Mus muscu 1357
 1285 63.6 2.8 4513 10 BC027791 Homo sapi 1358
 1286 63.6 2.8 5335 9 HSM803927 Homo sapi 1359
 1287 63.6 2.8 5405 10 BC038061 Mus muscu 1360
 1288 63.6 2.8 12951 6 AX3339144 Sequence 1361
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ALIGNMENTS

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VERSION AY358756.1 GI:37182630
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 2242)
Clark, H.F., Gurney, A.L., Abaya, E., Baker, K., Baldwin, D., Brush, J.,
Chen, J., Chow, B., Chui, C., Crowley, C., Currell, B., Deuel, B.,
Dowd, P., Eaton, D., Foster, J., Grimaldi, C., Gu, Q., Haas, P.E.,
Heldens, S., Huang, A., Kim, H.S., Klimowski, L., Jin, Y., Johnson, S.,
Lee, J., Lewis, L., Liao, D., Mark, M., Robbie, E., Sanchez, C.,
Schoenfeld, J., Seshagiri, S., Simmons, L., Singh, J., Smith, V.,
Stinson, J., Vagts, A., Vandlen, R., Watanabe, C., Wieand, D., Woods, K.,
Xie, M.H., Yansura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z.,
Goddard, A., Wood, W.I. and Godowski, P.
The Secreted Protein Discovery Initiative (SPDI), - a Large-Scale
Effort to Identify Novel Human Secreted and Transmembrane Proteins:
A Bioinformatics Assessment
Genome Res. 13 (10), 2265-2270 (2003)
JOURNAL 12975309
PUBMED 12975309
REFERENCE 2 (bases 1 to 2242)
Clark, H.F.
AUTHORS Direct Submission
TITLE Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
JOURNAL Inc., 1 DNA Way, South San Francisco, CA 94080, USA
FEATURES
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VERSION AX527744.1 GI:25172275
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REFERENCE 1
AUTHORS Kapeller-Libermann,R.
TITLE 55054, a novel human metalloprotease and uses therefor
JOURNAL Patent: WO 0226948-A 1 04-APR-2002;
Millennium Pharmaceuticals, Inc. (US)
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RESULT 3
LOCUS AX059560 2235 bp DNA linear PAT 17-JAN-2001
DEFINITION Sequence 8 from Patent WO0075298.
ACCESSION AX059560
VERSION AX059560.1 GI:12311667
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Hodgson,D.M., Lincoln,S.E., Russo,F.D., Spiro,P.A., Banville,S.C.,
Bratcher,S.R., Dufour,G.E., Cohen,H.J., Rosen,B.H., Chalup,M.S.,
Hillman,J.L., Jones,A.L., Yu,J.Y., Greenawalt,D.B., Panzer,S.R.,
Roseberry,A.M., Wright,R.J. and Daniels,S.E.
TITLE Molecules for disease detection and treatment
JOURNAL Patent: WO 0075298-A 8 14-DEC-2000;
INCYTE Incyte Genomics, Inc. (US)
LOCATION/Qualifiers
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Query Match 95.8%; Score 2147.4; DB 6; Length 2235;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 2148; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
QY 1 GAATGAATACCTCCGAAGCCGCTTTGTTCTCCAGATGTGAATAGTCCACTATACCAAGCC 60
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QY 121 CTGCGGGCTTTCAATGGGACTCCCTCTGCAATTTTTTTGGAGGTGGAAAGTTGCTAGA 180
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	Tanigami, A., Fujiwara, T., Shibahara, T., Goto, Y., Hirao, M.,	Db	465	TATGGACGAGAGCGACCGACAACAAAGGCGCTGTCTTGGCTTGGATCAATGTGTGAGC	524
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	Suzuki, Y., Hata, H., Nakagawa, K., Mizuno, S., Morinaga, M.,	Db	525	GCCTTCAGAGCCCTGGAGCAAGATCTTCTGTGAATATCAATTCATTCATTTGAGGGATG	584
	Kawamura, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H.,	Qy	795	GAAGAGCTCGCTCTGTGGCTGGAGAACTTGTGAAAAGAAAAGGACCGATTCTTC	854
	Nishikawa, T., Sugiyama, A., Kawakami, B., Nagai, K., Isogai, T. and	Db	585	GAAGAGCTCGCTCTGTGGCTGGAGAACTTGTGAAAAGAAAAGGACCGATTCTTC	644
	Sugano, S.	Qy	855	TCTGGTGTGGACTACATTTGTAATTTTCAGATAAACCCTGTGGATCAGCCAAAGGACCCAGCA	914
TITLE	NEDO human cDNA sequencing project	Db	645	TCTGGTGTGGACTACATTTGTAATTTTCAGATAAACCCTGTGGATCAGCCAAAGGACCCAGCA	704
JOURNAL	Unpublished	Qy	915	ATCATTTATGGAACCCGGGGGAAACAGCTACTTCATGTGTGGAGTGAATTCAGAGACCG	974
REFERENCE	2 (bases 1 to 1970)	Db	705	ATCATTTATGGAACCCGGGGGAAACAGCTACTTCATGTGTGGAGTGAATTCAGAGACCG	764
AUTHORS	Sugano, S. and Suzuki, Y.	Qy	975	GATTTTTCACCTCAGGAACCTTTTGGTGGCATCTTTCATGAACCAATGGCTGATCTGTTGCT	1034
TITLE	Direct Submission	Db	765	GATTTTTCACCTCAGGAACCTTTTGGTGGCATCTTTCATGAACCAATGGCTGATCTGTTGCT	824
JOURNAL	Submitted (08-JUL-2002) Sumio Sugano, Institute of Medical Science,	Qy	1035	CTTCTCGGTAGCTGTGGTAGACTCGTCTGGTTCATATCTCGTCTCGCTGGAATCTATGATGAA	1094
	University of Tokyo, Laboratory of Genome Structure, Human Genome	Db	825	CTTCTCGGTAGCTGTGGTAGACTCGTCTGGTTCATATCTCGTCTCGCTGGAATCTATGATGAA	884
	Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan	Qy	1095	GTGGTTCCTTTCAGAGAGGAAATAATACATACAAAGCCATCCATCTAGACCTAGAA	1154
	(E-mail: fclndna@ims.u-tokyo.ac.jp, Tel: 81-3-5449-5286,	Db	885	GTGGTTCCTTTCAGAGAGGAAATAATACATACAAAGCCATCCATCTAGACCTAGAA	944
	Fax: 81-3-5449-5416)	Qy	1155	GAATACCGGAATAGCAGCGGGTTGAGAAATTTCTGTTGCATATACTAGGAGGAGATCTA	1214
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	construction and 5'-end one pass sequencing: Institute of Medical	Qy	1275	CCTGGAACCTAAACAGTACATCTGCGCGAGTTATAGGAAATTTTCAATCCGCTCTAGTC	1334
	Science, University of Tokyo, Laboratory of Genome Structure, Human	Db	1065	CCTGGAACCTAAACAGTACATCTGCGCGAGTTATAGGAAATTTTCAATCCGCTCTAGTC	1124
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LOCUS HSA417564
DEFINITION Homo sapiens mRNA for glutamate carboxypeptidase-like protein 2
(CPGL2 gene).
ACCESSION AJ417564
VERSION AJ417564.1 GI:16555791
KEYWORDS CPGL2 gene; glutamate carboxypeptidase-like protein 2.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Chen, J.M. and Barrett, A.J.
TITLE Cloning and sequencing of a second human homologue of glutamate
carboxypeptidase in peptidase family M20
JOURNAL unpublished
REFERENCE 2
AUTHORS Chen, J.M.
TITLE Direct Submission
JOURNAL Submitted (24-OCT-2001) Chen J.M., MRC Molecular Enzymology
Laboratory, Babraham Institute, Babraham Hall, Babraham,
Cambridgeshire CB2 4AT, UNITED KINGDOM
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Query Match 72.1%; Score 1616; DB 9; Length 1640;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1632; Conservative 0; Mismatches 5; Indels 3; Gaps 1;
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RESULT 7
AX231101

LOCUS	AX231101	1587 bp	DNA	linear	PAT 11-SEP-2001
DEFINITION	Sequence 497 from Patent WO0162787.				
ACCESSION	AX231101				
VERSION	AX231101.1	GI:15592456			
KEYWORDS	.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				

Qy	1065	CATATCTCGTCCCTGGAACTATGATGAAGTGGTCTCTCTTACAGAAGAGGAAATAAAT	1124	Query Match	58.3%;	Score 1531.6;	DB 6;	Length 1587;	
Db	881	CATATCTCGTCCCTGGAACTATGATGAAGTGGTCTCTCTTACAGAAGAGGAAATAAAT	940	Best Local Similarity	99.1%;	Pred. No. 0;	Mismatches 14;	Indels 0;	Gaps 0;
Qy	1125	ACATACAAAGCCATCCATCTAGACTAGAGAAATACCGGAATAGCAGCCGGTTGAGAA	1184	Matches 1533;	Conservative	0;			
Db	941	ACATACAAAGCCATCCATCTAGACTAGAGAAATACCGGAATAGCAGCCGGTTGAGAA	1000						
Qy	1185	TTTCTGTTGATTAAGGAGAGATTTCTAATGCACTCTGAGGTACCCCATCTTTCT	1244						
Db	1001	TTTCTGTTGATTAAGGAGAGATTTCTAATGCACTCTGAGGTACCCCATCTTTCT	1060						
Qy	1245	ATTTCATGGGATCGAGGGCGGTTTATGAGCTGGAACTAAACAGTCATACCTGGCCGA	1304						
Db	1061	ATTTCATGGGATCGAGGGCGGTTTATGAGCTGGAACTAAACAGTCATACCTGGCCGA	1120						
Qy	1305	GTTATAGGAATTTTCAATCCGTTAGTCCCTACATGAATGTCTGCGGTGGAATAA	1364						
Db	1121	GTTATAGGAATTTTCAATCCGTTAGTCCCTACATGAATGTCTGCGGTGGAATAA	1180						
Qy	1365	CAGGTGACACGACATCTTGAAGATGTGTTCTCCAAAGAAATAGTTCACAAAGATGGTT	1424						
Db	1181	CAGGTGACACGACATCTTGAAGATGTGTTCTCCAAAGAAATAGTTCACAAAGATGGTT	1240						
Qy	1425	GTTTTCATGACTTAGACTACACCGGTGATTCGAAATATGATGACCCCATCTC	1484						
Db	1241	GTTTTCATGACTTAGACTACACCGGTGATTCGAAATATGATGACCCCATCTC	1300						
Qy	1485	GCAGCAAAAGACGATCAGAACAGTGTGTTGGAAACAGAACACAGATATGATCCGGATGGA	1544						
Db	1301	GCAGCAAAAGACGATCAGAACAGTGTGTTGGAAACAGAACACAGATATGATCCGGATGGA	1360						
Qy	1545	TCCACCAATCCAAATGCGAAAATGTTCCAGAGATCGTCCACAGAGCGTGGTCTTAAT	1604						
Db	1361	TCCACCAATCCAAATGCGAAAATGTTCCAGAGATCGTCCACAGAGCGTGGTCTTAAT	1420						
Qy	1605	CCGCTGGAGCTGTGATGATGAGAAACATTCGAGAAATGAGAAATCAAACAGTGGAAAC	1664						
Db	1421	CCGCTGGAGCTGTGATGATGAGAAACATTCGAGAAATGAGAAATCAAACAGTGGAAAC	1480						
Qy	1665	TACATAGAGGAAACCAAAATATTGCTGCTTTTCTTAGAGATGGCCAGCTCATTA	1724						
Db	1481	TACATAGAGGAAACCAAAATATTGCTGCTTTTCTTAGAGATGGCCAGCTCATTA	1540						
Qy	1725	TCACAGAACTTCTAGTCTGATCTCATCTCATCTGACAGATTCACCTC	1771						
Db	1541	TCACAGAACTTCTAGTCTGATCTCATCTCATCTGACAGATTCACCTC	1587						
RESULT	8								
LOCUS	AX231560	1587 bp	DNA	linear	PAT 11-SEP-2001				
DEFINITION	Sequence 458 from Patent WO0163294.								
ACCESSION	AX231560								
VERSION	AX231560.1	GI:15592465							
KEYWORDS									
SOURCE	Homo sapiens (human)								
ORGANISM	Homo sapiens								
REFERENCE	1								
AUTHORS	Herath, H.M., Parekh, R.B. and Rohlf, C.								
TITLE	Diagnosis of bipolar affective disorder (bad) and unipolar depression								
JOURNAL	Patent: WO 0163294-A 458 30-AUG-2001;								
FEATURES	Oxford GlycoSciences (UK) Limited (GB)								
source	Location/Qualifiers								
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[illegible]

585	Qy	TTTCTACGGCCACTTTGGACGCTGACAGCCTCTGTCACCGGGGCGATGGGTGGCTACGGAACCCC	544
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645	Qy	TATGTGCTGACGGAGGTAGACGGGAAACTTTTATGACGAGGAGCGACCGACAACAAGGC	704
461	Db	TATGTGCTGACGGAGGTAGACGGGAAACTTTTATGACGAGGAGCGACCGACAACAAGGC	520
705	Qy	CCTGTCTTGGCTTGGATCAATGCTGTGAGCGCTTTCAGAGCCCTCGAGCAAGATCTTCTCT	764
521	Db	CCTGTCTTGGCTTGGATCAATGCTGTGAGCGCTTTCAGAGCCCTCGAGCAAGATCTTCTCT	580
765	Qy	GTGAATATCAAAATTCAATCATGAGGGGATGGAAGAGCTGCTGTTGCCCTCGGAGGA	824
581	Db	GTGAATATCAAAATTCAATCATGAGGGGATGGAAGAGCTGCTGTTGCCCTCGGAGGA	640
825	Qy	CTTGTGAAAAAGAAAGACCGATTTCTTCTCTGCTGTGCACTTACATTTGTAATTTTCAGAT	884
641	Db	CTTGTGAAAAAGAAAGACCGATTTCTTCTCTGCTGTGCACTTACATTTGTAATTTTCAGAT	700
885	Qy	AACCTGTGGATCAGCCAAAGGAGCCAGCAATCACTTATGGAACCCGGGGGAACAGCTAC	944
701	Db	AACCTGTGGATCAGCCAAAGGAGCCAGCAATCACTTATGGAACCCGGGGGAACAGCTAC	760
945	Qy	TTTCATGGTCGAGGTGAAATGTCAGAGACAGGATTTTCACTCAGGAACCTTTTGGTGGCATC	1004
761	Db	TTTCATGGTCGAGGTGAAATGTCAGAGACAGGATTTTCACTCAGGAACCTTTTGGTGGCATC	820
1005	Qy	CTTTCATGAACCAATGCTGATCTGGTTGCTTCTTCGGTAGCTGTGTAGACTCGTCTGGT	1064
821	Db	CTTTCATGAACCAATGCTGATCTGGTTGCTTCTTCGGTAGCTGTGTAGACTCGTCTGGT	880
1065	Qy	CATATCCTGGTCCTCGGAATCTATGATGAAGTGGTTCCTCTTACAGAAGGAGAAATAAT	1124
881	Db	CATATCCTGGTCCTCGGAATCTATGATGAAGTGGTTCCTCTTACAGAAGGAGAAATAAT	940
1125	Qy	ACATACAAAGCCATCCATCTAGACCTTAGAAGAAATACCGGAATAGCACCGGGTTGAGAAA	1184
941	Db	ACATACAAAGCCATCCATCTAGACCTTAGAAGAAATACCGGAATAGCACCGGGTTGAGAAA	1000
1185	Qy	TTTCTGTTGATACTAAGAGGAGATCTTAATGCACTCTGGAGGTACCCATCTCTTTCT	1244
1001	Db	TTTCTGTTGATACTAAGAGGAGATCTTAATGCACTCTGGAGGTACCCATCTCTTTCT	1060
1245	Qy	ATTTCATGGGATCAGAGCGGGTTTGATGACCTTGGAACTAAACACAGTCATACCTGGCCGA	1304
1061	Db	ATTTCATGGGATCAGAGCGGGTTTGATGACCTTGGAACTAAACACAGTCATACCTGGCCGA	1120
1305	Qy	GTATATAGGAAAAATTTTCAATCCGTTAGTCCCTCAATGATGTGCTGGGTGGAAAAA	1364
1121	Db	GTATATAGGAAAAATTTTCAATCCGTTAGTCCCTCAATGATGTGCTGGGTGGAAAAA	1180
1365	Qy	CAGGTGACGACATCTTGAAGATGTGTTCTCCAAAAGAAATAGTTCCAAACAAGATGGTT	1424
1181	Db	CAGGTGACGACATCTTGAAGATGTGTTCTCCAAAAGAAATAGTTCCAAACAAGATGGTT	1240
1425	Qy	GTTTTCCATGACTCTAGGACTACACCCGTGGATGTCAAATATTGATGACACCCAGTATCTC	1484
1241	Db	GTTTTCCATGACTCTAGGACTACACCCGTGGATGTCAAATATTGATGACACCCAGTATCTC	1300
1485	Qy	GCAGCAAAAAGAGCGATCAGAACGTGTTTGGBAACAGAAACAGATATGATCCGGGATGGA	1544
1301	Db	GCAGCAAAAAGAGCGATCAGAACGTGTTTGGBAACAGAAACAGATATGATCCGGGATGGA	1360
1545	Qy	TCCACCATTCCAATTGCCAAAAATGTTTCCAGGAGATCGTCCACAAGCGTGGTCTAATT	1604
1361	Db	TCCACCATTCCAATTGCCAAAAATGTTTCCAGGAGATCGTCCACAAGCGTGGTCTAATT	1420
1605	Qy	CCGTGGGAGCTGTTGATGATGGAACATTCGCAGAAATGGAATAATCAACAGGTGGAAC	1664
1421	Db	CCGTGGGAGCTGTTGATGATGGAACATTCGCAGAAATGGAATAATCAACAGGTGGAAC	1480

Qy 1665 TACATAGAGGAAACAAATTAATTTGTCGCCCTTTTCTTAGAGATGGCCAGCTCCATTAA 1724
Db 1481 TACATAGAGGAAACAAATTAATTTGTCGCCCTTTTCTTAGAGATGGCCAGCTCCATTAA 1540
Qy 1725 TCACAAGAACCTTCTAGTCTGATCTGATCCACTACAGATTACCTC 1771
Db 1541 TCACAAGAACCTTCTAGTCTGATCTGATCCACTACAGATTACCTC 1587

RESULT 11
AX319869
LOCUS
DEFINITION Sequence 33 from Patent WO0183782.
ACCESSION AX319869
VERSION AX319869.1 GI:17901459
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Plowman, G.D., Whyte, D., Sudarsanam, S., Manning, G., Caenepeel, S. and
Payne, V.
Novel proteases
TITLE
JOURNAL
Sugen, Inc. (US)
LOCATION/Qualifiers
1. 1524
/organism="Homo sapiens"
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FEATURES

source
Query Match 68.0%; Score 1524; DB 6; Length 1524;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ORIGIN

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Db 1 ATGGATCCCAAACTCGGGAGAAATGGCTGCGTCCCTGCTGCTGCTGCTGCTGCTG 60
Qy 261 GAGCGCGGATGTTCTCTCACTCCCTCCCGCCCGCGGCTGTTAGAGAAAGTCTCCAG 320
Db 61 GAGCGCGGATGTTCTCTCACTCCCTCCCGCCCGCGGCTGTTAGAGAAAGTCTCCAG 120
Qy 321 TACATTACCTCCATCAGGATGAATTTGTCAGACGCTGAAGAGTGGTGGCCATCGAG 380
Db 121 TACATTACCTCCATCAGGATGAATTTGTCAGACGCTGAAGAGTGGTGGCCATCGAG 180
Qy 381 AGCGACTCTGTCCAGCCTGTGCTCGCTTCAGACAAGAGCTTTTCAAGATGATGGCCGTG 440
Db 181 AGCGACTCTGTCCAGCCTGTGCTCGCTTCAGACAAGAGCTTTTCAAGATGATGGCCGTG 240
Qy 441 GCTCGGACAGCTGACGCGCTGGGGCCCGCTGTCGCTGCTGCTGCTGCTGCTGCTG 500
Db 241 GCTCGGACAGCTGACGCGCTGGGGCCCGCTGTCGCTGCTGCTGCTGCTGCTGCTG 300
Qy 501 CAGTCCCGATGCTCAGAGTCTTCAATACCTCCCGTCACTCCGCGCAACTGGGGAGC 560
Db 301 CAGTCCCGATGCTCAGAGTCTTCAATACCTCCCGTCACTCCGCGCAACTGGGGAGC 360
Qy 561 GATCCCAAGAAAGCCAGCTGTGCTTACGGCCACCTTGACAGCTGCTGCTGCTGCTG 620
Db 361 GATCCCAAGAAAGCCAGCTGTGCTTACGGCCACCTTGACAGCTGCTGCTGCTGCTG 420
Qy 621 GCGATGGTGGCTCAGGACCCCTATGCTGACGAGGTAGACGGGAACTTTATGGA 680
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Qy 681 CGAGGAGCGCCGACAAAGGCCCTGCTTGGCTTGGATCAATGCTGTGAGCGCCTTC 740
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RESULT 12
AX527746
LOCUS
DEFINITION

AX527746 1521 bp DNA linear PAT 21-NOV-2002
Sequence 3 from Patent WO0226948.

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Db 541 AGAGCCCTGGAGCAAGATCTTCTGTGAATATCAAAATTCATTTAGGGGATGGAAGAG 600
Qy 801 GCTGGCTCTGTGGCCCTGGAGGAACCTTGTGGAAAAAGAAAGGACCCGATTTCTCTGGT 860
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Qy 861 GTGGACTACATTTGTAATTTTCAGATAACCTGTGGATCAGCCAAAGGAAGGACCAATCACT 920
Db 661 GTGGACTACATTTGTAATTTTCAGATAACCTGTGGATCAGCCAAAGGAAGGACCAATCACT 720
Qy 921 TATGGAAACCCGGGGGAAACAGCTACTTTCATGCTGGAGGTGAAATGTCAGAGACCAAGATTTT 980
Db 721 TATGGAAACCCGGGGGAAACAGCTACTTTCATGCTGGAGGTGAAATGTCAGAGACCAAGATTTT 780
Qy 981 CACTCAGGAACCTTTGGTGGCATCTTTCATGAACCAATGGCTGATCTGGTTCCTCTCTC 1040
Db 781 CACTCAGGAACCTTTGGTGGCATCTTTCATGAACCAATGGCTGATCTGGTTCCTCTCTC 840
Qy 1041 GGTAGCCTGTGTAGACTCGTCTGTGTCTATCTCTGTCTCCCTGGAATCTATGATGAAGTGGTT 1100
Db 841 GGTAGCCTGTGTAGACTCGTCTGTGTCTATCTCTGTCTCCCTGGAATCTATGATGAAGTGGTT 900
Qy 1101 CCTTTTACAGAAGAGGAAATAAATACATACAAAGCCCATCTAGACCTTAGAAGAATAC 1160
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Qy 1161 CGGAATAGCAGCGGGTGGAAAAATTTCTGTTGATCTAAGGAGGAGATCTTAATGGAC 1220
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Db 1141 ATGAATGTGTCTCGGTGGAAAAACAGGTGACACGATCTTGAAGATGTGTTCTCCAAA 1200
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Qy 1461 AATATTGATGACACCCAGTATCTCGCAGCAAAAAGAGCGATCAGAACAGTGTGTTGGAACA 1520
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Db 1441 AATGAGAAAAATCAACAGGTGGAACTACATAGAGGGAAACCAAAATTTATTTGCTGCTTTTC 1500
Qy 1701 TTAGAGATGGCCAGCTCCATTAA 1724
Db 1501 TTAGAGATGGCCAGCTCCATTAA 1524

ACCESSION	AX527746	Db	721	TATGGAACCCGGGGAACAGCTCTTTCATGCTGGAGTGAAATGCAGAGACAGGATTTT	780
VERSION	AX527746.1	QY	981	CACCTCAGGAACCTTTGGTGGCATCCTTCATGAACCAATGGCTGATCTCTGTTCTCTTC	1040
KEYWORDS	Homo sapiens (human)	Db	781	CACCTCAGGAACCTTTGGTGGCATCCTTCATGAACCAATGGCTGATCTCTGTTCTCTTC	840
SOURCE	Homo sapiens	QY	1041	GGTAGCCCTGGTAGACTCGTCTGGTGCATATCCTGGTCCCTGGAAATCTATGATGAAGTGGTT	1100
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Db	841	GGTAGCCCTGGTAGACTCGTCTGGTGCATATCCTGGTCCCTGGAAATCTATGATGAAGTGGTT	900
REFERENCE	Kapeller-Liebermann, R.	QY	1101	CCTCTTACAGAAGAGGAAATAAATACATACAAAGCCATCTCTAGACTAGAGAAATAC	1160
AUTHORS	55054, a novel human metalloproteinase and uses therefor	Db	901	CCTCTTACAGAAGAGGAAATAAATACATACAAAGCCATCTCTAGACTAGAGAAATAC	960
TITLE	Patent: WO 0236948-A 3 04-APR-2002;	QY	1161	CGGAATAGCAGCCGGGTTGAGAAATTTCTGTCGATCTAGAGGAGGAGATCTAATGCAC	1220
JOURNAL	Millennium Pharmaceuticals, Inc. (US)	Db	961	CGGAATAGCAGCCGGGTTGAGAAATTTCTGTCGATCTAGAGGAGGAGATCTAATGCAC	1020
FEATURES	Location/Qualifiers	QY	1221	CTCTGGAGTACCCATCTCTTCTTCTATTCATGGATCGAGGGCGCTTTTGATGAGCCTGGA	1280
source	1. .1521	Db	1021	CTCTGGAGTACCCATCTCTTCTTCTATTCATGGATCGAGGGCGCTTTTGATGAGCCTGGA	1080
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Query Match	67.8%; Score 1521; DB 6; Length 1521;	Db	1081	ACTAAACAGCTCATACCTGGCGAGTTATAGGAAATTTTCAATCCGCTAGTCCCTCAC	1140
Best Local Similarity	100.0%; Pred. No. 0;	QY	1341	ATGAATGTCTCGCGTGGGAAACACAGGTGACACGACATCTTGAAGATGTGTTCTCCAAA	1400
Matches 1521; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	Db	1141	ATGAATGTCTCGCGTGGGAAACACAGGTGACACGACATCTTGAAGATGTGTTCTCCAAA	1200
201	ATGGATCCCAAACTCGGAGATGGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	QY	1401	AGAAATAGTTCACAAAGATGGTGTCTTCCATGACTCTAGGACTACACCCGTGGATTCGA	1460
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261	GAGCGGGGCAATGTTCTCTCACCTCCCGCCCCCGCGCGCTGTTAGAGAAAGTCTTCCAG	QY	1461	ATATTTGATGACACCCAGTATCTCCGAGCAAAAGAGCGATCAGACAGTGTTCGGAACA	1520
61	GAGCGGGGCAATGTTCTCTCACCTCCCGCCCCCGCGCGCTGTTAGAGAAAGTCTTCCAG	Db	1261	ATATTTGATGACACCCAGTATCTCCGAGCAAAAGAGCGATCAGACAGTGTTCGGAACA	1320
321	TACATTTGACCTCAGATGAATTTGTCAGACCTGAGAGCTGGGTGGCCATCGAG	QY	1521	GAACAGATATGATCGGGATGGATCCACATTCOAATGCCAAATGTTCCAGAGAGATC	1580
121	TACATTTGACCTCAGATGAATTTGTCAGACCTGAGAGCTGGGTGGCCATCGAG	Db	1321	GAACAGATATGATCGGGATGGATCCACATTCOAATGCCAAATGTTCCAGAGAGATC	1380
381	AGCGACTCTGTCAGCTGTCCTCGCTTCAGACAGAGCTCTTCAGAAATGATGGCCGTG	QY	1581	GTCCAAGAGAGCGTGGTCTAAATCCGCTGGGAGCTGTTGATGATGGAGAAATTCGCGAG	1640
181	AGCGACTCTGTCAGCTGTCCTCGCTTCAGACAGAGCTCTTCAGAAATGATGGCCGTG	Db	1381	GTCCAAGAGAGCGTGGTCTAAATCCGCTGGGAGCTGTTGATGATGGAGAAATTCGCGAG	1440
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241	GCTCGGACACGCTGACAGCCCTGGGGCCCGTGTGGCTTCGTGAGCATGGGTCTCTCAG	Db	1441	ATGAGAAATCAACAGGTGGAACTACATAGAGGGAACCAATTAATTCGCTCTTTTC	1500
501	CAGTGCCTCATGGTCAGAGCTTCNAATACCTCCGTCATCTCGCGCAACTCGGGGAGC	QY	1701	TTAGAGATGGCCAGCTCCAT	1721
301	CAGTGCCTCATGGTCAGAGCTTCNAATACCTCCGTCATCTCGCGCAACTCGGGGAGC	Db	1501	TTAGAGATGGCCAGCTCCAT	1521
561	GATCCCAAGAAAGCAGCCGTGTCTTACGGCCACTTGGACCTGACGCTGCTGACCCGG	QY			
361	GATCCCAAGAAAGCAGCCGTGTCTTACGGCCACTTGGACCTGACGCTGCTGACCCGG	Db			
621	GGCGATGGGTGGCTCAGGACCCCTATGTGTCAGAGAGGTAGACGGGAACTTTATGGA	QY			
421	GGCGATGGGTGGCTCAGGACCCCTATGTGTCAGAGAGGTAGACGGGAACTTTATGGA	Db			
681	CGAGGAGCGGACGACAAAGCCCTGTCTGCTTGGATCAATGCTGAGCGCTTC	QY			
481	CGAGGAGCGGACGACAAAGCCCTGTCTGCTTGGATCAATGCTGAGCGCTTC	Db			
741	AGAGCCCTGGAGCAAGATCTTCTGTGAATATCAAAATTCATCATTTAGGGGATGGAAGAG	QY			
541	AGAGCCCTGGAGCAAGATCTTCTGTGAATATCAAAATTCATCATTTAGGGGATGGAAGAG	Db			
801	GCTGGCTGTGTGGCTGGAGAACTTGTGAAAAGAAAGGACCAATCTCTCTGGT	QY			
601	GCTGGCTGTGTGGCTGGAGAACTTGTGAAAAGAAAGGACCAATCTCTCTGGT	Db			
861	GTGACTACATTTGATTTTCAGATAAAGCTGTGGATCAGCAAGAGGAGCCAGCAATCACT	QY			
661	GTGACTACATTTGATTTTCAGATAAAGCTGTGGATCAGCAAGAGGAGCCAGCAATCACT	Db			
921	TATGGAACCCGGGGAACAGCTCTTTCATGCTGAGGTGAAATGCAGAGACCGAGATTTT	QY			

RESULT 13
AX139747
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

AX139747
Sequence 1 from Patent EP1097997.
AX139747
AX139747.1
GI:14275329
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Saudek, V., Smirnova-Robert, T. and Teufel, M.
Human carnosinase, its isolation and uses
Patent: EP 1097997-A 1 09-MAY-2001;
SANOFI-SYNTHELABO (FR)
Location/Qualifiers
1. .1524

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Db	781	TTTCACTCAGGAACCTTTTGGTGGCATCCCTTTCATGAACCAATGGCTGATCTGGTTGCTCTT	840
Qy	1038	CTCGGTAGCCTGGTAGACTCGTCTGGTTCATATCTCTGGTCCCTCGGAATCTATGATGAAGTG	1097
Db	841	CTCGGTAGCCTGGTAGACTCGTCTGGTTCATATCTCTGGTCCCTCGGAATCTATGATGAAGTG	900
Qy	1098	GTTCTCTTTACAGAAGAGGAATAAATACATACAAAGCCATCCATCTAGACCTTAGAAGAA	1157
Db	901	GTTCTCTTTACAGAAGAGGAATAAATACATACAAAGCCATCCATCTAGACCTTAGAAGAA	960
Qy	1158	TACCGGAATAGCAGCGGGTTAGAAATTTCTGTTCCGATCTAAGGAGGAGATCTCTAATG	1217
Db	961	TACCGGAATAGCAGCGGGTTAGAAATTTCTGTTCCGATCTAAGGAGGAGATCTCTAATG	1020
Qy	1218	CACCTCTGGAGGTACCCATCTCTTTCTTATTCATGGGATCGAGGCGCGTTTGTATGAGCCT	1277
Db	1021	CACCTCTGGAGGTACCCATCTCTTTCTTATTCATGGGATCGAGGCGCGTTTGTATGAGCCT	1080
Qy	1278	GGAACCTAAACAGTCTATCTCTGGCCGAGTTATAGGAAAAATTTTCAATCCGCTTAGTCCCT	1337
Db	1081	GGAACCTAAACAGTCTATCTCTGGCCGAGTTATAGGAAAAATTTTCAATCCGCTTAGTCCCT	1140
Qy	1338	CACATGAATGTGCTCGGGTGGAAAAACAGGTGACACGACATCTTCAAGATGTGTTCTCC	1397
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Qy	1398	AAAAAGAAATAGTTCCTCAACAGATGGTGTGTTTCATGACTCTAGGACTACACCCGCTGGATT	1457
Db	1201	AAAAAGAAATAGTTCCTCAACAGATGGTGTGTTTCATGACTCTAGGACTACACCCGCTGGATT	1260
Qy	1458	GCAAAATATTGATGACACCCAGTATCTCGCAGCAAAAAGAGCGATCAGAACAGTGTGTTGGA	1517
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Qy	1518	ACAGAACCCAGATGATCGGGATGGATCCACATTCCTCAATTCGCCAAATGTTCCAGGAG	1577
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Qy	1578	ATCGTCCCAAGAGCGGTGCTGCTAAATTCGGCTGGGAGCTGTTGATGATGAGAGAACATTG	1637
Db	1381	ATCGTCCCAAGAGCGGTGCTGCTAAATTCGGTGGGAGCTGTTGATGATGAGAGAACATTG	1440
Qy	1638	CAGAATGAGAAAAATCAACAGGTGGAACTACATAGAGGGAAACCAAAATTTTGTGCTGCTTT	1697
Db	1441	CAGAATGAGAAAAATCAACAGGTGGAACTACATAGAGGGAAACCAAAATTTTGTGCTGCTTT	1500
Qy	1698	TTCTTAGAGATGCCCGAGTCCAT	1721
Db	1501	TTCTTAGAGATGCCCGAGTCCAT	1524
RESULT 14			
BC081877			
LOCUS	BC081877 Rattus norvegicus cdna clone MGC:93742 IMAGE:7107931, complete cds.		
DEFINITION	Rattus norvegicus cdna clone MGC:93742 IMAGE:7107931, complete cds.		
ACCESSION	BC081877		
VERSION	BC081877.1 GI:51859149		
KEYWORDS	MGC.		
SOURCE	Rattus norvegicus (Norway rat)		
ORGANISM	Rattus norvegicus		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;		
	Rattus.		
REFERENCE	1 (bases 1 to 2675)		
AUTHORS	Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,		

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Musny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahney, J., Helton, E., Kettman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smal, D.E., Scherch, A., Schein, J.E., Jones, S.J., and Marra, M.A.,
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 2675)
Director MGC Project.
Direct Submission
Submitted (01-SEP-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabs@mail.nih.gov
Tissue Procurement: Howard Jacobs
cDNA Library Preparation: Express Genomics
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) mcdpaxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LILNL at: <http://image.lilnl.gov>
Series: IRAC Plate: 181 Row: 1 Column: 1
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, similarity but not identity to protein.

FEATURES

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CDS

ORIGIN

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Matches 1242; Conservative 0; Mismatches 303; Indels 9; Gaps 2;

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RESULT 15

BC043305

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

BC043305

2774 bp

mrna

linear

ROD 30-JUN-2004

Mus musculus carnosine dipeptidase 1 (metallopeptidase M20 family), mRNA (cDNA clone MGC:49227 IMAGE:5040944), complete cds.

BC043305

GI:27695038

MGC.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 2774)

Strausberg,R.L., Reingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shennan,C.M., Schuler,G.D., Altschul,S.F., Zebberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Schetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullaly,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunatirane,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettner,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Bickertfield,Y.S., Krzywinski,M.I., Skalska,U., Smalys,D.E., Schnerch,A., Schein,J.E., Jones,S.O., and Marra,M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932

2 (bases 1 to 2774)

Strausberg,R.

Direct Submission

Submitted (09-JAN-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer

JOURNAL

TITLE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 1, 2005, 15:45:48 ; Search time 9249 Seconds
(without alignments)
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Perfect score: 2242
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Scoring table: OLIGO NUC
Gapop_60.0 , Gapext 60.0

Searched: 4526729 seqs, 23644849745 residues

Word size : 6
Total number of hits satisfying chosen parameters: 8998214

Minimum DB seq length: 0
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Post-processing: Listing first 1500 summaries

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- 3: gb_in.*
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- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1865	83.2	2235	6	AX059560 Sequence
5	1602	71.5	1970	9	AX098369 Homo sapi
6	1524	68.0	1524	6	AX319869 Sequence
7	1521	67.8	1521	6	AX527746 Sequence
8	1427	63.6	1524	6	AX139747 Sequence
9	1375	61.3	1587	6	AX231101 Sequence
10	1375	61.3	1587	6	AX231560 Sequence
11	1375	61.3	1587	6	AX232218 Sequence
12	1375	61.3	1587	6	AX233356 Sequence
13	1298	57.9	1640	9	HSA417564 Homo sapi
14	525	23.4	175905	2	AC127485 Homo sapi
15	518	23.1	3755	6	C0845803 Sequence
16	518	23.1	3755	9	AK131263 Homo sapi
17	423	18.9	164394	9	AK116904 Homo sapi
18	314	14.0	672	6	AR412460 Sequence
19	314	14.0	672	6	AX969294 Sequence

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112	60	2.7	2512	9	BC009355	BC009355	Homo sapi	c 185	59	2.6	506	6	CQ517637	CQ517637	Sequence
113	60	2.7	2958	5	BC054564	BC054564	Danio rer	c 186	59	2.6	516	6	CQ410493	CQ410493	Sequence
114	60	2.7	3021	9	BC033086	BC033086	Homo sapi	c 187	59	2.6	526	6	CQ524536	CQ524536	Sequence
115	60	2.7	3348	10	BC066211	BC066211	Mus muscu	c 188	59	2.6	535	6	CQ524620	CQ524620	Sequence
116	60	2.7	4086	6	BD227299	BD227299	Secreted	c 189	59	2.6	549	6	CQ524814	CQ524814	Sequence
117	60	2.7	4086	6	AR274048	AR274048	Sequence	c 190	59	2.6	555	6	CQ482852	CQ482852	Sequence
118	60	2.7	4086	6	AR277629	AR277629	Sequence	c 191	59	2.6	566	6	CQ410439	CQ410439	Sequence
119	60	2.7	4086	6	AR441754	AR441754	Sequence	c 192	59	2.6	585	9	BSM800245	BSM800245	Sequence
120	60	2.7	4086	6	AX369091	AX369091	Sequence	c 193	59	2.6	610	6	CQ398031	CQ398031	Sequence
121	60	2.7	4154	9	BSM803629	BSM803629	Homo sapi	c 194	59	2.6	611	6	CQ404323	CQ404323	Sequence
122	60	2.7	4397	6	CQ498439	CQ498439	Sequence	c 195	59	2.6	639	6	AX187144	AX187144	Sequence
123	60	2.7	202089	2	CR382364	CR382364	Danio rer	c 196	59	2.6	664	6	BD218567	BD218567	Sequence
124	60	2.7	217898	5	BX649377	BX649377	Zebrafish	c 200	59	2.6	664	6	CQ397668	CQ397668	Sequence
125	60	2.7	291762	2	AC125887	AC125887	Rattus no	c 202	59	2.6	671	10	BC022592	BC022592	Sequence
126	59	2.6	81	6	AX381811	AX381811	Sequence	c 204	59	2.6	682	10	BC049545	BC049545	Mus muscu
127	59	2.6	90	6	AX381219	AX381219	Sequence	c 205	59	2.6	693	4	SSAPOAT	SSAPOAT	Mus muscu
128	59	2.6	157	6	AR418774	AR418774	Sequence	c 206	59	2.6	699	10	BC053692	BC053692	Mus muscu
129	59	2.6	157	6	AX979468	AX979468	Sequence	c 207	59	2.6	771	6	BD019001	BD019001	Novel gen
130	59	2.6	157	6	BD114327	BD114327	Sequence	c 208	59	2.6	771	6	BD098939	BD098939	Novel gen
131	59	2.6	190	6	AX985981	AX985981	Sequence	c 209	59	2.6	810	6	CQ398775	CQ398775	Sequence
132	59	2.6	190	6	BD120840	BD120840	EST and e	c 210	59	2.6	810	6	CQ405056	CQ405056	Sequence
133	59	2.6	196	6	CQ527157	CQ527157	Sequence	c 211	59	2.6	841	6	AX575537	AX575537	Sequence
134	59	2.6	197	8	CNS01A8P	CNS01A8P	Sequence	c 212	59	2.6	856	9	BC027918	BC027918	Homo sapi
135	59	2.6	198	6	CQ487842	CQ487842	Sequence	c 213	59	2.6	856	10	BC005592	BC005592	Mus muscu
136	59	2.6	201	11	BV200932	BV200932	sgnm20544	c 214	59	2.6	856	10	BC005592	BC005592	Mus muscu
137	59	2.6	211	6	CQ487475	CQ487475	Sequence	c 215	59	2.6	875	9	BC001470	BC001470	Homo sapi
138	59	2.6	220	6	CQ415635	CQ415635	Sequence	c 216	59	2.6	882	9	AK025383	AK025383	Homo sapi
139	59	2.6	225	11	BV174883	BV174883	sgnm75005	c 217	59	2.6	882	9	BSM801969	BSM801969	Homo sapi
140	59	2.6	228	6	CQ529214	CQ529214	Sequence	c 218	59	2.6	911	9	BSM801969	BSM801969	Homo sapi
141	59	2.6	244	6	AX201931	AX201931	Sequence	c 219	59	2.6	913	3	AF252289	AF252289	Leishmani
142	59	2.6	246	6	CQ398352	CQ398352	Sequence	c 220	59	2.6	926	10	BD248890	BD248890	47 human
143	59	2.6	246	6	CQ404639	CQ404639	Sequence	c 221	59	2.6	932	6	BC035045	BC035045	Mus muscu
144	59	2.6	257	6	CQ506050	CQ506050	Sequence	c 222	59	2.6	995	6	BD249159	BD249159	27 human
145	59	2.6	270	6	CQ517277	CQ517277	Sequence	c 223	59	2.6	1017	10	BC049561	BC049561	Mus muscu
146	59	2.6	281	6	CQ529993	CQ529993	Sequence	c 224	59	2.6	1030	8	BT009386	BT009386	Triticum
147	59	2.6	294	6	CQ529167	CQ529167	Sequence	c 225	59	2.6	1045	9	BC004880	BC004880	Homo sapi
148	59	2.6	305	6	CQ487458	CQ487458	Sequence	c 226	59	2.6	1055	10	BC049675	BC049675	Mus muscu
149	59	2.6	308	6	CQ517578	CQ517578	Sequence	c 227	59	2.6	1073	9	BC032697	BC032697	Homo sapi
150	59	2.6	309	6	AX185718	AX185718	Sequence	c 228	59	2.6	1080	9	BC063605	BC063605	Homo sapi
151	59	2.6	313	6	CQ433394	CQ433394	Sequence	c 229	59	2.6	1107	6	AX430924	AX430924	Sequence
152	59	2.6	324	6	CQ410808	CQ410808	Sequence	c 230	59	2.6	1108	8	AY639596	AY639596	Salicorni
153	59	2.6	333	6	CQ487783	CQ487783	Sequence	c 231	59	2.6	1112	3	SCU96099	SCU96099	Sarcophaga
154	59	2.6	339	6	CQ467400	CQ467400	Sequence	c 232	59	2.6	1115	3	AK000652	AK000652	Homo sapi
155	59	2.6	359	6	CQ529133	CQ529133	Sequence	c 233	59	2.6	1118	9	AK000652	AK000652	Homo sapi
156	59	2.6	360	6	CQ483087	CQ483087	Sequence	c 234	59	2.6	1167	10	BC068254	BC068254	Mus muscu
157	59	2.6	374	6	CQ483087	CQ483087	Sequence	c 235	59	2.6	1178	9	BC003392	BC003392	Homo sapi
158	59	2.6	375	6	CQ473918	CQ473918	Sequence	c 236	59	2.6	1180	6	BD132791	BD132791	Apo-2bCr.
159	59	2.6	376	6	CQ524552	CQ524552	Sequence	c 237	59	2.6	1180	6	BD132792	BD132792	Apo-2bCr.
160	59	2.6	376	6	CQ526144	CQ526144	Sequence	c 238	59	2.6	1180	9	AF012536	AF012536	Homo sapi
161	59	2.6	394	6	CQ410884	CQ410884	Sequence								
162	59	2.6	396	6	CQ481648	CQ481648	Sequence								
163	59	2.6	400	6	CQ482962	CQ482962	Sequence								
164	59	2.6	402	6	CQ411023	CQ411023	Sequence								
165	59	2.6	417	6	CQ433349	CQ433349	Sequence								

239	59	2.6	1202	9	BC041171	BC041171 Homo sapi	312	59	2.6	2066	10	BC046399	BC046399 Mus muscu
240	59	2.6	1214	10	BC014865	BC014865 Mus muscu	313	59	2.6	2083	6	AR409309	AR409309 Sequence
241	59	2.6	1223	9	BC051848	BC051848 Homo sapi	314	59	2.6	2083	6	BD140654	BD140654 36 human
242	59	2.6	1228	5	BC054600	BC054600 Danio rer	315	59	2.6	2094	10	BC037443	BC037443 Mus muscu
243	59	2.6	1293	6	BD242878	BD242878 Secreted	316	59	2.6	2111	10	BC018235	BC018235 Mus muscu
244	59	2.6	1315	10	BC003736	BC003736 Mus muscu	317	59	2.6	2132	9	BC042102	BC042102 Homo sapi
245	59	2.6	1319	9	BC003683	BC003683 Homo sapi	318	59	2.6	2159	9	BC033286	BC033286 Homo sapi
246	59	2.6	1328	3	AK114307	AK114307 Ciona int	319	59	2.6	2167	10	BC028325	BC028325 Mus muscu
247	59	2.6	1335	5	BC067557	BC067557 Danio rer	320	59	2.6	2176	9	BC051801	BC051801 Homo sapi
248	59	2.6	1341	9	BC018707	BC018707 Homo sapi	321	59	2.6	2219	4	AB044390	AB044390 Sus scrofa
249	59	2.6	1351	3	AY069618	AY069618 Drosophila	322	59	2.6	2236	6	CQ412293	CQ412293 Sequence
250	59	2.6	1390	9	BC064533	BC064533 Homo sapi	323	59	2.6	2242	6	CQ490721	CQ490721 Sequence
251	59	2.6	1390	10	BC062169	BC062169 Mus muscu	324	59	2.6	2269	6	CQ496562	CQ496562 Sequence
252	59	2.6	1405	10	BC064681	BC064681 Mus muscu	325	59	2.6	2269	6	AX535086	AX535086 Sequence
253	59	2.6	1413	10	BC026675	BC026675 Mus muscu	326	59	2.6	2307	10	BC057127	BC057127 Mus muscu
254	59	2.6	1417	5	BC067701	BC067701 Danio rer	327	59	2.6	2328	9	BC028034	BC028034 Homo sapi
255	59	2.6	1420	10	BC035539	BC035539 Mus muscu	328	59	2.6	2348	9	BC007998	BC007998 Homo sapi
256	59	2.6	1444	9	BC035354	BC035354 Homo sapi	329	59	2.6	2364	9	BC008711	BC008711 Homo sapi
257	59	2.6	1456	5	BC077897	BC077897 Xenopus l	330	59	2.6	2370	10	BC034555	BC034555 Mus muscu
258	59	2.6	1464	9	AL389978	AL389978 Homo sapi	331	59	2.6	2375	10	BC028239	BC028239 Homo sapi
259	59	2.6	1480	5	BC074071	BC074071 Danio rer	332	59	2.6	2404	9	BC042542	BC042542 Homo sapi
260	59	2.6	1487	8	BT008916	BT008916 Triticum	333	59	2.6	2413	9	BC002342	BC002342 Homo sapi
261	59	2.6	1490	9	BC063409	BC063409 Homo sapi	334	59	2.6	2422	9	BC043488	BC043488 Homo sapi
262	59	2.6	1513	6	AX921981	AX921981 Sequence	335	59	2.6	2426	9	BC004874	BC004874 Homo sapi
263	59	2.6	1534	10	RNC21	X99257 R.norvegicus	336	59	2.6	2430	5	BC056717	BC056717 Danio rer
264	59	2.6	1554	5	AF065135	AF065135 Xenopus l	337	59	2.6	2435	9	BC051753	BC051753 Homo sapi
265	59	2.6	1554	6	BD132843	BD132843 WA545 com	338	59	2.6	2447	5	BC064881	BC064881 Xenopus t
266	59	2.6	1555	5	BC049526	BC049526 Danio rer	339	59	2.6	2460	10	BC036985	BC036985 Mus muscu
267	59	2.6	1573	10	BC057679	BC057679 Mus muscu	340	59	2.6	2474	9	BSM806789	BSM806789 Homo sapi
268	59	2.6	1598	10	BC082643	BC082643 Mus muscu	341	59	2.6	2503	8	AF061107	AF061107 Zea mays
269	59	2.6	1609	9	BC010738	BC010738 Homo sapi	342	59	2.6	2504	6	BD139957	BD139957 Secreted
270	59	2.6	1609	8	BT008970	BT008970 Triticum	343	59	2.6	2507	9	BC006411	BC006411 Homo sapi
271	59	2.6	1620	10	BC046632	BC046632 Mus muscu	344	59	2.6	2630	10	BC064659	BC064659 Rattus no
272	59	2.6	1625	9	BC065733	BC065733 Homo sapi	345	59	2.6	2641	9	BC020219	BC020219 Homo sapi
273	59	2.6	1640	5	BC058535	BC058535 Danio rer	346	59	2.6	2647	9	BC043484	BC043484 Homo sapi
274	59	2.6	1651	6	BC035844	BC035844 Homo sapi	347	59	2.6	2660	10	BC046050	BC046050 Danio rer
275	59	2.6	1651	6	AR374741	AR374741 Sequence	348	59	2.6	2660	10	BC046318	BC046318 Mus muscu
276	59	2.6	1651	6	AX146877	AX146877 Sequence	349	59	2.6	2673	9	BC036711	BC036711 Homo sapi
277	59	2.6	1651	9	AF067420	AF067420 Homo sapi	350	59	2.6	2765	9	BC009113	BC009113 Homo sapi
278	59	2.6	1670	9	BSM806969	BSM806969 Homo sapi	351	59	2.6	2817	9	BC000556	BC000556 Homo sapi
279	59	2.6	1693	9	BC042110	BC042110 Homo sapi	352	59	2.6	2825	9	BC028203	BC028203 Homo sapi
280	59	2.6	1704	10	BC048726	BC048726 Mus muscu	353	59	2.6	2836	3	AB016609	AB016609 Dictyoste
281	59	2.6	1705	9	BC032249	BC032249 Homo sapi	354	59	2.6	2841	10	BC045601	BC045601 Mus muscu
282	59	2.6	1754	4	AY312278	AY312278 Bos tauru	355	59	2.6	2931	3	PPTUBEA	X14213 Physarum po
283	59	2.6	1755	9	BC036846	BC036846 Homo sapi	356	59	2.6	2988	9	BC073907	BC073907 Homo sapi
284	59	2.6	1759	6	AX358752	AX358752 Sequence	357	59	2.6	2989	6	AR364635	AR364635 Sequence
285	59	2.6	1759	6	AX362245	AX362245 Sequence	358	59	2.6	2998	10	BC051114	BC051114 Mus muscu
286	59	2.6	1759	9	AY358724	AY358724 Homo sapi	359	59	2.6	3004	10	BC031128	BC031128 Mus muscu
287	59	2.6	1800	10	BC042440	BC042440 Mus muscu	360	59	2.6	3076	8	AF205791	AF205791 Botryococ
288	59	2.6	1812	9	BC018774	BC018774 Homo sapi	361	59	2.6	3095	10	BC063752	BC063752 Mus muscu
289	59	2.6	1815	6	AX098200	AX098200 Sequence	362	59	2.6	3105	9	BSM800649	BSM800649 Homo sapi
290	59	2.6	1816	3	AK112765	AK112765 Ciona int	363	59	2.6	3115	10	BC058780	BC058780 Mus muscu
291	59	2.6	1820	9	BC035606	BC035606 Homo sapi	364	59	2.6	3132	9	BSM802176	BSM802176 Homo sapi
292	59	2.6	1868	6	AX709314	AX709314 Sequence	365	59	2.6	3160	9	BC028067	BC028067 Homo sapi
293	59	2.6	1878	6	AR217827	AR217827 Sequence	366	59	2.6	3217	6	BD015772	BD015772 Antbody
294	59	2.6	1878	6	AX787069	AX787069 Sequence	367	59	2.6	3315	9	AB056768	AB056768 Macaca fa
295	59	2.6	1881	5	BC049494	BC049494 Danio rer	368	59	2.6	3329	9	BC051862	BC051862 Homo sapi
296	59	2.6	1882	9	BC043565	BC043565 Homo sapi	369	59	2.6	3418	9	BC037539	BC037539 Homo sapi
297	59	2.6	1885	6	CQ412300	CQ412300 Sequence	370	59	2.6	3481	9	BC065509	BC065509 Homo sapi
298	59	2.6	1899	9	BC013872	BC013872 Homo sapi	371	59	2.6	3481	10	BC064007	BC064007 Mus muscu
299	59	2.6	1923	9	BC001349	BC001349 Homo sapi	372	59	2.6	3531	10	BC060084	BC060084 Mus muscu
300	59	2.6	1932	9	BC014126	BC014126 Homo sapi	373	59	2.6	3585	10	BC063072	BC063072 Mus muscu
301	59	2.6	1968	9	BC011262	BC011262 Homo sapi	374	59	2.6	3599	9	BC064543	BC064543 Homo sapi
302	59	2.6	1968	10	BC006016	BC006016 Mus muscu	375	59	2.6	3626	9	BC012147	BC012147 Homo sapi
303	59	2.6	1982	3	AK112713	AK112713 Ciona int	376	59	2.6	3645	10	BC062916	BC062916 Mus muscu
304	59	2.6	1993	9	BC013377	BC013377 Homo sapi	377	59	2.6	3715	9	BC054004	BC054004 Homo sapi
305	59	2.6	1995	10	BC050759	BC050759 Mus muscu	378	59	2.6	3724	9	BSM805632	BSM805632 Homo sapi
306	59	2.6	2029	10	BC050265	BC050265 Mus muscu	379	59	2.6	3832	9	HSU75370	HSU75370 Human mitoc
307	59	2.6	2030	10	BC037434	BC037434 Mus muscu	380	59	2.6	4067	5	BC077182	BC077182 Xenopus l
308	59	2.6	2032	10	BC057123	BC057123 Mus muscu	381	59	2.6	4083	9	BC062341	BC062341 Homo sapi
309	59	2.6	2035	9	BC036799	BC036799 Homo sapi	382	59	2.6	4124	9	BC032311	BC032311 Homo sapi
310	59	2.6	2042	9	BC044947	BC044947 Homo sapi	383	59	2.6	4271	10	BC060275	BC060275 Mus muscu
311	59	2.6	2049	9	BC065235	BC065235 Homo sapi	384	59	2.6	4508	10	BC053013	BC053013 Mus muscu

385	59	2.6	4592	3	AY118673	AY118673 Drosophil	458	58	2.6	453	6	CQ517526	CQ517526 Sequence
386	59	2.6	4710	10	BC060613	BC060613 Mus muscu	c 459	58	2.6	461	3	AX284240	AX284240 Sequence
387	59	2.6	4863	3	BSM808808	BSM808808 Homo sapi	c 460	58	2.6	467	3	AF156168	AF156168 Butus ma
388	59	2.6	5000	3	AY392433	AY392433 Dictyoste	c 461	58	2.6	470	6	BD242015	BD242015 Compounds
389	59	2.6	5124	9	BSM805736	BSM805736 Homo sapi	c 462	58	2.6	470	6	AR237198	AR237198 Sequence
390	59	2.6	5344	6	AX470393	AX470393 Sequence	c 463	58	2.6	470	6	AR278222	AR278222 Sequence
391	59	2.6	5701	6	AX470390	AX470390 Sequence	c 464	58	2.6	470	6	AR366918	AR366918 Sequence
392	59	2.6	7028	9	BSM803514	BSM803514 Homo sapi	c 465	58	2.6	470	6	AR370814	AR370814 Sequence
393	59	2.6	33651	3	AC114261	AC114261 Dictyoste	c 466	58	2.6	470	6	AR392319	AR392319 Sequence
394	59	2.6	49306	3	AC115606	AC115606 Dictyoste	c 467	58	2.6	470	6	AR399954	AR399954 Sequence
395	59	2.6	79284	2	BX927314	BX927314 Danio rer	c 468	58	2.6	470	6	AR405221	AR405221 Sequence
396	59	2.6	125958	3	AC115592	AC115592 Dictyoste	c 469	58	2.6	470	6	AR439425	AR439425 Sequence
397	59	2.6	130701	2	AC009889	AC009889 Homo sapi	c 470	58	2.6	470	6	AX106321	AX106321 Sequence
398	59	2.6	141427	2	AL929185	AL929185 Danio rer	c 471	58	2.6	470	6	AX140612	AX140612 Sequence
399	59	2.6	161823	2	AL36947	AL36947 Homo sapi	c 472	58	2.6	470	6	AX267128	AX267128 Sequence
400	59	2.6	167780	9	AL844892	AL844892 Human DNA	c 473	58	2.6	470	6	BD070251	BD070251 Compounds
401	59	2.6	170655	2	AP001012	AP001012 Homo sapi	c 474	58	2.6	470	6	AX267128	AX267128 Sequence
402	59	2.6	172915	2	AC010160	AC010160 Homo sapi	c 475	58	2.6	470	6	AX200472	AX200472 Sequence
403	59	2.6	179739	2	CR352231	CR352231 Danio rer	c 476	58	2.6	470	6	AX200472	AX200472 Sequence
404	59	2.6	184182	2	CR352231	CR352231 Rattus no	c 477	58	2.6	470	6	AX376118	AX376118 Sequence
405	59	2.6	211091	2	AC132973	AC132973 Apis mell	c 478	58	2.6	470	6	AX376118	AX376118 Sequence
406	59	2.6	223920	2	AC141733	AC141733 Rattus no	c 479	58	2.6	470	6	AX403358	AX403358 Sequence
407	59	2.6	229316	2	AC117604	AC117604 Mus muscu	c 480	58	2.6	470	6	AX358669	AX358669 Homo sapi
408	59	2.6	349980	6	AX344563	AX344563 Sequence	c 481	58	2.6	470	6	CQ525211	CQ525211 Sequence
409	58	2.6	80	6	AR001312	AR001312 Sequence	c 482	58	2.6	490	6	BD242108	BD242108 Compounds
410	58	2.6	80	6	AR130410	AR130410 Sequence	c 483	58	2.6	509	6	AR237291	AR237291 Sequence
411	58	2.6	80	6	AX494448	AX494448 Sequence	c 484	58	2.6	509	6	AR278315	AR278315 Sequence
412	58	2.6	101	6	CQ677570	CQ677570 Sequence	c 485	58	2.6	509	6	AR367011	AR367011 Sequence
413	58	2.6	147	6	AX182151	AX182151 Sequence	c 486	58	2.6	509	6	AR370907	AR370907 Sequence
414	58	2.6	153	6	CQ473920	CQ473920 Sequence	c 487	58	2.6	509	6	AR392412	AR392412 Sequence
415	58	2.6	177	6	CQ526416	CQ526416 Sequence	c 488	58	2.6	509	6	AR400047	AR400047 Sequence
416	58	2.6	201	6	CQ525565	CQ525565 Sequence	c 489	58	2.6	509	6	AR405314	AR405314 Sequence
417	58	2.6	206	6	CQ525561	CQ525561 Sequence	c 490	58	2.6	509	6	AX106421	AX106421 Sequence
418	58	2.6	234	6	CQ524931	CQ524931 Sequence	c 491	58	2.6	509	6	AX140712	AX140712 Sequence
419	58	2.6	247	6	AR421302	AR421302 Sequence	c 492	58	2.6	509	6	AX200572	AX200572 Sequence
420	58	2.6	253	6	AX981996	AX981996 Sequence	c 493	58	2.6	509	6	AX267228	AX267228 Sequence
421	58	2.6	253	6	BD116855	BD116855 EST and e	c 494	58	2.6	509	6	BD070344	BD070344 Compounds
422	58	2.6	253	6	BD116855	BD116855 Sequence	c 495	58	2.6	509	6	BC061178	BC061178 Mus muscu
423	58	2.6	254	6	CQ487594	CQ487594 Sequence	c 496	58	2.6	516	9	AJ628244	AJ628244 Homo sapi
424	58	2.6	254	6	CQ517598	CQ517598 Sequence	c 497	58	2.6	516	9	AK026592	AK026592 Homo sapi
425	58	2.6	260	6	CQ704761	CQ704761 Sequence	c 498	58	2.6	519	9	BC051915	BC051915 Homo sapi
426	58	2.6	263	6	E15582	E15582 cDNA encodi	c 499	58	2.6	525	9	BC032225	BC032225 Homo sapi
427	58	2.6	263	6	AR222772	AR222772 Sequence	c 500	58	2.6	527	9	BC049628	BC049628 Mus muscu
428	58	2.6	278	6	CQ518107	CQ518107 Sequence	c 501	58	2.6	528	10	BC049628	BC049628 Sequence
429	58	2.6	282	6	CQ427703	CQ427703 Sequence	c 502	58	2.6	530	6	BC064908	BC064908 Homo sapi
430	58	2.6	285	6	AX284863	AX284863 Sequence	c 503	58	2.6	530	6	BC031454	BC031454 Mus muscu
431	58	2.6	285	6	CQ467734	CQ467734 Sequence	c 504	58	2.6	539	10	CQ522382	CQ522382 Sequence
432	58	2.6	312	6	CQ699683	CQ699683 Sequence	c 505	58	2.6	540	6	BC038211	BC038211 Homo sapi
433	58	2.6	321	6	AX361391	AX361391 Sequence	c 506	58	2.6	541	9	BC046339	BC046339 Mus muscu
434	58	2.6	325	6	CQ527169	CQ527169 Sequence	c 507	58	2.6	541	10	BC046339	BC046339 Sequence
435	58	2.6	342	6	AX381435	AX381435 Sequence	c 508	58	2.6	550	6	CQ655455	CQ655455 Sequence
436	58	2.6	360	6	CQ482995	CQ482995 Sequence	c 509	58	2.6	550	9	BC043570	BC043570 Homo sapi
437	58	2.6	367	6	CQ523839	CQ523839 Sequence	c 510	58	2.6	559	9	BD223440	BD223440 94 human
438	58	2.6	372	10	BC027531	BC027531 Mus muscu	c 511	58	2.6	569	6	AR243074	AR243074 Sequence
439	58	2.6	373	6	CQ526228	CQ526228 Sequence	c 512	58	2.6	569	6	AR404255	AR404255 Sequence
440	58	2.6	377	6	CQ517394	CQ517394 Sequence	c 513	58	2.6	569	6	AY554050	AY554050 Oryza sat
441	58	2.6	390	9	BC035731	BC035731 Homo sapi	c 514	58	2.6	571	8	AY554050	AY554050 Oryza sat
442	58	2.6	392	6	CQ507200	CQ507200 Sequence	c 515	58	2.6	572	5	AF612435	AF612435 Rhinobato
443	58	2.6	396	6	CQ525748	CQ525748 Sequence	c 516	58	2.6	580	10	AF036941	AF036941 Rattus no
444	58	2.6	400	6	CQ483089	CQ483089 Sequence	c 517	58	2.6	581	6	CQ467009	CQ467009 Sequence
445	58	2.6	404	6	CQ507110	CQ507110 Sequence	c 518	58	2.6	581	6	CQ524342	CQ524342 Sequence
446	58	2.6	409	10	BC055712	BC055712 Mus muscu	c 519	58	2.6	586	6	AX381934	AX381934 Sequence
447	58	2.6	413	6	CQ427117	CQ427117 Sequence	c 520	58	2.6	586	6	BD192969	BD192969 Sequence
448	58	2.6	423	6	CQ412615	CQ412615 Sequence	c 521	58	2.6	588	6	CQ821965	CQ821965 Sequence
449	58	2.6	423	6	CQ526104	CQ526104 Sequence	c 522	58	2.6	588	6	BD270370	BD270370 50 human
450	58	2.6	429	6	CQ473793	CQ473793 Sequence	c 523	58	2.6	604	6	CQ503221	CQ503221 Sequence
451	58	2.6	441	6	AX344256	AX344256 Sequence	c 524	58	2.6	606	6	CQ512068	CQ512068 Sequence
452	58	2.6	441	6	AX019230	AX019230 Sequence	c 525	58	2.6	612	10	BC024419	BC024419 Mus muscu
453	58	2.6	441	6	BD130456	BD130456 Expressio	c 526	58	2.6	612	8	AF165421	AF165421 Mesembrya
454	58	2.6	441	6	BD130456	BD130456 P.bicolor m	c 527	58	2.6	620	9	BD107858	BD107858 36 human
455	58	2.6	443	5	PBDRSPB	PBDRSPB Transgeni	c 528	58	2.6	634	9	BC047681	BC047681 Homo sapi
456	58	2.6	446	6	CQ487730	CQ487730 Sequence	c 529	58	2.6	635	4	AR038969	AR038969 Sequence
457	58	2.6	451	6	CQ524930	CQ524930 Sequence	c 530	58	2.6	638	4	AB063244	AB063244 Sus scrofa

531	58	2.6	638	6	BD181688	BD181688 Polypepti	604	58	2.6	942	6	AX709468	AX709468 Sequence
532	58	2.6	638	6	E49221	E49221 Polypeptide	605	58	2.6	942	6	AX709469	AX709469 Sequence
533	58	2.6	638	6	BD142627	BD142627 Use of po	606	58	2.6	943	6	AX098202	AX098202 Sequence
534	58	2.6	650	9	BC034814	BC034814 Homo sapi	607	58	2.6	945	9	BC002688	BC002688 Homo sapi
535	58	2.6	673	9	BC063401	BC063401 Homo sapi	608	58	2.6	949	6	BD223099	BD223099 98 human
536	58	2.6	673	9	BC073915	BC073915 Homo sapi	609	58	2.6	949	6	AR243797	AR243797 98 human
537	58	2.6	682	10	BC053379	BC053379 Mus muscu	610	58	2.6	951	6	BD021498	BD021498 Novel gen
538	58	2.6	688	6	AR365490	AR365490 Sequence	611	58	2.6	951	6	BD101436	BD101436 Novel gen
539	58	2.6	693	6	AX055710	AX055710 Sequence	612	58	2.6	973	9	BC043578	BC043578 Homo sapi
540	58	2.6	693	6	AX299998	AX299998 Sequence	613	58	2.6	979	9	BC031875	BC031875 Homo sapi
541	58	2.6	693	6	AX358922	AX358922 Sequence	614	58	2.6	981	9	BC000007	BC000007 Homo sapi
542	58	2.6	693	6	AX362415	AX362415 Sequence	615	58	2.6	990	3	AF466601	AF466601 Aedes aeg
543	58	2.6	693	6	AX454614	AX454614 Sequence	616	58	2.6	995	9	BC043534	BC043534 Homo sapi
544	58	2.6	693	6	AX464366	AX464366 Sequence	617	58	2.6	996	6	AX406866	AX406866 Sequence
545	58	2.6	693	6	AX491092	AX491092 Sequence	618	58	2.6	997	5	BC061271	BC061271 Xenopus t
546	58	2.6	693	6	AX697075	AX697075 Sequence	619	58	2.6	1003	5	BC067645	BC067645 Danio rer
547	58	2.6	693	9	AX358935	AX358935 Homo sapi	620	58	2.6	1004	10	BC045153	BC045153 Mus muscu
548	58	2.6	693	10	BC049621	BC049621 Mus muscu	621	58	2.6	1006	9	AF111112	AF111112 Homo sapi
549	58	2.6	700	10	BC035545	BC035545 Mus muscu	622	58	2.6	1008	6	AR404675	AR404675 Sequence
550	58	2.6	705	10	BC059084	BC059084 Mus muscu	623	58	2.6	1011	6	AX709470	AX709470 Sequence
551	58	2.6	708	5	AY190729	AY190729 Pagrus ma	624	58	2.6	1013	4	AF155148	AF155148 Canis fam
552	58	2.6	710	10	BC024378	BC024378 Mus muscu	625	58	2.6	1013	6	BD211499	BD211499 Canine an
553	58	2.6	710	10	BC049608	BC049608 Mus muscu	626	58	2.6	1013	6	BD211500	BD211500 Canine an
554	58	2.6	716	9	BC015172	BC015172 Homo sapi	627	58	2.6	1013	6	AR241477	AR241477 Sequence
555	58	2.6	716	9	BC044236	BC044236 Homo sapi	628	58	2.6	1013	6	AR241478	AR241478 Sequence
556	58	2.6	730	3	AY113197	AY113197 Drosophil	629	58	2.6	1013	6	AR254433	AR254433 Sequence
557	58	2.6	732	6	CQ487253	CQ487253 Sequence	630	58	2.6	1013	6	AR254434	AR254434 Sequence
c 558	58	2.6	735	6	CQ467402	CQ467402 Sequence	631	58	2.6	1016	6	BD135263	BD135263 110 human
559	58	2.6	737	9	BC0113410	BC0113410 Homo sapi	632	58	2.6	1016	10	BC024487	BC024487 Mus muscu
560	58	2.6	740	6	CQ430280	CQ430280 Sequence	633	58	2.6	1020	5	BC066621	BC066621 Danio rer
561	58	2.6	741	6	AR414257	AR414257 Sequence	634	58	2.6	1026	9	BC031650	BC031650 Homo sapi
562	58	2.6	741	6	AX971091	AX971091 Sequence	635	58	2.6	1032	8	LETHM18GE	X98308 L. esculentu
563	58	2.6	741	6	BD109810	BD109810 EST and e	636	58	2.6	1042	9	BC036790	BC036790 Homo sapi
564	58	2.6	749	10	BC049667	BC049667 Mus muscu	637	58	2.6	1046	9	BC032585	BC032585 Homo sapi
565	58	2.6	759	6	AR423329	AR423329 Sequence	638	58	2.6	1056	3	AY069254	AY069254 Drosophil
566	58	2.6	759	8	BT008966	BT008966 Triticum	639	58	2.6	1062	6	AR438054	AR438054 Sequence
567	58	2.6	759	9	BC043514	BC043514 Homo sapi	640	58	2.6	1063	9	BC047332	BC047332 Homo sapi
568	58	2.6	761	9	BC037214	BC037214 Homo sapi	641	58	2.6	1065	8	ZMYPTM2A	X63278 Z. mays YPTM
569	58	2.6	762	9	BC070287	BC070287 Homo sapi	642	58	2.6	1065	9	BC073914	BC073914 Homo sapi
570	58	2.6	763	9	BC040916	BC040916 Homo sapi	643	58	2.6	1069	6	BD192979	BD192979 207 human
571	58	2.6	781	9	AK000690	AK000690 Homo sapi	644	58	2.6	1069	6	CQ821975	CQ821975 Sequence
572	58	2.6	781	9	AK074413	AK074413 Homo sapi	645	58	2.6	1074	9	BC052808	BC052808 Homo sapi
573	58	2.6	791	3	AY156926	AY156926 Pinctada	646	58	2.6	1082	9	BC029908	BC029908 Homo sapi
574	58	2.6	791	8	BT009373	BT009373 Triticum	647	58	2.6	1083	9	HSMB000561	AL080060 Homo sapi
575	58	2.6	794	9	BC058920	BC058920 Homo sapi	648	58	2.6	1088	10	BC014283	BC014283 Mus muscu
576	58	2.6	809	6	BD252094	BD252094 47. secret	649	58	2.6	1092	10	BC005748	BC005748 Mus muscu
577	58	2.6	814	10	BC025933	BC025933 Mus muscu	650	58	2.6	1097	8	BT009078	BT009078 Triticum
578	58	2.6	815	10	AF035161	AF035161 Mus muscu	651	58	2.6	1102	9	HSMB005713	BX537414 Homo sapi
579	58	2.6	816	6	CQ486089	CQ486089 Sequence	652	58	2.6	1105	10	BC005696	BC005696 Mus muscu
580	58	2.6	822	6	BD271590	BD271590 49 human	653	58	2.6	1108	9	BC018104	BC018104 Homo sapi
581	58	2.6	851	9	BC016844	BC016844 Homo sapi	654	58	2.6	1112	5	BC060917	BC060917 Danio rer
582	58	2.6	859	9	BC043551	BC043551 Homo sapi	655	58	2.6	1113	10	BC013777	BC013777 Mus muscu
583	58	2.6	866	10	BC026557	BC026557 Mus muscu	656	58	2.6	1113	10	BC071717	BC071717 Homo sapi
584	58	2.6	868	9	BC033502	BC033502 Homo sapi	657	58	2.6	1120	9	BC035904	BC035904 Homo sapi
c 585	58	2.6	870	6	CQ482086	CQ482086 Sequence	658	58	2.6	1126	6	BD275148	BD275148 48 Human
586	58	2.6	870	8	BT009293	BT009293 Triticum	659	58	2.6	1130	10	BC061770	BC061770 Rattus no
587	58	2.6	872	9	BC058073	BC058073 Homo sapi	660	58	2.6	1133	10	BC044743	BC044743 Mus muscu
588	58	2.6	875	9	AF242525	AF242525 Homo sapi	661	58	2.6	1138	4	AF360872	AF360872 Oryctolag
589	58	2.6	878	9	BC009521	BC009521 Homo sapi	662	58	2.6	1148	8	OSY15009	Y15009 Oryza sativ
590	58	2.6	880	9	AF207829	AF207829 Homo sapi	663	58	2.6	1159	9	BC067119	BC067119 Homo sapi
591	58	2.6	880	9	BC018139	BC018139 Homo sapi	664	58	2.6	1164	9	BC006332	BC006332 Homo sapi
592	58	2.6	882	10	BC062186	BC062186 Mus muscu	665	58	2.6	1174	9	AF094850	AF094850 Homo sapi
593	58	2.6	887	3	AY099474	AY099474 Haematobi	666	58	2.6	1178	6	BD275922	BD275922 Uncouplin
594	58	2.6	892	9	BC000077	BC000077 Homo sapi	667	58	2.6	1178	10	BC048734	BC048734 Mus muscu
595	58	2.6	900	10	BC020073	BC020073 Mus muscu	668	58	2.6	1183	10	BC046431	BC046431 Mus muscu
596	58	2.6	907	10	BC058959	BC058959 Mus muscu	669	58	2.6	1195	9	HSMB02132	AL137429 Homo sapi
597	58	2.6	910	10	BC049687	BC049687 Mus muscu	670	58	2.6	1197	9	BC031811	BC031811 Homo sapi
598	58	2.6	914	9	BC036297	BC036297 Homo sapi	671	58	2.6	1197	10	BC036984	BC036984 Mus muscu
599	58	2.6	923	10	BC026487	BC026487 Mus muscu	672	58	2.6	1198	9	BC000051	BC000051 Homo sapi
600	58	2.6	931	9	BC064491	BC064491 Homo sapi	673	58	2.6	1198	10	BC033305	BC033305 Mus muscu
601	58	2.6	935	10	BC049693	BC049693 Mus muscu	674	58	2.6	1200	10	BC038126	BC038126 Mus muscu
602	58	2.6	939	5	BC061437	BC061437 Xenopus t	675	58	2.6	1203	3	AF187063	AF187063 Oryza sat
603	58	2.6	940	10	BC060548	BC060548 Rattus no	676	58	2.6	1208	9	BC046635	BC046635 Homo sapi

677	58	2.6	1238	5	BC041264	BC041264 Xenopus l	750	58	2.6	1493	6	I40996	I40996 Sequence 24
678	58	2.6	1238	9	BC025970	BC025970 Homo sapi	751	58	2.6	1500	5	BC065586	BC065586 Danio rer
679	58	2.6	1238	9	BSM802295	AL137556 Homo sapi	752	58	2.6	1500	5	BC049755	BC049755 Mus muscu
680	58	2.6	1242	9	BC017721	BC017721 Homo sapi	753	58	2.6	1500	10	BC065307	BC065307 Rattus no
681	58	2.6	1244	10	MMBASII	Y16258 Mus musculu	754	58	2.6	1507	9	BC002839	BC002839 Homo sapi
682	58	2.6	1254	9	BC054506	BC054506 Homo sapi	755	58	2.6	1509	10	BC071190	BC071190 Mus muscu
683	58	2.6	1257	8	AY367058	AY367058 Pisum sat	756	58	2.6	1510	5	BC074510	BC074510 Xenopus t
684	58	2.6	1259	8	BC051778	BC051778 Danio rer	757	58	2.6	1511	10	BC061104	BC061104 Mus muscu
685	58	2.6	1259	9	BC018847	BC018847 Homo sapi	758	58	2.6	1516	8	OSABTU01	X78142 O.sativa (A
686	58	2.6	1261	9	BC029647	BC029647 Homo sapi	759	58	2.6	1519	6	AX546769	AX546769 Sequence
687	58	2.6	1276	6	AS7389	A57389 Sequence 4	760	58	2.6	1520	9	AK026597	AK026597 Homo sapi
688	58	2.6	1290	9	BC062599	BC062599 Homo sapi	761	58	2.6	1520	10	BC027081	BC027081 Mus muscu
689	58	2.6	1294	8	AF394890	AF394890 Filobasid	762	58	2.6	1523	10	BC027081	BC027081 Mus muscu
690	58	2.6	1298	5	BC053261	BC053261 Danio rer	763	58	2.6	1525	6	AR144464	AR144464 Sequence
691	58	2.6	1298	10	MMBASII	Y16257 Mus musculu	764	58	2.6	1525	6	BD224149	BD224149 REC2 kina
692	58	2.6	1299	6	BD227288	BD227288 Secreted	765	58	2.6	1525	6	AR214787	AR214787 Sequence
693	58	2.6	1302	6	E02756	E02756 DNA encodin	766	58	2.6	1525	6	BD003352	BD003352 Mammalian
694	58	2.6	1302	6	BD140113	BD140113 Secreted	767	58	2.6	1525	10	MMU92068	U92068 Mus musculu
695	58	2.6	1302	10	MMBASII	Y16256 Mus musculu	768	58	2.6	1531	9	BC042073	BC042073 Homo sapi
696	58	2.6	1303	9	BSM802259	AL137526 Homo sapi	769	58	2.6	1535	9	BC025659	BC025659 Homo sapi
697	58	2.6	1311	3	BT011164	BT011164 Drosophil	770	58	2.6	1537	8	CAK400861	CAK400861 Cicer ari
698	58	2.6	1311	10	BC0310932	BC0310932 Mus muscu	771	58	2.6	1540	9	BC053865	BC053865 Homo sapi
699	58	2.6	1315	5	BC055585	BC055585 Danio rer	772	58	2.6	1547	5	BC076743	BC076743 Xenopus l
700	58	2.6	1316	9	BC089049	BC089049 Homo sapi	773	58	2.6	1547	6	BD275163	BD275163 48 Human
701	58	2.6	1317	10	BC059775	BC059775 Mus muscu	774	58	2.6	1551	9	BC017072	BC017072 Homo sapi
702	58	2.6	1319	9	BC057971	BC057971 Mus muscu	775	58	2.6	1559	9	BC009822	BC009822 Homo sapi
703	58	2.6	1329	9	BC071737	BC071737 Homo sapi	776	58	2.6	1570	6	AX376268	AX376268 Sequence
704	58	2.6	1330	10	BC064023	BC064023 Mus muscu	777	58	2.6	1570	9	AX358532	AX358532 Homo sapi
705	58	2.6	1339	9	BC016998	BC016998 Homo sapi	778	58	2.6	1570	9	BC025726	BC025726 Homo sapi
706	58	2.6	1339	9	BC048255	BC048255 Homo sapi	779	58	2.6	1577	9	BD231696	BD231696 31 human
707	58	2.6	1342	6	AR223153	BD23153 98 human	780	58	2.6	1580	6	BC037569	BC037569 Homo sapi
708	58	2.6	1342	6	AR243851	AR243851 Sequence	781	58	2.6	1580	9	BC042270	BC042270 Xenopus l
709	58	2.6	1343	5	BC057508	BC057508 Danio rer	782	58	2.6	1584	5	BC042270	BC042270 Xenopus l
710	58	2.6	1343	9	BC052989	BC052989 Homo sapi	783	58	2.6	1588	5	BC049408	BC049408 Danio rer
711	58	2.6	1344	8	BT009299	BT009299 Triticum	784	58	2.6	1588	5	BC032331	BC032331 Homo sapi
712	58	2.6	1348	5	BC057423	BC057423 Danio rer	785	58	2.6	1591	9	BSM807298	BSM807298 Homo sapi
713	58	2.6	1350	10	BC057639	BC057639 Mus muscu	786	58	2.6	1591	10	AB041801	AB041801 Mus muscl
714	58	2.6	1362	3	AY070872	AY070872 Drosophil	787	58	2.6	1598	9	AK000432	AK000432 Homo sapi
715	58	2.6	1366	9	BC065486	BC065486 Homo sapi	788	58	2.6	1601	9	BC010419	BC010419 Homo sapi
716	58	2.6	1368	5	BC064278	BC064278 Xenopus t	789	58	2.6	1609	9	BC040703	BC040703 Homo sapi
717	58	2.6	1372	8	ATCOQ3	Y15055 Arabidopsis	790	58	2.6	1624	6	AX464048	AX464048 Sequence
718	58	2.6	1377	5	BC063336	BC063336 Xenopus t	791	58	2.6	1624	6	AY359115	AY359115 Homo sapi
719	58	2.6	1388	3	AF182511	AF182511 Drosophil	792	58	2.6	1636	8	ATASDZET	X94938 A.thaliana
720	58	2.6	1389	5	XLNLPN038	X56039 X.laavis mR	793	58	2.6	1637	6	BD193083	BD193083 207 human
721	58	2.6	1391	5	BC074604	BC074604 Xenopus t	794	58	2.6	1637	6	CQ822079	CQ822079 Sequence
722	58	2.6	1402	9	BC040630	BC040630 Homo sapi	795	58	2.6	1641	9	BC010739	BC010739 Homo sapi
723	58	2.6	1405	6	AR337570	AR337570 Sequence	796	58	2.6	1642	9	BSM805977	BSM805977 Homo sapi
724	58	2.6	1405	6	BD130049	BD130049 Human ser	797	58	2.6	1646	8	AF058708	AF058708 Zea mays
725	58	2.6	1412	6	AR452913	AR452913 Sequence	798	58	2.6	1646	9	BC051812	BC051812 Homo sapi
726	58	2.6	1414	10	BC049767	BC049767 Mus muscu	799	58	2.6	1652	8	BT009431	BT009431 Triticum
727	58	2.6	1416	8	AY443040	AY443040 Arabidops	800	58	2.6	1654	9	AB055370	AB055370 Macaca fa
728	58	2.6	1416	9	BC004950	BC004950 Homo sapi	801	58	2.6	1660	3	AY069770	AY069770 Drosophil
729	58	2.6	1418	9	BC075806	BC075806 Homo sapi	802	58	2.6	1660	3	AY069770	AY069770 Drosophil
730	58	2.6	1423	6	I09360	I09360 Sequence 1	803	58	2.6	1660	10	BC062018	BC062018 Rattus no
731	58	2.6	1424	5	BC063367	BC063367 Xenopus t	804	58	2.6	1662	8	AY243851	AY243851 Galdieria
732	58	2.6	1441	9	BC050568	BC050568 Homo sapi	805	58	2.6	1664	9	BC048288	BC048288 Homo sapi
733	58	2.6	1444	9	BC064535	BC064535 Homo sapi	806	58	2.6	1674	3	AY070845	AY070845 Drosophil
734	58	2.6	1444	9	BSM801370	AL133093 Homo sapi	807	58	2.6	1674	6	AR252574	AR252574 Sequence
735	58	2.6	1452	10	BC030672	BC030672 Mus muscu	808	58	2.6	1674	6	AX403413	AX403413 Sequence
736	58	2.6	1455	5	BC053247	BC053247 Danio rer	809	58	2.6	1674	6	AX454576	AX454576 Sequence
737	58	2.6	1456	9	BC025257	BC025257 Homo sapi	810	58	2.6	1674	6	AX464320	AX464320 Sequence
738	58	2.6	1460	5	BC065641	BC065641 Danio rer	811	58	2.6	1674	6	AX491054	AX491054 Sequence
739	58	2.6	1469	5	XLUB50GAP4	X87582 X.laavis B-	812	58	2.6	1674	3	DDRAX	Z11804 D.discoideu
740	58	2.6	1469	10	BC055305	BC055305 Mus muscu	813	58	2.6	1676	5	BC074594	BC074594 Xenopus t
741	58	2.6	1475	6	BD249092	BD249092 49 human	814	58	2.6	1677	5	BC048049	BC048049 Danio rer
742	58	2.6	1479	9	BC018977	BC018977 Homo sapi	815	58	2.6	1685	9	BC009889	BC009889 Homo sapi
743	58	2.6	1480	10	BC062376	BC062376 Mus muscu	816	58	2.6	1685	9	BC018841	BC018841 Homo sapi
744	58	2.6	1481	6	BD275459	BD275459 47 Human	817	58	2.6	1685	3	AF044679	AF044679 Leishmani
745	58	2.6	1486	6	BD223469	BD223469 94 human	818	58	2.6	1691	3	AK025549	AK025549 Homo sapi
746	58	2.6	1486	6	AR243103	AR243103 Sequence	819	58	2.6	1691	10	BC019184	BC019184 Mus muscu
747	58	2.6	1486	6	AR404284	AR404284 Sequence	820	58	2.6	1691	6	AR360374	AR360374 Sequence
748	58	2.6	1493	6	E05822	E05822 DNA encodin	821	58	2.6	1692	6	AR360374	AR360374 Sequence
749	58	2.6	1493	6	I19901	I19901 Sequence 24	822	58	2.6	1692	9	AF132676	AF132676 Homo sapi

823	58	2.6	1697	10	AF166267	AF166267 Rattus no	896	58	2.6	1960	9	BC007355	BC007355 Homo sapi
824	58	2.6	1702	9	BC006832	BC006832 Homo sapi	897	58	2.6	1962	9	BC009848	BC009848 Homo sapi
825	58	2.6	1710	9	AB047897	AB047897 Macaca fa	898	58	2.6	1966	10	BC024430	BC024430 Mus muscu
826	58	2.6	1717	5	BC056693	BC056693 Danio rer	899	58	2.6	1975	9	BC017376	BC017376 Homo sapi
827	58	2.6	1725	6	AR451632	AR451632 Sequence	900	58	2.6	1981	3	AFACHA	X84584 A. fulica Fe
828	58	2.6	1733	10	BC017530	BC017530 Mus muscu	901	58	2.6	1984	9	AB071103	AB071103 Macaca fa
829	58	2.6	1738	9	BSM801162	BSM801162 Homo sapi	902	58	2.6	1985	6	BD175393	BD175393 Secretary
830	58	2.6	1744	8	BT009253	BT009253 Triticum	903	58	2.6	1985	6	AR410771	AR410771 Sequence
831	58	2.6	1761	9	BC054519	BC054519 Homo sapi	904	58	2.6	1985	6	AR439135	AR439135 Sequence
832	58	2.6	1762	10	BC022118	BC022118 Mus muscu	905	58	2.6	1985	6	AR473155	AR473155 Sequence
833	58	2.6	1768	8	SCSACPD	X78935 S. commerson	906	58	2.6	1985	6	AX375960	AX375960 Sequence
834	58	2.6	1769	9	BC025749	BC025749 Homo sapi	907	58	2.6	1985	6	AX697621	AX697621 Sequence
835	58	2.6	1780	10	BC062053	BC062053 Rattus no	908	58	2.6	1985	6	BD075542	BD075542 Secretary
836	58	2.6	1788	9	BC044944	BC044944 Homo sapi	909	58	2.6	1985	6	BD172402	BD172402 Secreted
837	58	2.6	1788	9	BSM801263	BSM801263 Homo sapi	910	58	2.6	1985	6	BD172721	BD172721 Secreted
838	58	2.6	1790	10	BC024638	BC024638 Mus muscu	911	58	2.6	1985	6	BD173040	BD173040 Secreted
839	58	2.6	1791	9	BC015779	BC015779 Homo sapi	912	58	2.6	1985	6	BD173359	BD173359 Secreted
840	58	2.6	1797	9	AK027161	AK027161 Homo sapi	913	58	2.6	1985	9	AY358500	AY358500 Homo sapi
841	58	2.6	1798	9	BC042845	BC042845 Homo sapi	914	58	2.6	1987	9	EX957216	EX957216 Homo sapi
842	58	2.6	1805	6	CQ413955	CQ413955 Sequence	915	58	2.6	1993	9	AK026793	AK026793 Homo sapi
843	58	2.6	1805	8	AY036609	AY036609 Triticum	916	58	2.6	1996	9	BC062574	BC062574 Homo sapi
844	58	2.6	1808	9	AK000636	AK000636 Homo sapi	917	58	2.6	2005	9	BC040276	BC040276 Homo sapi
845	58	2.6	1811	6	CQ414890	CQ414890 Sequence	918	58	2.6	2005	9	BSM803426	BSM803426
846	58	2.6	1817	9	BC020499	BC020499 Homo sapi	919	58	2.6	2009	9	BC050391	BC050391 Homo sapi
847	58	2.6	1819	9	BC009930	BC009930 Homo sapi	920	58	2.6	2009	10	BC031165	BC031165 Mus muscu
848	58	2.6	1820	5	BC066434	BC066434 Danio rer	921	58	2.6	2016	8	AF428076	AF428076 Paracocci
849	58	2.6	1820	9	BC064387	BC064387 Homo sapi	922	58	2.6	2016	8	BC066638	BC066638 Danio rer
850	58	2.6	1822	9	AF061836	AF061836 Homo sapi	923	58	2.6	2021	5	BC044045	BC044045 Xenopus 1
851	58	2.6	1822	10	BC058602	BC058602 Mus muscu	924	58	2.6	2027	10	BC052191	BC052191 Mus muscu
852	58	2.6	1823	9	BC008904	BC008904 Homo sapi	925	58	2.6	2030	9	BC041637	BC041637 Homo sapi
853	58	2.6	1824	9	BC028094	BC028094 Homo sapi	926	58	2.6	2030	10	BC058229	BC058229 Mus muscu
854	58	2.6	1825	9	BC063388	BC063388 Homo sapi	927	58	2.6	2033	10	BC021915	BC021915 Mus muscu
855	58	2.6	1831	10	BC028896	BC028896 Mus muscu	928	58	2.6	2034	5	BC067669	BC067669 Danio rer
856	58	2.6	1833	9	BSM802685	BSM802685 Homo sapi	929	58	2.6	2045	6	AR229196	AR229196 Sequence
857	58	2.6	1838	5	BC053151	BC053151 Danio rer	930	58	2.6	2045	6	AX810698	AX810698 Sequence
858	58	2.6	1839	10	BC053440	BC053440 Mus muscu	931	58	2.6	2045	6	BD084173	BD084173 28 human
859	58	2.6	1842	10	BC055473	BC055473 Mus muscu	932	58	2.6	2047	10	BC053455	BC053455 Mus muscu
860	58	2.6	1846	9	BC008280	BC008280 Homo sapi	933	58	2.6	2048	9	BC044243	BC044243 Homo sapi
861	58	2.6	1847	3	AY069729	AY069729 Drosophila	934	58	2.6	2050	5	BC066614	BC066614 Danio rer
862	58	2.6	1849	5	BC061396	BC061396 Xenopus t	935	58	2.6	2060	10	BC049179	BC049179 Mus muscu
863	58	2.6	1851	10	BC017684	BC017684 Mus muscu	936	58	2.6	2063	10	BC003900	BC003900 Mus muscu
864	58	2.6	1856	3	BT003792	BT003792 Drosophila	937	58	2.6	2064	8	BT009245	BT009245 Triticum
865	58	2.6	1860	9	BC058897	BC058897 Homo sapi	938	58	2.6	2065	9	BC024260	BC024260 Homo sapi
866	58	2.6	1864	14	SMVAJ6202	AY006202 Sugarcane	939	58	2.6	2069	9	BC007641	BC007641 Homo sapi
867	58	2.6	1872	6	AR208578	AR208578 Sequence	940	58	2.6	2070	10	BC046278	BC046278 Mus muscu
868	58	2.6	1872	8	BT009301	BT009301 Triticum	941	58	2.6	2072	9	BC044245	BC044245 Homo sapi
869	58	2.6	1872	10	BC023437	BC023437 Mus muscu	942	58	2.6	2073	10	BC060677	BC060677 Mus muscu
870	58	2.6	1879	10	BC060146	BC060146 Mus muscu	943	58	2.6	2074	9	BC035912	BC035912 Homo sapi
871	58	2.6	1880	6	CQ769491	CQ769491 Sequence	944	58	2.6	2076	10	BC010309	BC010309 Mus muscu
872	58	2.6	1884	9	AF086921	AF086921 Homo sapi	945	58	2.6	2079	10	BC029014	BC029014 Mus muscu
873	58	2.6	1885	10	BC051143	BC051143 Mus muscu	946	58	2.6	2081	5	BSM802275	BSM802275
874	58	2.6	1888	5	BC068332	BC068332 Danio rer	947	58	2.6	2082	9	BC071171	BC071171 Homo sapi
875	58	2.6	1889	5	AB025103	AB025103 Gallus ga	948	58	2.6	2090	9	BC038500	BC038500 Mus muscu
876	58	2.6	1889	9	AB066553	AB066553 Macaca fa	949	58	2.6	2094	10	BC033384	BC033384 Mus muscu
877	58	2.6	1890	9	AK025208	AK025208 Homo sapi	950	58	2.6	2094	10	BC006472	BC006472 Homo sapi
878	58	2.6	1892	9	BC065843	BC065843 Homo sapi	951	58	2.6	2095	9	BC006472	BC006472 Homo sapi
879	58	2.6	1894	9	BC011889	BC011889 Homo sapi	952	58	2.6	2096	3	AY061097	AY061097 Drosophila
880	58	2.6	1894	9	BSM803495	BSM803495 Homo sapi	953	58	2.6	2103	10	BC022603	BC022603 Mus muscu
881	58	2.6	1900	9	BC025963	BC025963 Homo sapi	954	58	2.6	2104	10	BC023321	BC023321 Mus muscu
882	58	2.6	1900	9	BC063603	BC063603 Homo sapi	955	58	2.6	2106	9	BC027948	BC027948 Homo sapi
883	58	2.6	1903	10	BC023012	BC023012 Mus muscu	956	58	2.6	2115	5	BC051611	BC051611 Danio rer
884	58	2.6	1908	9	AK025209	AK025209 Homo sapi	957	58	2.6	2116	10	BC030862	BC030862 Mus muscu
885	58	2.6	1915	10	BC046597	BC046597 Mus muscu	958	58	2.6	2119	8	BT009049	BT009049 Triticum
886	58	2.6	1920	10	BC059229	BC059229 Mus muscu	959	58	2.6	2122	9	BC037277	BC037277 Homo sapi
887	58	2.6	1928	9	BC039741	BC039741 Homo sapi	960	58	2.6	2134	5	XLCTG	X84990 X. laevis CC
888	58	2.6	1929	10	BC058811	BC058811 Mus muscu	961	58	2.6	2138	9	BC067301	BC067301 Homo sapi
889	58	2.6	1932	9	AK026947	AK026947 Homo sapi	962	58	2.6	2140	9	BC062566	BC062566 Homo sapi
890	58	2.6	1934	9	AK025407	AK025407 Homo sapi	963	58	2.6	2145	9	BC037968	BC037968 Homo sapi
891	58	2.6	1935	9	BC042416	BC042416 Homo sapi	964	58	2.6	2149	9	BC072428	BC072428 Homo sapi
892	58	2.6	1945	9	BC072393	BC072393 Homo sapi	965	58	2.6	2151	9	BC032474	BC032474 Homo sapi
893	58	2.6	1953	9	BC029049	BC029049 Homo sapi	966	58	2.6	2153	10	RNF4502C	X55446 Rat mRNA fo
894	58	2.6	1956	9	BC052580	BC052580 Homo sapi	967	58	2.6	2159	3	AY119209	AY119209 Drosophila
895	58	2.6	1958	5	BC064256	BC064256 Xenopus t	968	58	2.6	2164	9	BC028132	BC028132 Homo sapi

969	58	2.6	2207	9	BC058880	BC058880 Homo sapi	1042	58	2.6	2667	5	BC064852	BC064852 Xenopus t
970	58	2.6	2217	9	BC073932	BC073932 Homo sapi	1043	58	2.6	2690	10	BC058562	BC058562 Mus muscu
971	58	2.6	2220	9	BC007556	BC007556 Homo sapi	1044	58	2.6	2699	9	BC013364	BC013364 Homo sapi
972	58	2.6	2230	9	BC069230	BC069230 Homo sapi	1045	58	2.6	2702	9	BC017163	BC017163 Homo sapi
973	58	2.6	2238	10	AF356506	AF356506 Mus muscu	1046	58	2.6	2710	3	DMORPROT	X92840 D.melanogas
974	58	2.6	2246	6	AR212256	AR212256 Sequence	1047	58	2.6	2736	9	HSN801348	AL133077 Homo sapi
975	58	2.6	2246	6	AR265251	AR265251 Sequence	1048	58	2.6	2754	10	BC066817	BC066817 Mus muscu
976	58	2.6	2246	10	AF017152	AF017152 Mus muscu	1049	58	2.6	2762	10	BC006698	BC006698 Mus muscu
977	58	2.6	2247	5	BC058510	BC058510 Danio rer	1050	58	2.6	2771	10	BC027055	BC027055 Mus muscu
978	58	2.6	2257	6	AX048774	AX048774 Sequence	1051	58	2.6	2773	10	BC064468	BC064468 Mus muscu
979	58	2.6	2266	9	BC041164	BC041164 Homo sapi	1052	58	2.6	2789	10	BC026672	BC026672 Mus muscu
980	58	2.6	2275	9	AF218023	AF218023 Homo sapi	1053	58	2.6	2791	10	BC046625	BC046625 Mus muscu
981	58	2.6	2287	9	BC044220	BC044220 Homo sapi	1054	58	2.6	2800	9	BC014632	BC014632 Homo sapi
982	58	2.6	2291	9	AK000753	AK000753 Homo sapi	1055	58	2.6	2800	9	BC053596	BC053596 Homo sapi
983	58	2.6	2298	5	BC074532	BC074532 Xenopus t	1056	58	2.6	2809	10	BC053333	BC053333 Mus muscu
984	58	2.6	2298	9	BC029162	BC029162 Homo sapi	1057	58	2.6	2811	10	BC051178	BC051178 Mus muscu
985	58	2.6	2313	10	BC029670	BC029670 Mus muscu	1058	58	2.6	2813	9	AF217991	AF217991 Homo sapi
986	58	2.6	2322	9	BC017240	BC017240 Homo sapi	1059	58	2.6	2816	9	BC013375	BC013375 Homo sapi
987	58	2.6	2324	5	BC062381	BC062381 Danio rer	1060	58	2.6	2827	9	HSN807053	BC013975 Homo sapi
988	58	2.6	2327	10	MMU96683	U96683 Mus musculu	1061	58	2.6	2855	6	AX574572	AX574572 Sequence
989	58	2.6	2330	9	BC006555	BC006555 Homo sapi	1062	58	2.6	2855	9	AX358127	AX358127 Homo sapi
990	58	2.6	2366	9	BC017481	BC017481 Homo sapi	1063	58	2.6	2873	9	BC042488	BC042488 Homo sapi
991	58	2.6	2368	9	HSN802593	AL162062 Homo sapi	1064	58	2.6	2873	10	BC046232	BC046232 Mus muscu
992	58	2.6	2369	9	AK074384	AK074384 Homo sapi	1065	58	2.6	2874	6	AX815603	AX815603 Sequence
993	58	2.6	2371	9	HSN805927	EX537833 Homo sapi	1066	58	2.6	2875	9	HSN808745	EX648594 Homo sapi
994	58	2.6	2374	3	AY119126	AY119126 Drosophil	1067	58	2.6	2881	9	IR2004669	AL389951 Homo sapi
995	58	2.6	2379	9	BC025698	BC025698 Homo sapi	1068	58	2.6	2886	10	BC025599	BC025599 Mus muscu
996	58	2.6	2388	10	BC030895	BC030895 Mus muscu	1069	58	2.6	2890	10	BC036168	BC036168 Mus muscu
997	58	2.6	2397	9	BC052990	BC052990 Homo sapi	1070	58	2.6	2907	9	BC042125	BC042125 Homo sapi
998	58	2.6	2400	9	BC053347	BC053347 Homo sapi	1071	58	2.6	2908	10	BC043702	BC043702 Mus muscu
999	58	2.6	2403	9	HSN808752	EX648601 Homo sapi	1072	58	2.6	2909	10	BC053050	BC053050 Mus muscu
1000	58	2.6	2415	9	BC028002	BC028002 Homo sapi	1073	58	2.6	2924	6	AX683129	AX683129 Sequence
1001	58	2.6	2415	9	BC032459	BC032459 Homo sapi	1074	58	2.6	2924	9	BC063554	BC063554 Homo sapi
1002	58	2.6	2432	10	BC0303959	BC0303959 Mus muscu	1075	58	2.6	2924	10	S68736	S68736 Rattus sap.
1003	58	2.6	2438	6	AR310306	AR310306 Sequence	1076	58	2.6	2940	9	HSN803172	AL832219 Homo sapi
1004	58	2.6	2438	6	AX097774	AX097774 Sequence	1077	58	2.6	2943	9	HSN803526	BC017172 Homo sapi
1005	58	2.6	2443	9	BC063448	BC063448 Homo sapi	1078	58	2.6	2968	9	BC041697	AL832219 Homo sapi
1006	58	2.6	2445	9	BC038798	BC038798 Homo sapi	1079	58	2.6	2975	9	BC012172	BC012172 Homo sapi
1007	58	2.6	2453	9	HSN807676	EX647530 Homo sapi	1080	58	2.6	2980	6	BD270060	BD270060 Secretd
1008	58	2.6	2454	10	BC031113	BC031113 Mus muscu	1081	58	2.6	2993	10	BC052189	BC052189 Mus muscu
1009	58	2.6	2465	5	BC070798	BC070798 Xenopus l	1082	58	2.6	3002	6	AX354181	AX354181 Sequence
1010	58	2.6	2466	9	HSN802197	AL137712 Homo sapi	1083	58	2.6	3002	9	HSN808510	AX648362 Homo sapi
1011	58	2.6	2468	8	AF053585	AF053585 Oryza sat	1084	58	2.6	3039	3	AY280848	AY280848 Apis mell
1012	58	2.6	2474	3	AY220909	AY220909 Helicover	1085	58	2.6	3039	3	AY220924	AY129024 Homo sapi
1013	58	2.6	2490	5	BC073845	BC073845 Homo sapi	1086	58	2.6	3046	9	AY129024	AY129024 Homo sapi
1014	58	2.6	2496	5	BC079755	BC079755 Xenopus l	1087	58	2.6	3048	10	BC054124	BC054124 Mus muscu
1015	58	2.6	2500	9	BC035690	BC035690 Homo sapi	1088	58	2.6	3055	6	AX430977	AX430977 Sequence
1016	58	2.6	2533	5	HSN803787	BC064702 Danio rer	1089	58	2.6	3057	9	BC019256	BC019256 Homo sapi
1017	58	2.6	2533	9	BC006690	BC006690 Mus muscu	1090	58	2.6	3061	10	AF180525	AF180525 Rattus no
1018	58	2.6	2533	10	BC006690	BC006690 Mus muscu	1091	58	2.6	3096	9	BC035284	BC035284 Homo sapi
1019	58	2.6	2539	10	BC006050	BC006050 Mus muscu	1092	58	2.6	3120	9	BC038443	BC038443 Homo sapi
1020	58	2.6	2542	10	BC060983	BC060983 Mus muscu	1093	58	2.6	3124	6	AR235862	AR235862 Sequence
1021	58	2.6	2553	10	BC061558	BC061558 Rattus no	1094	58	2.6	3124	6	AX350342	AX350342 Sequence
1022	58	2.6	2562	6	AX477654	AX477654 Sequence	1095	58	2.6	3141	3	BT011466	BT011466 Drosophil
1023	58	2.6	2562	9	AK025708	AK025708 Homo sapi	1096	58	2.6	3143	10	BC029653	BC029653 Homo sapi
1024	58	2.6	2564	9	BC017181	BC017181 Homo sapi	1097	58	2.6	3151	9	BC027028	BC027028 Mus muscu
1025	58	2.6	2565	9	BC007198	BC007198 Homo sapi	1098	58	2.6	3154	10	BC065074	BC065074 Mus muscu
1026	58	2.6	2565	9	BC017438	BC017438 Homo sapi	1099	58	2.6	3166	10	BC053054	BC053054 Mus muscu
1027	58	2.6	2565	9	BC030233	BC030233 Homo sapi	1100	58	2.6	3166	10	BC053054	BC060096 Mus muscu
1028	58	2.6	2578	9	BC064805	BC064805 Homo sapi	1101	58	2.6	3211	10	AX060096	AX060096 Mus muscu
1029	58	2.6	2586	9	BC006207	BC006207 Homo sapi	1102	58	2.6	3224	6	AX754970	AX754970 Sequence
1030	58	2.6	2594	6	AX5787	AX5787 Sequence 25	1103	58	2.6	3224	9	BC032429	BC032429 Homo sapi
1031	58	2.6	2594	8	CNACON	X82840 C.melo mRNA	1104	58	2.6	3224	5	BC068779	BC068779 Xenopus l
1032	58	2.6	2600	5	BC035596	BC035596 Homo sapi	1105	58	2.6	3254	9	BC030523	AF522186 Rattus no
1033	58	2.6	2601	5	BC072034	BC072034 Xenopus l	1106	58	2.6	3254	9	BC030523	BC030523 Homo sapi
1034	58	2.6	2626	10	BC013637	BC013637 Mus muscu	1107	58	2.6	3282	10	AF030513	AF030513 Mus muscu
1035	58	2.6	2628	5	BC053210	BC053210 Danio rer	1108	58	2.6	3287	10	BC028722	BC028722 Mus muscu
1036	58	2.6	2628	6	I66342	I66342 Sequence 1	1109	58	2.6	3305	10	BC040407	BC040407 Mus muscu
1037	58	2.6	2630	6	BC033813	BC033813 Homo sapi	1110	58	2.6	3305	9	BC035372	BC035372 Homo sapi
1038	58	2.6	2634	6	AR241385	AR241385 Sequence	1111	58	2.6	3325	9	HSN802260	AL137527 Homo sapi
1039	58	2.6	2634	6	AX006092	AX006092 Sequence	1112	58	2.6	3327	9	HSN802260	BC054371 Mus muscu
1040	58	2.6	2634	6	BD080224	BD080224 Starch de	1113	58	2.6	3329	10	BC054371	BC054371 Mus muscu
1041	58	2.6	2634	8	AY132998	AY132998 Solanum t	1114	58	2.6	3330	9	BC037992	BC037992 Homo sapi

1115	58	2.6	3350	6	AR068182 Sequence	1188	58	2.6	4856	10	BC052326	BC052326 Mus muscu
1116	58	2.6	3350	6	AR076934 Sequence	1189	58	2.6	4857	10	BC030187	BC030187 Mus muscu
1117	58	2.6	3350	6	AR078767 Sequence	1190	58	2.6	5223	5	BC044985	BC044985 Xenopus 1
1118	58	2.6	3392	3	AF300334	1191	58	2.6	5280	10	BC052198	BC052198 Mus muscu
1119	58	2.6	3395	5	AF300334 Dictyoste	1192	58	2.6	5344	6	AX346356	AX346356 Homo sapi
1120	58	2.6	3399	5	BC077830	1193	58	2.6	5418	6	AX346356	AX346356 Homo sapi
1121	58	2.6	3401	9	BC041867	1194	58	2.6	5559	9	AX346356	AX346356 Homo sapi
1122	58	2.6	3402	3	BT003641	1195	58	2.6	5644	9	AX346356	AX346356 Homo sapi
1123	58	2.6	3410	10	BC037109	1196	58	2.6	5735	5	BC063260	BC063260 Homo sapi
1124	58	2.6	3412	10	BC066648	1197	58	2.6	5735	5	AB034701	AB034701 Xenopus 1
1125	58	2.6	3415	10	BC023677	1198	58	2.6	6163	10	BC052150	BC052150 Mus muscu
1126	58	2.6	3418	9	HSB04646	1199	58	2.6	6200	9	AF324064	AF324064 Homo sapi
1127	58	2.6	3430	3	BT003625	1200	58	2.6	6239	9	AF324064	AF324064 Homo sapi
1128	58	2.6	3447	9	BC052983	1201	58	2.6	6430	6	CO491854	CO491854 Sequence
1129	58	2.6	3447	9	HSB01484	1202	58	2.6	6430	6	CO491854	CO491854 Sequence
1130	58	2.6	3459	9	BC052964	1203	58	2.6	6559	5	BC063724	BC063724 Xenopus 1
1131	58	2.6	3469	9	HSB000438	1204	58	2.6	7165	9	HSB003503	HSB003503 Homo sapi
1132	58	2.6	3505	9	HSB086327	1205	58	2.6	7240	9	HSB0808174	HSB0808174 Homo sapi
1133	58	2.6	3505	10	BC068304	1206	58	2.6	8000	6	BD226819	BD226819 Alphaviru
1134	58	2.6	3506	9	BC062616	1207	58	2.6	8100	6	BD226819	BD226819 Alphaviru
1135	58	2.6	3520	9	HSB04704	1208	58	2.6	8100	6	AR243302	AR243302 Sequence
1136	58	2.6	3544	10	BC042521	1209	58	2.6	8694	9	HSB0808392	HSB0808392 Homo sapi
1137	58	2.6	3582	10	BC053927	1210	58	2.6	10467	6	AX323839	AX323839 Sequence
1138	58	2.6	3620	9	HSB04516	1211	58	2.6	11000	6	BD138792	BD138792 Alphaviru
1139	58	2.6	3621	5	BC068908	1212	58	2.6	11517	6	AR001293	AR001293 Sequence
1140	58	2.6	3657	10	BC050054	1213	58	2.6	11517	6	AR001293	AR001293 Sequence
1141	58	2.6	3694	10	AF05809	1214	58	2.6	11517	6	AR130391	AR130391 Sequence
1142	58	2.6	3697	9	AB048948	1215	58	2.6	12295	6	BD138799	BD138799 Alphaviru
1143	58	2.6	3713	9	HSB0807381	1216	58	2.6	12464	6	BD263357	BD263357 Compositi
1144	58	2.6	3724	5	BC068927	1217	58	2.6	12972	3	AF088979	AF088979 Dictyoste
1145	58	2.6	3747	9	HSB05597	1218	58	2.6	15418	6	BD226816	BD226816 Alphaviru
1146	58	2.6	3768	9	BC051845	1219	58	2.6	15528	6	A93016	A93016 Sequence 4
1147	58	2.6	3782	9	HSB04515	1220	58	2.6	15528	12	PEAVEN	Y07862 Cloning vec
1148	58	2.6	3835	9	BC063854	1221	58	2.6	15538	6	AR243299	AR243299 Sequence
1149	58	2.6	3857	10	BC040362	1222	58	2.6	39984	3	AC114258	AC114258 Dictyoste
1150	58	2.6	3864	3	AF122110	1223	58	2.6	64814	8	NCB11J21	NCB11J21 Neurospor
1151	58	2.6	3870	9	HSB06049	1224	58	2.6	79554	8	NCB11B23	NCB11B23 Neurospor
1152	58	2.6	3911	10	BC031166	1225	58	2.6	80272	5	AC004438	AC004438 Drosophil
1153	58	2.6	3916	10	BC018439	1226	58	2.6	83240	3	AC004438	AC004438 Drosophil
1154	58	2.6	3919	10	BC067070	1227	58	2.6	89232	5	AL591175	AL591175 Zebrafish
1155	58	2.6	3960	9	BC038239	1228	58	2.6	94153	2	AC139443	AC139443 Rattus no
1156	58	2.6	4008	10	BC025619	1229	58	2.6	110000	2	AC131059	AC131059 Continnuation (3 of
1157	58	2.6	4050	9	BC047244	1230	58	2.6	111158	9	AP004987	AP004987 Homo sapi
1158	58	2.6	4121	6	AR344255	1231	58	2.6	126590	2	AP001112	AP001112 Homo sapi
1159	58	2.6	4121	6	AX019229 Sequence	1232	58	2.6	126611	10	AL928592	AL928592 Mouse DNA
1160	58	2.6	4121	6	BD130455	1233	58	2.6	136240	3	AC117070	AC117070 Dictyoste
1161	58	2.6	4143	5	GSDYNACT	1234	58	2.6	136240	3	AC117070	AC117070 Dictyoste
1162	58	2.6	4168	6	AX393305	1235	58	2.6	137436	9	AF348209	AF348209 Homo sapi
1163	58	2.6	4169	10	BC053919	1236	58	2.6	138426	10	AC142451	AC142451 Mus muscu
1164	58	2.6	4184	10	BC058993	1237	58	2.6	138426	10	AC142451	AC142451 Mus muscu
1165	58	2.6	4204	10	BC052212	1238	58	2.6	139936	2	AC139411	AC139411 Rattus no
1166	58	2.6	4236	5	BC071048	1239	58	2.6	139936	9	AY233855	AY233855 Homo sapi
1167	58	2.6	4250	9	HSB003434	1240	58	2.6	142951	2	CR391966	CR391966 Danlo rer
1168	58	2.6	4274	6	AX042021	1241	58	2.6	146846	2	AC150264	AC150264 Aedes aeg
1169	58	2.6	4274	10	AF192401	1242	58	2.6	147889	2	AC018534	AC018534 Homo sapi
1170	58	2.6	4295	10	BC057367	1243	58	2.6	148250	9	AL353625	AL353625 Human DNA
1171	58	2.6	4318	9	BC016029	1244	58	2.6	149152	10	AC124388	AC124388 Mus muscu
1172	58	2.6	4362	10	BC052329	1245	58	2.6	157847	10	AC122511	AC122511 Mus muscu
1173	58	2.6	4380	9	AF000145	1246	58	2.6	157998	10	AC140354	AC140354 Mus muscu
1174	58	2.6	4432	3	AY095206	1247	58	2.6	162972	10	AC144579	AC144579 Mus muscu
1175	58	2.6	4486	10	BC054123	1248	58	2.6	163121	2	AC122406	AC122406 Mus muscu
1176	58	2.6	4487	10	BC023962	1249	58	2.6	165978	2	AC087132	AC087132 Mus muscu
1177	58	2.6	4493	9	BC064843	1250	58	2.6	172830	10	AC131329	AC131329 Mus muscu
1178	58	2.6	4499	9	HSB003130	1251	58	2.6	175611	2	AC020621	AC020621 Homo sapi
1179	58	2.6	4508	10	AF192402	1252	58	2.6	176306	3	AC007186	AC007186 Drosophil
1180	58	2.6	4519	10	BC058994	1253	58	2.6	176329	2	AC117968	AC117968 Rattus no
1181	58	2.6	4538	5	AF182215	1254	58	2.6	179439	2	AC018874	AC018874 Homo sapi
1182	58	2.6	4543	10	BC049133	1255	58	2.6	179676	2	AC012221	AC012221 Homo sapi
1183	58	2.6	4598	9	BC032463	1256	58	2.6	186950	10	BX855608	BX855608 Mouse DNA
1184	58	2.6	4659	9	HSB0806121	1257	58	2.6	190516	10	AC110376	AC110376 Mus muscu
1185	58	2.6	4723	5	BC063192	1258	58	2.6	190792	10	AC129019	AC129019 Mus muscu
1186	58	2.6	4841	9	BC052565	1259	58	2.6	192874	10	AL672019	AL672019 Mouse DNA
1187	58	2.6	4845	9	HSB0808798	1260	58	2.6	197571	10	BX890555	BX890555 Mouse DNA

1261	58	2.6	199372	2	AC135219	AC135219 Sus scrofa	1334	57	2.5	165	6	AX977324	AX977324 Sequence
1262	58	2.6	203225	5	BX255942	BX255942 Zebrafish	1335	57	2.5	165	6	BD112183	BD112183 EST and e
c1263	58	2.6	204021	2	AC139352	AC139352 Rattus no	1336	57	2.5	169	6	CQ663079	CQ663079 Sequence
1264	58	2.6	204334	10	AC079644	AC079644 Mus muscu	1337	57	2.5	169	6	AX419752	AX419752 Sequence
c1265	58	2.6	204591	2	AC136341	AC136341 Mus muscu	1338	57	2.5	169	6	AX980446	AX980446 Sequence
c1266	58	2.6	205515	2	AC118905	AC118905 Rattus no	1339	57	2.5	169	6	BD115305	BD115305 EST and e
c1267	58	2.6	210688	2	AC139257	AC139257 Homo sapi	1340	57	2.5	173	6	AX284784	AX284784 Sequence
1268	58	2.6	213167	9	AC008588	AC008588 Homo sapi	1341	57	2.5	175	6	CQ769330	CQ769330 Sequence
1269	58	2.6	213565	2	CR354428	CR354428 Danio rer	1342	57	2.5	176	6	CQ677241	CQ677241 Sequence
1270	58	2.6	217279	2	AC117787	AC117787 Mus muscu	1343	57	2.5	176	6	AX422406	AX422406 Sequence
c1271	58	2.6	217327	2	AC111930	AC111930 Rattus no	1344	57	2.5	176	6	AX983100	AX983100 Sequence
1272	58	2.6	219673	2	AC139283	AC139283 Homo sapi	1345	57	2.5	176	6	BD117959	BD117959 EST and e
c1273	58	2.6	219941	2	AC099717	AC099717 Mus muscu	1346	57	2.5	177	6	AX970244	AX970244 Sequence
1274	58	2.6	227074	2	AC060772	AC060772 Mus muscu	1347	57	2.5	177	6	BD108963	BD108963 EST and e
1275	58	2.6	228428	2	AC099217	AC099217 Rattus no	1348	57	2.5	177	6	CQ486695	CQ486695 Sequence
c1276	58	2.6	228878	2	AC112329	AC112329 Rattus no	1349	57	2.5	178	6	AX486695	AX486695 Sequence
c1277	58	2.6	230886	10	AL935264	AL935264 Mouse DNA	1350	57	2.5	179	6	AX418078	AX418078 Sequence
1278	58	2.6	236489	2	AC110553	AC110553 Mus muscu	1351	57	2.5	179	6	AX978772	AX978772 Sequence
c1279	58	2.6	237913	2	AC104208	AC104208 Mus muscu	1352	57	2.5	179	6	BD113631	BD113631 EST and e
c1280	58	2.6	244105	2	AC098897	AC098897 Rattus no	1353	57	2.5	185	6	CQ524628	CQ524628 Sequence
1281	58	2.6	249995	2	AC121434	AC121434 Rattus no	1354	57	2.5	187	6	CQ701146	CQ701146 Sequence
1282	58	2.6	253149	2	AC107527	AC107527 Rattus no	1355	57	2.5	188	6	CQ527214	CQ527214 Sequence
1283	58	2.6	253313	2	AC102731	AC102731 Mus muscu	1356	57	2.5	189	6	AX284585	AX284585 Sequence
1284	58	2.6	254733	3	AC117075	AC117075 Dictyoste	1357	57	2.5	189	6	AX413164	AX413164 Sequence
1285	58	2.6	256673	2	AC087146	AC087146 Mus muscu	1358	57	2.5	194	6	AX969998	AX969998 Sequence
1286	58	2.6	263283	2	AC109389	AC109389 Rattus no	1359	57	2.5	194	6	BD108717	BD108717 EST and e
c1287	58	2.6	263319	2	AC125258	AC125258 Mus muscu	1360	57	2.5	195	6	AX361368	AX361368 Sequence
c1288	58	2.6	272652	2	AC109709	AC109709 Rattus no	1361	57	2.5	196	6	CQ525476	CQ525476 Sequence
c1289	58	2.6	274909	2	AC131169	AC131169 Rattus no	1362	57	2.5	198	6	CQ487384	CQ487384 Sequence
1290	58	2.6	289460	3	AE003630	AE003630 Drosophi	1363	57	2.5	198	6	CQ820245	CQ820245 Sequence
c1291	58	2.6	302156	3	AC116977	AC116977 Dictyoste	1364	57	2.5	198	6	CQ820246	CQ820246 Sequence
c1292	58	2.6	308479	2	AC094671	AC094671 Rattus no	1365	57	2.5	199	6	CQ523406	CQ523406 Sequence
1293	58	2.6	318145	2	AC122576	AC122576 Rattus no	1366	57	2.5	201	11	BV199973	BV199973 sqmnm20284
c1294	58	2.6	349980	6	AX344553	AX344553 Sequence	1367	57	2.5	201	11	BV200358	BV200358 sqmnm20393
c1295	58	2.6	349980	6	AX344558	AX344558 Sequence	1368	57	2.5	201	11	BV200361	BV200361 sqmnm20395
1296	57	2.5	92	6	AX422123	AX422123 Sequence	1369	57	2.5	201	11	BV200378	BV200378 sqmnm20400
1297	57	2.5	92	6	AX982817	AX982817 Sequence	1370	57	2.5	201	11	BV200379	BV200379 sqmnm20400
1298	57	2.5	92	6	BD117676	BD117676 EST and e	c1371	57	2.5	201	11	BV200460	BV200460 sqmnm20420
1299	57	2.5	97	6	AX417589	AX417589 Sequence	c1372	57	2.5	201	11	BV201749	BV201749 sqmnm20728
1300	57	2.5	97	6	AX978283	AX978283 Sequence	1373	57	2.5	201	11	BV202083	BV202083 sqmnm20814
1301	57	2.5	97	6	BD113142	BD113142 EST and e	1374	57	2.5	201	11	BV202595	BV202595 sqmnm20945
1302	57	2.5	106	6	BD021994	BD021994 Secrete	1375	57	2.5	201	11	BV204012	BV204012 sqmnm21375
c1303	57	2.5	107	9	S77771	S77771 aspartylglu	1376	57	2.5	201	11	BV204551	BV204551 sqmnm21558
1304	57	2.5	109	6	AR423095	AR423095 Sequence	1377	57	2.5	201	11	BV207013	BV207013 sqmnm22249
1305	57	2.5	109	6	AX983789	AX983789 Sequence	1378	57	2.5	201	11	BV208193	BV208193 sqmnm22575
1306	57	2.5	109	6	BD118648	BD118648 EST and e	1379	57	2.5	202	11	BV088830	BV088830 RPAWMSBQ
1307	57	2.5	127	6	AR422436	AR422436 Sequence	1380	57	2.5	202	11	BV097344	BV097344 RPAWMSBQ
1308	57	2.5	127	6	AX983130	AX983130 Sequence	1381	57	2.5	205	6	CQ525020	CQ525020 Sequence
1309	57	2.5	127	6	BD117989	BD117989 EST and e	1382	57	2.5	209	10	BC036353	BC036353 Mus muscu
1310	57	2.5	134	6	AR426936	AR426936 Sequence	1383	57	2.5	210	6	CQ525883	CQ525883 Sequence
1311	57	2.5	134	6	AX987630	AX987630 Sequence	1384	57	2.5	214	6	CQ487824	CQ487824 Sequence
1312	57	2.5	134	6	BD122489	BD122489 EST and e	1385	57	2.5	215	6	CQ526670	CQ526670 Sequence
1313	57	2.5	137	6	AR426937	AR426937 Sequence	1386	57	2.5	216	6	CQ525470	CQ525470 Sequence
1314	57	2.5	137	6	AX987631	AX987631 Sequence	1387	57	2.5	218	9	BC051786	BC051786 Sequence
1315	57	2.5	137	6	BD122490	BD122490 EST and e	1388	57	2.5	218	9	BC055094	BC055094 Homo sapi
1316	57	2.5	142	6	AR419304	AR419304 Sequence	1389	57	2.5	221	6	CQ663915	CQ663915 Sequence
1317	57	2.5	142	6	AX979998	AX979998 Sequence	1390	57	2.5	224	6	CQ525227	CQ525227 Sequence
1318	57	2.5	142	6	BD114857	BD114857 EST and e	1391	57	2.5	235	6	CQ677257	CQ677257 Sequence
1319	57	2.5	147	6	AX418757	AX418757 Sequence	1392	57	2.5	236	6	CQ664217	CQ664217 Sequence
1320	57	2.5	147	6	AX979451	AX979451 Sequence	1393	57	2.5	241	6	CQ487383	CQ487383 Sequence
1321	57	2.5	147	6	BD114310	BD114310 EST and e	1394	57	2.5	241	6	CQ526281	CQ526281 Sequence
1322	57	2.5	150	6	AR417159	AR417159 Sequence	1395	57	2.5	244	6	AX408053	AX408053 Sequence
1323	57	2.5	150	6	AX977853	AX977853 Sequence	1396	57	2.5	244	6	CQ524135	CQ524135 Sequence
1324	57	2.5	150	6	BD112712	BD112712 EST and e	1397	57	2.5	249	6	AX427647	AX427647 Sequence
1325	57	2.5	153	6	CQ700107	CQ700107 Sequence	1398	57	2.5	249	6	AX988341	AX988341 Sequence
1326	57	2.5	160	6	AR418838	AR418838 Sequence	1399	57	2.5	249	6	BD123200	BD123200 EST and e
1327	57	2.5	160	6	AX979532	AX979532 Sequence	1400	57	2.5	250	6	CQ526214	CQ526214 Sequence
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DEFINITION AX358756
ACCESSION AX358756
VERSION AX358756.1 GI:37182630
KEYWORDS FLI CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 2242)
Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,
Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,
Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,
Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V.,
Stinson,J., Vagts,A., Vanden,R., Watanabe,C., Wieand,D., Woods,K.,
Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
Goddard,A., Wood,W.I. and Godowski,P.
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
Effort to Identify Novel Human Secreted and Transmembrane Proteins:
A Bioinformatics Assessment
Genome Res. 13 (10), 2265-2270 (2003)
12975309
JOURNAL
PUBMED
REFERENCE
2 (bases 1 to 2242)
Clark,H.F.
Direct Submission
TITLE
Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
Inc., 1 DNA Way, South San Francisco, CA 94080, USA
JOURNAL
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gene
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VERSION AX527744.1 GI:25172275
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ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Kapeller-Libermann R.
TITLE 55054, a novel human metalloprotease and uses therefor
JOURNAL Patent: WO 0226948-A 1 04-APR-2002;
Millennium Pharmaceuticals, Inc. (US)
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RESULT 3

BD205653

LOCUS BD205653 2152 bp DNA linear PAT 17-JUL-2003

DEFINITION 97 human secreted proteins.

ACCESSION BD205653

VERSION BD205653.1 GI:33015423

KEYWORDS JP 2002533058-A/30.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2152)

Ruben, S.M., Florence, K., Ni, J., Rosen, C.A., Carter, K.C., Moore, P.A., Olsen, H.S., Shi, Y., Young, P.E., Wei, F.F., Brewer, L.A., Soppet, D.R., Lafleur, D.W., Endress, G.A. and Ebner, R.

97 human secreted proteins

Patent: JP 2002533058-A 30 08-OCT-2002;

HUMAN GENOME SCIENCES INC

OS Homo sapiens (human)

PN JP 2002533058-A/30

PD 08-OCT-2002

PF 06-MAY-1999 JP 2000548451

PR 12-MAY-1998 US 60/085093,12-MAY-1998 US 60/085094 PR

12-MAY-1998 US 60/085105,12-MAY-1998 US 60/085180 PR

18-MAY-1998 US 60/085927,18-MAY-1998 US 60/085906 PR

18-MAY-1998 US 60/085924,18-MAY-1998 US 60/085922 PR

18-MAY-1998 US 60/085923,18-MAY-1998 US 60/085921 PR

18-MAY-1998 US 60/085925,18-MAY-1998 US 60/085928 PR

18-MAY-1998 US 60/085920

PI STEVEN M RUBEN, KIMBERLY FLORENCE, JIAN NI, CRAIG A ROSEN, KENNETH C CARTER,

PI PAUL A MOORE, HENRIK S OLSEN, YANGGU SHI, PAUL E YOUNG, FING FEI WEI,

PI LAURIE A BREWER, DANIEL R SOPPET, DAVID W LAFLEUR, GREGORY A PI ENDRESS,

PI REINHARD EBNER

PC C12N15/09, C07K14/00, C07K14/435, C07K16/18, C12N1/15, C12N1/19, PC C12N1/21,

PC C12N5/10, C12P21/02, C12N15/00, C12N5/00

CC 97 human secreted proteins.

PH Key Location/Qualifiers

FT source 1..2152

FT /organism='Homo sapiens (human)'. Location/Qualifiers

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FEATURES

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Matches 1891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	1609	ATGAGAAACATTCGAGAA	ATGAGAAATCAACAGGTGGAACTACATAGAGGGAAACCAAT	1668
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Db	1969	TGCNATAGCCCCCAGGATTTGGATTTCCTTCCAACTTTTAGCATATCTTCCAACTTGCNAT	2028
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AX059560			
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DEFINITION	Sequence: 8 from Patent WO0075298.		
ACCESSION	AX059560		
VERSION	AX059560.1	GI:12311667	
KEYWORDS	Homo sapiens (human)		
SOURCE	Homo sapiens		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1		
AUTHORS	Hodgson,D.M., Lincoln,S.E., Russo,P.D., Spiro,P.A., Banville,S.C., Bratcher,S.R., Dufour,G.E., Cohen,H.J., Rosen,B.H., Chalup,M.S., Hillman,J.L., Jones,A.L., Yu,J.Y., Greenawalt,L.B., Panzer,S.R., Roseberry,A.M., Wright,R.J. and Daniels,S.E.		
TITLE	Molecules for disease detection and treatment		
JOURNAL	Patent: WO 0075298-A 8 14-DEC-2000;		
FEATURES	Incyte Genomics, Inc. (US)		
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Qy	625	ATGGGTGGCTCACGGACCCCTATGTGCTGCACGGAGGTAGACGGGAAACTTTATGACGAG	684
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Query Match	71.5%;	Score 1602;	DB 9;	Length 1970;
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Qy	537	GTCAATCTGGCCGAACCTGGGGAGCGATCCACGAAAGCCACCGTGTCTTCTACGGCCAC	596	
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Qy	597	TTGGACCTGCAGCCCTGCTGACCCGGGGCGATGGGTGGCTCACGGACCCCTATGTCTGACG	656	
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Qy	777	TTCAATCAATGAGGGGATGGAAGGCCTGGCTCTGTGCTCCCTGGAGGAACTTGTGAAAAA	836	
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RESULT 8
AX139747
LOCUS
DEFINITION
Sequence 1 from Patent EP1097997.
ACCESSION
AX139747
VERSION
AX139747.1 GI:14275329
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
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AUTHORS
Saudek, V., Smirnova-Robert, T. and Teufel, M.
TITLE
Human carnosinase, its isolation and uses
JOURNAL
Patent: EP 1097997-A 1 09-MAY-2001;
SANOFI-SYNTHELABO (FR)
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Query Match 63.6%; Score 1427; DB 6; Length 1524;
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DEFINITION Sequence 497 from Patent WO0162787.
ACCESSION AX231101
VERSION AX231101.1 GI:15592456
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AUTHORS Herath,H.M., Parekh,R.B., Rohlf,C.O., Terrett,J.A. and Tyson,K.L.
TITLE Diagnosis and treatment of bipolar affective disorder
JOURNAL Patent: WO 0162787-A 497 30-AUG-2001;
Oxford GlycoSciences (UK) Limited (GB)
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LOCUS Sequence 458 from Patent WO0163294.
ACCESSION AX231560
VERSION AX231560.1 GI:15592465
SOURCE
ORGANISM Homo sapiens (human)
AUTHORS Homo sapiens
TITLE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
Herath,H.M., Parekh,R.B. and Rohlf,C.
Diagnosis of bipolar affective disorder (bad) and unipolar
depression
Patent: WO 0163294-A 458 30-AUG-2001;
JOURNAL Oxford GlycoSciences (UK) Limited (GB)
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Best Local Similarity 99.8%; Pred. No. 0;
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RESULT 11
AX232218
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS

AX232218
Sequence 496 from Patent WO0163293.
AX232218
AX232218.1 GI:15592548

1587 bp
DNA
linear
PAT 11-SEP-2001

SOURCE	Homo sapiens (human)									
ORGANISM	Homo sapiens									
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.									
AUTHORS	Herath, M.A., Parekh, R.B. and Rohlf, C.O.									
TITLE	Diagnosis and treatment of schizophrenia									
JOURNAL	Patent: WO 0163293-A 496 30-AUG-2001;									
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DEFINITION (CPGL2 gene).
ACCESSION AJ417564
VERSION AJ417564.1 GI:16555791
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE 1
AUTHORS Chen, J.M. and Barrett, A.J.
TITLE Cloning and sequencing of a second human homologue of glutamate
carboxypeptidase in peptidase family M20
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 1640)
TITLE Chen, J.M.
JOURNAL Direct Submission
TITLE Submitted (24-OCT-2001) Chen J.M., MRC Molecular Enzymology
Laboratory, Babraham Institute, Babraham Hall, Babraham,
Cambridgeshire CB2 4AT, UNITED KINGDOM
FEATURES
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QY 364 AGTGGGTGGCCATCAGAGCGACTCTGTCCAGCTGTGTGCTTTCAGACAGAGCTCT 423
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QY 904 GGAAGCCAGCAATCACTTATGGAACCCGGGGGAAACAGTACTTCTATGTTGAGGTGAAAT 963
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DEFINITION	Homo sapiens chromosome 18 clone RP13-482C18 map 18, WORKING DRAFT SEQUENCE, 3 unordered pieces.		
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VERSION	AC127485.2 GI:2267793		
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ORGANISM	Homo sapiens		
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REFERENCE	1 (bases 1 to 175905)		
AUTHORS	Birren, B., Nussbaum, C. and Lander, E.		
TITLE	Homo sapiens chromosome 18, clone RP13-482C18		
JOURNAL	Unpublished		

REFERENCE
AUTHORS

2 (bases 1 to 175905)
Birren, B., Nussbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,
Barra, N., Bastien, V., Bloom, T., Boguslavskiy, L., Boukhgalter, B.,
Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A.,
Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S.,
Faros, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J.,
Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B.,
Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kanat, A.,
Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K.,
Liu, G., Maclean, C., Macdonald, P., Major, J., Matthews, C.,
McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mienga, V.,
Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H.,
O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K.,
Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P.,
Roman, J., Roy, A., Schauer, S., Schuback, R., Seaman, S., Severy, P.,
Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J.,
Teefaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J.,
Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

Submitted (17-JUL-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 175905)

Birren, B., Nussbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,
Barra, N., Bastien, V., Bloom, T., Boguslavskiy, L., Boukhgalter, B.,
Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A.,
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Faros, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J.,
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Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kanat, A.,
Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K.,
Liu, G., Maclean, C., Macdonald, P., Major, J., Matthews, C.,
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Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H.,
O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K.,
Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P.,
Roman, J., Roy, A., Schauer, S., Schuback, R., Seaman, S., Severy, P.,
Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J.,
Teefaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J.,
Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

Submitted (16-AUG-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

On Aug 16, 2002 this sequence version replaced gi:21886892.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WTB

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L27777

Center clone name: 482 C 18

----- Summary Statistics

Sequencing vector: Plasmid; n/a; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 174971 bases at least Q40

Consensus quality: 175423 bases at least Q30

Consensus quality: 175606 bases at least Q20

Insert size: 175000; agarose-fp

Insert size: 175705; sum-of-contigs

Quality coverage: 15.3 in Q20 bases; agarose-fp

Quality coverage: 15.3 in Q20 bases; sum-of-contigs

- * NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.


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Scoring table: OLIGO_NUC

Searched: Gapop 60.0 , Gapext 60.0
Total number of hits satisfying chosen parameters: 8142013
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Database : N_Geneseq_23Sep04.*
1: Geneseqn1980s.*
2: Geneseqn1990s.*
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4: Geneseqn2001as.*
5: Geneseqn2001bs.*
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7: Geneseqn2002bs.*
8: Geneseqn2003as.*
9: Geneseqn2003bs.*
10: Geneseqn2003cs.*
11: Geneseqn2003ds.*
12: Geneseqn2004s.*

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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DE cDNA encoding a novel polypeptide designated PRO4380.
PN WO200056889-A2.
PD 28-SEP-2000.
PA (GETH ) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 0;
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PN US2003027249-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 0;
RESULT 3
ID ACA06111 standard; cDNA; 2242 BP.
DE cDNA encoding human PRO polypeptide #13.
PN US2003008348-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 0;
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DE cDNA encoding human secreted polypeptide PRO4380.
PN US2002192751-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 0;
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ID ADA76581 standard; cDNA; 2242 BP.
DE Novel human secreted and transmembrane protein PRO4380 cDNA.
PN US2003036114-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 0;
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ID ACD42296 standard; cDNA; 2242 BP.
DE Human secreted protein coding sequence, SEQ ID 137.
DE Human cDNA encoding secreted/transmembrane protein PRO4380.
PN US2003044842-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 0;
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ID AAD59362 standard; cDNA; 2242 BP.
DE Human PRO4380 cDNA.
PN US2003049733-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 0;
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DE Human PRO4380 cDNA.
PN US2003049734-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2242; DB 10; Length 2242;
Best Local Similarity 100.0%; Pred. No. 0;
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ID ADC29812 standard; cDNA; 2242 BP.
DE Novel human secreted and transmembrane protein PRO4380 cDNA.
PN US2003092063-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 0;
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ID ACA06168 standard; cDNA; 2242 BP.
DE cDNA encoding human PRO polypeptide #13.
PN US2003032061-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 0;
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ID ADF09255 standard; cDNA; 2242 BP.
DE Human secreted and transmembrane protein PRO4380 cDNA.
PN US2003134327-A1.
PD 17-JUL-2003.
PA (GETH ) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 0;
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PN WO200226948-A2.
PD 04-APR-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 97.2%; Score 2180; DB 6; Length 2784;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 13
ID ADF0847 standard; DNA; 2851 BP.
DE Human hepatic-fibrosis disease marker SEQ ID 309.
PN JP2003259877-A.
PD 16-SEP-2003.
PA (SUMU ) SUMITOMO SEIYAKU KK.
Query Match 97.2%; Score 2180; DB 10; Length 2851;
Best Local Similarity 100.0%; Pred. No. 0;
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ID AAZ65270 standard; DNA; 2152 BP.
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PN WO9958660-A1.
PD 18-NOV-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
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Best Local Similarity 100.0%; Pred. No. 0;
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DE Human secreted protein coding sequence, SEQ ID 137.
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PN WO200295010-A2.
 PD 28-NOV-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
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 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 16
 ID ABZ71261 standard; cDNA; 2152 BP.
 DE Human secreted protein-encoding gene 72 cDNA clone HHPEN62, SEQ ID NO:82.
 PN WO200276488-A1.
 PD 03-OCT-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
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 Best Local Similarity 100.0%; Pred. No. 0;
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 DE Human secreted protein cDNA #SEQ ID 113.
 PN WO2003004622-A2.
 PD 16-JAN-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
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 Best Local Similarity 100.0%; Pred. No. 0;
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 ID ADC73537 standard; DNA; 2152 BP.
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 PN WO2003038063-A2.
 PD 08-MAY-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 84.3%; Score 1891; DB 10; Length 2152;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 19
 ID ADE11660 standard; cDNA; 2152 BP.
 DE Human secreted polypeptide cDNA #22.
 PN US2003100051-A1.
 PD 29-MAY-2003.
 PA (RUBE/) RUBEN S M.
 PA (FLOR/) FLORENCE K A.
 PA (NIJ/) NI J.
 PA (ROSE/) ROSEN C A.
 PA (CART/) CARTER K C.
 PA (MOOR/) MOORE P A.
 PA (OLSE/) OLSEN H S.
 PA (SHY/) SHI Y.
 PA (YOUN/) YOUNG P E.
 PA (WEI/) WEI Y.
 PA (BREW/) BREWER L A.
 PA (SOPP/) SOPPET D R.
 PA (LAPL/) LAFLEUR D W.
 PA (ENDR/) ENDRESS G A.
 PA (EBNE/) EBNER R.
 PA (BIRS/) BIRSE C E.
 Query Match 84.3%; Score 1891; DB 10; Length 2152;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 20
 ID AAH64725 standard; cDNA; 2201 BP.
 DE Human secreted protein cDNA, SEQ ID NO: 1.
 PN WO200142451-A2.
 PD 14-JUN-2001.
 PA (GEST/) GENSET.
 Query Match 84.1%; Score 1886; DB 5; Length 2201;
 Best Local Similarity 99.9%; Pred. No. 0;
 RESULT 21
 ID AAC54452 standard; cDNA; 2235 BP.
 DE Nucleotide sequence of mdt cDNA clone ID No: 436857.2.
 PN WO200075298-A2.
 PD 14-DEC-2000.
 PA (INCY-) INCYTE GENOMICS INC.
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 Best Local Similarity 99.9%; Pred. No. 0;
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 PN WO200183782-A2.
 PD 08-NOV-2001.
 PA (SUGE-) SUGEN INC.
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 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 23
 ID ABL58477 standard; cDNA; 1521 BP.
 DE Human metalloprotease, 55054 coding sequence.
 PN WO200226948-A2.
 PD 04-APR-2002.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 67.8%; Score 1521; DB 6; Length 1521;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 24
 ID AAH27154 standard; cDNA; 1524 BP.
 DE Human carnosinase cDNA.
 PN EP1097997-A1.
 PD 05-MAY-2001.
 PA (SNFI) SANOFI-SYNTHELABO.
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 Best Local Similarity 99.9%; Pred. No. 0;
 RESULT 25
 ID AAS12574 standard; DNA; 1587 BP.
 DE DNA encoding DPI-45 and DPI-213.
 PN WO200162787-A1.
 PD 30-AUG-2001.
 PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 Query Match 61.3%; Score 1375; DB 4; Length 1587;
 Best Local Similarity 99.8%; Pred. No. 0;
 RESULT 26
 ID AAS42478 standard; DNA; 1587 BP.
 DE Human Schizophrenia-Associated Protein Isoform (SPI) 238/240 DNA.
 PN WO200162785-A2.
 PD 30-AUG-2001.
 PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 Query Match 61.3%; Score 1375; DB 4; Length 1587;
 Best Local Similarity 99.8%; Pred. No. 0;
 RESULT 27
 ID AAS43075 standard; DNA; 1587 BP.
 DE EST AAS26679/AIS89129 complete sequence.
 PN WO200163294-A2.
 PD 30-AUG-2001.
 PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 Query Match 61.3%; Score 1375; DB 4; Length 1587;
 Best Local Similarity 99.8%; Pred. No. 0;
 RESULT 28
 ID AAS23811 standard; DNA; 1587 BP.
 DE DNA encoding schizophrenia-associated isoform SPI-238/240.
 PN WO200163293-A2.
 PD 30-AUG-2001.
 PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
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 Best Local Similarity 99.8%; Pred. No. 0;
 RESULT 29
 ID AD079057 standard; DNA; 1587 BP.
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 PN US2004110938-A1.
 PD 10-JUN-2004.
 PA (PARE/) PAREKH R B.
 PA (HERA/) CHANDRASIRI HERATH H M A.
 PA (ROHL/) ROHLF C.
 PA (TERR/) TERRETT J A.
 PA (TYSO/) TYSON K L.
 Query Match 61.3%; Score 1375; DB 12; Length 1587;
 Best Local Similarity 99.8%; Pred. No. 0;
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 ID ADC77690 standard; cDNA; 1640 BP.
 DE Human S5054 protein encoding cDNA SEQ ID NO:53.
 PN WO2003073983-A2.
 PD 12-SEP-2003.
 PA (MILL-) MILLENNIUM PHARM INC.
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 Best Local Similarity 99.7%; Pred. No. 0;
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DE Human polynucleotide SEQ ID NO 1508.
PN WO200153112-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 52.8%; Score 1184; DB 4; Length 1343;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 32
ID AAI61091 standard; cDNA; 1569 BP.
DE Human polynucleotide SEQ ID NO 5080.
PN WO200153112-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 45.5%; Score 1021; DB 4; Length 1569;
Best Local Similarity 99.7%; Pred. No. 0;
RESULT 33
ID ABL90090 standard; cDNA; 2039 BP.
DE Human polynucleotide SEQ ID NO 652.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 42.1%; Score 945; DB 6; Length 2039;
Best Local Similarity 99.5%; Pred. No. 1.1e-311;
RESULT 34
ID ADF90810 standard; DNA; 742 BP.
DE Human hepatic-fibrosis disease marker SEQ ID 272.
PN JP2003259877-A.
PD 16-SEP-2003.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match 25.7%; Score 576; DB 10; Length 742;
Best Local Similarity 100.0%; Pred. No. 3e-186;
RESULT 35
ID AAH98942 standard; cDNA; 639 BP.
DE Human EST-derived coding sequence SEQ ID NO: 799.
PN WO200154477-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 14.8%; Score 332; DB 4; Length 639;
Best Local Similarity 100.0%; Pred. No. 2.4e-103;
RESULT 36
ID AAH99853 standard; cDNA; 639 BP.
DE Human protein encoding cDNA sequence SEQ ID NO:688.
PN WO200153455-A2.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 14.8%; Score 332; DB 4; Length 639;
Best Local Similarity 100.0%; Pred. No. 2.4e-103;
RESULT 37
ID ACH13751 standard; cDNA; 456 BP.
DE Human adult brain cDNA #963.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRNA) DRMANAC R T.
PA (LABA) LABAT I.
PA (STAC) STACHE-CRAIN B.
PA (DICK) DICKSON M C.
PA (JONE) JONES L W.
Query Match 14.0%; Score 313; DB 9; Length 456;
Best Local Similarity 100.0%; Pred. No. 7.3e-97;
RESULT 38
ID AAC09875 standard; cDNA; 300 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 13950.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match 8.0%; Score 180; DB 3; Length 300;
Best Local Similarity 99.6%; Pred. No. 1.2e-51;
RESULT 39
ID ACH74305 standard; DNA; 582 BP.
DE Human genome derived single exon probe #7500.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN) PENN S G.
PA (RANK) RANK D R.

PA (HANZ) HANZEL D K.
Query Match 6.8%; Score 152; DB 12; Length 582;
Best Local Similarity 100.0%; Pred. No. 3.4e-42;
RESULT 40
ID ACH88005 standard; DNA; 156 BP.
DE Human genome derived single exon probe #21200.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN) PENN S G.
PA (RANK) RANK D R.
PA (HANZ) HANZEL D K.
Query Match 6.7%; Score 150; DB 12; Length 156;
Best Local Similarity 100.0%; Pred. No. 2.2e-41;
RESULT 41
ID AAS65841 standard; cDNA; 643 BP.
DE DNA encoding novel human diagnostic protein #1645.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.4%; Score 144; DB 5; Length 643;
Best Local Similarity 99.5%; Pred. No. 1.7e-39;
RESULT 42
ID AAS65840 standard; cDNA; 497 BP.
DE DNA encoding novel human diagnostic protein #1644.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.9%; Score 132; DB 5; Length 497;
Best Local Similarity 100.0%; Pred. No. 2.2e-35;
RESULT 43
ID AAX10638 standard; DNA; 127 BP.
DE Human biallelic polymorphic DNA fragment WI-15225.
PN WO9820165-A2.
PD 14-MAY-1998.
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
Query Match 3.6%; Score 80; DB 2; Length 127;
Best Local Similarity 100.0%; Pred. No. 1.4e-17;
RESULT 44
ID AAI84805 standard; cDNA; 402 BP.
DE Human polynucleotide SEQ ID NO 4865.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.7%; Score 61; DB 4; Length 402;
Best Local Similarity 100.0%; Pred. No. 3e-11;
RESULT 45
ID ABA77130 standard; DNA; 433 BP.
DE Proliferative glomerular nephritis-associated gene sequence SEQ ID:137.
PN WO200173022-A1.
PD 04-OCT-2001.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 2.7%; Score 61; DB 4; Length 433;
Best Local Similarity 100.0%; Pred. No. 2.9e-11;
RESULT 46
ID ABN96930 standard; DNA; 770 BP.
DE Gene #3428 used to diagnose liver cancer.
PN WO200229103-A2.
PD 11-APR-2002.
PA (GENE) GENE LOGIC INC.
Query Match 2.7%; Score 61; DB 6; Length 770;
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
RESULT 47
ID ADQ22074 standard; DNA; 980 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 4894.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT) PROTEIN DESIGN LABS INC.
Query Match 2.7%; Score 61; DB 12; Length 980;
Best Local Similarity 100.0%; Pred. No. 2.4e-11;
RESULT 48
ID ADQ33279 standard; DNA; 1225 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6099.
PN WO2004048938-A2.

PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.7%; Score 61; DB 12; Length 1225;
Best Local Similarity 100.0%; Pred. No. 2.3e-11;
RESULT 49
ID RAD16506 standard; DNA; 1367 BP.
DE Human ABC transporter-encoding gene 3 cDNA clone HJMBP48, SEQ ID NO:21.
PN WO200155208-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 61; DB 4; Length 1367;
Best Local Similarity 100.0%; Pred. No. 2.3e-11;
RESULT 50
ID AAS29733 standard; cDNA; 1367 BP.
DE Human endocrine polypeptide encoding cDNA SEQ ID NO 233.
PN WO200155364-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 61; DB 5; Length 1367;
Best Local Similarity 100.0%; Pred. No. 2.3e-11;
RESULT 51
ID ADA27261 standard; cDNA; 1367 BP.
DE cDNA encoding human ABC transport receptor #11.
PN US2003049652-A1.
PD 13-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 61; DB 9; Length 1367;
Best Local Similarity 100.0%; Pred. No. 2.3e-11;
RESULT 52
ID ADA12864 standard; cDNA; 1367 BP.
DE Human ABC transporter-related cDNA HJMBP48 #2.
PN US2002161208-A1.
PD 31-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 2.7%; Score 61; DB 10; Length 1367;
Best Local Similarity 100.0%; Pred. No. 2.3e-11;
RESULT 53
ID ACC72015 standard; DNA; 1422 BP.
DE BCU0021 gene #SEQ ID 7.
PN WO2003029421-A2.
PD 10-APR-2003.
PA (ORIG-) ORIGENE TECHNOLOGIES INC.
Query Match 2.7%; Score 61; DB 8; Length 1422;
Best Local Similarity 100.0%; Pred. No. 2.2e-11;
RESULT 54
ID AAS27477 standard; cDNA; 1661 BP.
DE cDNA encoding novel signal transduction pathway protein, Seq ID 512.
PN WO200154733-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 61; DB 4; Length 1661;
Best Local Similarity 100.0%; Pred. No. 2.2e-11;
RESULT 55
ID AAL02553 standard; cDNA; 1661 BP.
DE Human reproductive system related antigen cDNA SEQ ID NO: 2554.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 61; DB 4; Length 1661;
Best Local Similarity 100.0%; Pred. No. 2.2e-11;
RESULT 56
ID ABA07672 standard; cDNA; 1661 BP.
DE Human ovarian and breast cancer associated polynucleotide SEQ ID NO 229.
PN WO200155325-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 61; DB 4; Length 1661;
Best Local Similarity 100.0%; Pred. No. 2.2e-11;
RESULT 57
ID ABK43975 standard; cDNA; 1661 BP.
DE DNA encoding novel central nervous system protein #555.
PN WO200155318-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 61; DB 4; Length 1661;
Best Local Similarity 100.0%; Pred. No. 2.2e-11;
RESULT 58
ID ADB93655 standard; cDNA; 1661 BP.
DE Human cDNA encoding a novel protein #502.
PN US2002168711-A1.
PD 14-NOV-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 2.7%; Score 61; DB 10; Length 1661;
Best Local Similarity 100.0%; Pred. No. 2.2e-11;
RESULT 59
ID ADI54362 standard; cDNA; 1661 BP.
DE cDNA encoding novel human protein seq id 565.
PN US2004018969-A1.
PD 29-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 2.7%; Score 61; DB 12; Length 1661;
Best Local Similarity 100.0%; Pred. No. 2.2e-11;
RESULT 60
ID ABQ54695 standard; cDNA; 1663 BP.
DE Human ovarian antigen HCOMM05 cDNA, SEQ ID NO:575.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 61; DB 6; Length 1663;
Best Local Similarity 100.0%; Pred. No. 2.2e-11;
RESULT 61
ID AAV81394 standard; DNA; 1733 BP.
DE Human tumour antigen zsig15 coding sequence.
PN WO9850552-A1.
PD 12-NOV-1998.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 2.7%; Score 61; DB 2; Length 1733;
Best Local Similarity 100.0%; Pred. No. 2.1e-11;
RESULT 62
ID ADN04967 standard; cDNA; 2161 BP.
DE Antipsoriatic cDNA sequence #698.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 61; DB 12; Length 2161;
Best Local Similarity 100.0%; Pred. No. 2e-11;
RESULT 63
ID ABK69135 standard; cDNA; 3714 BP.
DE DNA encoding human secreted protein, SEQ ID NO 59.
PN WO200224721-A1.
PD 28-MAR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 61; DB 6; Length 3714;
Best Local Similarity 100.0%; Pred. No. 1.8e-11;
RESULT 64
ID ABQ54814 standard; cDNA; 3714 BP.
DE Human ovarian antigen HSPSI42 cDNA, SEQ ID NO:694.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 61; DB 6; Length 3714;
Best Local Similarity 100.0%; Pred. No. 1.8e-11;
RESULT 65
ID ABV07975 standard; cDNA; 309 BP.
DE Human prostate expression marker cDNA 7966.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.7%; Score 60; DB 5; Length 309;
Best Local Similarity 100.0%; Pred. No. 7e-11;

RESULT 66
 ID ADL37681 standard; DNA; 309 BP.
 DE Human ovarian cancer DNA marker #11571.
 PN WO200170979-A2.
 PD 27-SEP-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 2.7%; Score 60; DB 5; Length 309;
 Best Local Similarity 100.0%; Pred. No. 7e-11;
 RESULT 67
 ID ADI72542 standard; DNA; 309 BP.
 DE Human ovarian cancer DNA marker #5284.
 PN WO200170979-A2.
 PD 27-SEP-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 2.7%; Score 60; DB 5; Length 309;
 Best Local Similarity 100.0%; Pred. No. 7e-11;
 RESULT 68
 ID ABX41000 standard; cDNA; 321 BP.
 DE Bovine EST associated with lactation/muscle/fat deposition #6165.
 PN US2002137139-A1.
 PD 26-SEP-2002.
 PA (BYAT/) BYATT J C.
 PA (MATH/) MATHIALAGAN N.
 PA (TAON/) TAO N.
 PA (WARR/) WARREN W C.
 Query Match 2.7%; Score 60; DB 8; Length 321;
 Best Local Similarity 100.0%; Pred. No. 6.9e-11;
 RESULT 69
 ID AAC78443 standard; cDNA; 386 BP.
 DE Human cancer associated gene sequence SEQ ID NO:837.
 PN WO200053350-A1.
 PD 21-SEP-2000.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.7%; Score 60; DB 3; Length 386;
 Best Local Similarity 100.0%; Pred. No. 6.6e-11;
 RESULT 70
 ID AAI92146 standard; cDNA; 386 BP.
 DE Human polynucleotide SEQ ID NO 12206.
 PN WO200164835-A2.
 PD 07-SEP-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 2.7%; Score 60; DB 4; Length 386;
 Best Local Similarity 100.0%; Pred. No. 6.6e-11;
 RESULT 71
 ID ADK61475 standard; DNA; 438 BP.
 DE Ovarian cancer-related DNA #630 with altered ovarian cancer expression.
 PN WO2003068034-A2.
 PD 21-AUG-2003.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA (SLOK) SLOAN KETTERING INST CANCER RES.
 Query Match 2.7%; Score 60; DB 10; Length 438;
 Best Local Similarity 100.0%; Pred. No. 6.4e-11;
 RESULT 72
 ID AAS60503 standard; cDNA; 509 BP.
 DE Human cancer agent-sensitive marker #234.
 PN WO200179556-A2.
 PD 25-OCT-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 2.7%; Score 60; DB 4; Length 509;
 Best Local Similarity 100.0%; Pred. No. 6.2e-11;
 RESULT 73
 ID AAF81806 standard; cDNA; 712 BP.
 DE Human secreted protein gene 20 SEQ ID NO:30.
 PN WO200112775-A2.
 PD 22-FEB-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.7%; Score 60; DB 4; Length 712;
 Best Local Similarity 100.0%; Pred. No. 5.7e-11;
 RESULT 74
 ID AAL23455 standard; cDNA; 752 BP.
 DE Human breast cancer expressed polynucleotide 15912.
 PN WO200151628-A2.
 PD 19-JUL-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 2.7%; Score 60; DB 4; Length 752;
 Best Local Similarity 100.0%; Pred. No. 5.7e-11;
 RESULT 75
 ID ADI15961 standard; cDNA; 759 BP.
 DE Human PP 83 cDNA.
 PN WO2003008450-A1.
 PD 30-JAN-2003.
 PA (ITOH/) ITOH K.
 Query Match 2.7%; Score 60; DB 10; Length 759;
 Best Local Similarity 100.0%; Pred. No. 5.7e-11;
 RESULT 76
 ID ADES8855 standard; DNA; 774 BP.
 DE Human gene AK026608, SEQ ID NO 4743.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 Query Match 2.7%; Score 60; DB 10; Length 774;
 Best Local Similarity 100.0%; Pred. No. 5.6e-11;
 RESULT 77
 ID ADES8852 standard; DNA; 774 BP.
 DE Human gene AK026608, SEQ ID NO 4740.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 Query Match 2.7%; Score 60; DB 10; Length 774;
 Best Local Similarity 100.0%; Pred. No. 5.6e-11;
 RESULT 78
 ID AAL24400 standard; cDNA; 781 BP.
 DE Human breast cancer expressed polynucleotide 16857.
 PN WO200151628-A2.
 PD 19-JUL-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 2.7%; Score 60; DB 4; Length 781;
 Best Local Similarity 100.0%; Pred. No. 5.6e-11;
 RESULT 79
 ID AAD64841 standard; cDNA; 1249 BP.
 DE M. charantia FUSCA homologue transcription factor EST cDNA #2.
 PN US2003119165-A1.
 PD 26-JUN-2003.
 PA (CAHO) CAHOON R E.
 PA (LUGG) LU G.
 PA (WILL) WILLIAMS M E.
 Query Match 2.7%; Score 60; DB 10; Length 1249;
 Best Local Similarity 100.0%; Pred. No. 5e-11;
 RESULT 80
 ID ADI42365 standard; DNA; 1262 BP.
 DE Plant transcription factor polynucleotide #503.
 PN US2004019927-A1.
 PD 29-JAN-2004.
 PA (SHER) SHERMAN B K.
 PA (RIEC) RIECHMANN J L.
 PA (JIAN) JIANG C.
 PA (HEAR) HEARD J E.
 PA (HAAK) HAAKE V.
 PA (CREE) CREELMAN R A.
 PA (RATC) RATCLIFFE O.
 PA (ADAM) ADAM L J.
 PA (REUB) REUBER T L.
 PA (KEDD) KEDDIE J.
 PA (BROU) BROUN P E.
 PA (PILG) PILGRIM M L.
 PA (DUBE) DUBELL A N.
 PA (PINE) PINEDA O.
 PA (YUGG) YU G.
 Query Match 2.7%; Score 60; DB 12; Length 1262;
 Best Local Similarity 100.0%; Pred. No. 5e-11;
 RESULT 81
 ID ADO02769 standard; cDNA; 1262 BP.
 DE Soybean orthologue of Thalecress transcription factor, cDNA #103.
 PN US2004045049-A1.

PD 04-MAR-2004.
PA (ZHAN/) ZHANG J.
PA (FROM/) FROM M E.
PA (HEAR/) HEARD J E.
PA (RIEC/) RIECHMANN J L.
PA (ADAM/) ADAM L J.
PA (BROU/) BROUN P E.
PA (PINE/) PINEDA O.
PA (REUB/) REUBER T L.
PA (KEDD/) KEDDIE J S.
PA (YUGG/) YU G.
PA (JIAN/) JIANG C.
PA (SAMA/) SAMAHA R S.
PA (PILG/) PILGRIM M L.
PA (CREE/) CREELMAN R A.
PA (DUBE/) DUBELL A N.
PA (RATC/) RATCLIFFE O.
PA (KUMI/) KUMIMOTO R.
PA (SHER/) SHERMAN B K.
Query Match
Best Local Similarity 2.7%; Score 60; DB 12; Length 1262;
Best Local Similarity 100.0%; Pred. No. 5e-11;
RESULT 82
ID AAA99029 standard; cDNA; 1360 BP.
DE Human TGC839 nucleotide sequence.
PN WO200055197-A1.
PD 21-SEP-2000.
PA (TAKE/) TAKEDA CHEM IND LTD.
Query Match
Best Local Similarity 2.7%; Score 60; DB 3; Length 1360;
Best Local Similarity 100.0%; Pred. No. 4.9e-11;
RESULT 83
ID ADM47789 standard; DNA; 1455 BP.
DE Polynucleotide sequence #207 useful in producing transgenic plants.
PN US2003233670-A1.
PD 18-DEC-2003.
PA (EDGE/) EDGERTON M D.
PA (CHOM/) CHOMET P S.
PA (LACC/) LACCETTI L B.
Query Match
Best Local Similarity 2.7%; Score 60; DB 12; Length 1455;
Best Local Similarity 100.0%; Pred. No. 4.9e-11;
RESULT 84
ID ADQ24546 standard; DNA; 1478 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7366.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match
Best Local Similarity 2.7%; Score 60; DB 12; Length 1478;
Best Local Similarity 100.0%; Pred. No. 4.8e-11;
RESULT 85
ID RAD07771 standard; cDNA; 1480 BP.
DE Human secreted protein-encoding gene 2 cDNA clone HCGBB81, SEQ ID NO:12.
PN WO200132687-A1.
PD 10-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 2.7%; Score 60; DB 4; Length 1480;
Best Local Similarity 100.0%; Pred. No. 4.8e-11;
RESULT 86
ID ABQ54640 standard; cDNA; 1583 BP.
DE Human ovarian antigen HWIU46 cDNA, SEQ ID NO:520.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 2.7%; Score 60; DB 6; Length 1583;
Best Local Similarity 100.0%; Pred. No. 4.8e-11;
RESULT 87
ID AAC68122 standard; cDNA; 1751 BP.
DE Human secreted protein cDNA sequence #42.
PN WO200058335-A1.
PD 05-OCT-2000.
PA (ROSE/) ROSEN C A.
PA (ROSE/) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 2.7%; Score 60; DB 3; Length 1751;
Best Local Similarity 100.0%; Pred. No. 4.7e-11;
RESULT 88
ID ADA61322 standard; cDNA; 1904 BP.
DE Human colon cancer antigen encoding cDNA SEQ ID NO:229.
PN WO200122920-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 2.7%; Score 60; DB 4; Length 1751;
Best Local Similarity 100.0%; Pred. No. 4.7e-11;
RESULT 89
ID AAS21293 standard; cDNA; 1904 BP.
DE Human cDNA sequence encoding for PRO4403 polypeptide.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH-) GENENTECH INC.
Query Match
Best Local Similarity 2.7%; Score 60; DB 4; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 90
ID ACA03652 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH-) GENENTECH INC.
Query Match
Best Local Similarity 2.7%; Score 60; DB 8; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 91
ID ABX89190 standard; cDNA; 1904 BP.
DE DNA encoding novel secreted and transmembrane protein PRO4403.
PN US2003017583-A1.
PD 23-JAN-2003.
PA (GETH-) GENENTECH INC.
Query Match
Best Local Similarity 2.7%; Score 60; DB 8; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 92
ID ACD41844 standard; cDNA; 1904 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #50.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH-) GENENTECH INC.
Query Match
Best Local Similarity 2.7%; Score 60; DB 8; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 93
ID ACA04073 standard; cDNA; 1904 BP.
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 99.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH-) GENENTECH INC.
Query Match
Best Local Similarity 2.7%; Score 60; DB 8; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 94
ID ADA45618 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH-) GENENTECH INC.
Query Match
Best Local Similarity 2.7%; Score 60; DB 9; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 95
ID ADA76049 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH-) GENENTECH INC.
Query Match
Best Local Similarity 2.7%; Score 60; DB 9; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 96
ID ADA18699 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH-) GENENTECH INC.
Query Match
Best Local Similarity 2.7%; Score 60; DB 9; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 97
ID ADA61322 standard; cDNA; 1904 BP.

DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 9; Length 1904;
Query Match 100.0%; Pred. No. 4.6e-11;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 98
ID ADB19107 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 9; Length 1904;
Query Match 100.0%; Pred. No. 4.6e-11;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 99
ID ADB27648 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 9; Length 1904;
Query Match 100.0%; Pred. No. 4.6e-11;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 100
ID ADA86127 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 9; Length 1904;
Query Match 100.0%; Pred. No. 4.6e-11;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 101
ID ADB15691 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 9; Length 1904;
Query Match 100.0%; Pred. No. 4.6e-11;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 102
ID ADA47477 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 9; Length 1904;
Query Match 100.0%; Pred. No. 4.6e-11;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 103
ID ADA67272 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 9; Length 1904;
Query Match 100.0%; Pred. No. 4.6e-11;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 104
ID ADB30279 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 9; Length 1904;
Query Match 100.0%; Pred. No. 4.6e-11;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 105
ID ADA85575 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 9; Length 1904;
Query Match 100.0%; Pred. No. 4.6e-11;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 106
ID ADA96787 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.

PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 9; Length 1904;
Query Match 100.0%; Pred. No. 4.6e-11;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 107
ID ADA79091 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 9; Length 1904;
Query Match 100.0%; Pred. No. 4.6e-11;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 108
ID ADA87230 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 9; Length 1904;
Query Match 100.0%; Pred. No. 4.6e-11;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 109
ID ADB16432 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 9; Length 1904;
Query Match 100.0%; Pred. No. 4.6e-11;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 110
ID ADA91524 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 9; Length 1904;
Query Match 100.0%; Pred. No. 4.6e-11;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 111
ID ADB14587 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 9; Length 1904;
Query Match 100.0%; Pred. No. 4.6e-11;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 112
ID ADB18548 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 9; Length 1904;
Query Match 100.0%; Pred. No. 4.6e-11;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 113
ID ADA93763 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 9; Length 1904;
Query Match 100.0%; Pred. No. 4.6e-11;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 114
ID ADB19659 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 9; Length 1904;
Query Match 100.0%; Pred. No. 4.6e-11;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 115
ID ADB12971 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003082710-A1.

PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 9; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 116
ID ACD98473 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 9; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 117
ID ADA74225 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003086798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 9; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 118
ID ADB24458 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide SEQ ID NO 99.
PN US2003077113-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 9; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 119
ID ADA81982 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 9; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 120
ID ADA74945 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 9; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 121
ID ADA85023 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 9; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 122
ID ADA84471 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 9; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 123
ID ADB29727 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 9; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 124
ID ADA80255 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.

PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 9; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 125
ID ADA75497 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 9; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 126
ID ADA46722 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 9; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 127
ID ADB25018 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide SEQ ID NO 99.
PN US2003077115-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 9; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 128
ID ADA93194 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US200307721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 9; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 129
ID ADB26544 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 9; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 130
ID ADB30831 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 9; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 131
ID ADA60759 standard; cDNA; 1904 BP.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 9; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 132
ID ADB23906 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide SEQ ID NO 99.
PN US2003077114-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 9; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 133
ID ADA96235 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity 2.7%; Score 60; DB 9; Length 1904;
RESULT 134
ID ADAB0807 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.7%; Score 60; DB 9; Length 1904;
RESULT 135
ID ADA95683 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.7%; Score 60; DB 9; Length 1904;
RESULT 136
ID ADB25992 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.7%; Score 60; DB 9; Length 1904;
RESULT 137
ID ADB21477 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.7%; Score 60; DB 9; Length 1904;
RESULT 138
ID ADA77256 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.7%; Score 60; DB 9; Length 1904;
RESULT 139
ID ADB17996 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2003077110-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.7%; Score 60; DB 9; Length 1904;
RESULT 140
ID ADA86679 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.7%; Score 60; DB 9; Length 1904;
RESULT 141
ID ADA87782 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.7%; Score 60; DB 9; Length 1904;
RESULT 142
ID ADA6170 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.7%; Score 60; DB 9; Length 1904;
RESULT 143
ID ADB28200 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2003082899-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.7%; Score 60; DB 9; Length 1904;
RESULT 144
ID ADB28752 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.7%; Score 60; DB 9; Length 1904;
RESULT 145
ID ADA76704 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.7%; Score 60; DB 9; Length 1904;
RESULT 146
ID ADA88334 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.7%; Score 60; DB 9; Length 1904;
RESULT 147
ID ADA97339 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.7%; Score 60; DB 9; Length 1904;
RESULT 148
ID ADB27096 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2003022239-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.7%; Score 60; DB 9; Length 1904;
RESULT 149
ID ADB22029 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003087344-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.7%; Score 60; DB 9; Length 1904;
RESULT 150
ID ADA66720 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.7%; Score 60; DB 9; Length 1904;
RESULT 151
ID ADB22581 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.7%; Score 60; DB 9; Length 1904;
RESULT 152
ID ADB23354 standard; cDNA; 1904 BP.

DE Human PRO polynucleotide SEQ ID NO 99.
PN US200307712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 9; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 153
ID ADA92076 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 9; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 154
ID ADB15139 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 9; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 155
ID ADB38391 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 9; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 156
ID ADB37839 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 9; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 157
ID ADB66311 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 158
ID ADB9391 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 159
ID ADB90123 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 160
ID ADB39224 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 161
ID ADB46847 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.

PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 162
ID ADB86454 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 163
ID ADB77059 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 164
ID ADB34216 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide SEQ ID NO 99.
PN US200307717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 165
ID ADB35320 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide SEQ ID NO 99.
PN US200307719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 166
ID ADB33664 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide SEQ ID NO 99.
PN US200307716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 167
ID ADB34768 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide SEQ ID NO 99.
PN US200307718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 168
ID ADB35872 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide SEQ ID NO 99.
PN US200307720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 169
ID ADB46267 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 170
ID ADC50140 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003092106-A1.

PD 15-MAY-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 171
ID ADC71687 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 172
ID ADC59666 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 173
ID ADC52673 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID99.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 174
ID ADC57027 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID99.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 175
ID ADC60218 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 176
ID ADC50693 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 177
ID ADC65220 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 178
ID ADC54318 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID99.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 179
ID ADC53279 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID99.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 180
ID ADC58802 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID99.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 181
ID ADC55680 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID99.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 182
ID ADC58250 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID99.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 183
ID ADD02924 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 184
ID ADC89916 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 185
ID ADC9335 standard; cDNA; 1904 BP.
DE CDNA encoding human PRO polypeptide #50.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 186
ID ADC48224 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 187
ID ADD09753 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 188
ID ADD04328 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;

Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 189
ID ADC80284 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 190
ID ADD10791 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 191
ID ADC47672 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 192
ID ADC79732 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 193
ID ADD09201 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 194
ID ADD40914 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 195
ID ADD52053 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 196
ID ADD52793 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 197
ID ADD53345 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;

Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 198
ID ADD51501 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 199
ID ADD02300 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 200
ID ADD01734 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 201
ID ADD53916 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 202
ID ADD92233 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 203
ID ADD91129 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 204
ID ADE03743 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 205
ID ADE32040 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 206
ID ADE21972 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 10; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;

RESULT 207
ID ADE18653 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 208
ID ADE41732 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 209
ID ADE17549 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 210
ID ADD91681 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 211
ID ADE33144 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 212
ID ADE33696 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 213
ID ADD79748 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 214
ID ADD32785 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 215
ID ADE19205 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 216
ID ADE40612 standard; cDNA; 1904 BP.

ID ADE18653 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 217
ID ADE42849 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 218
ID ADD95638 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 219
ID ADE22524 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 220
ID ADD78642 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 221
ID ADE32592 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 222
ID ADE42284 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 223
ID ADD80300 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 224
ID ADD89328 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 225
ID ADE40612 standard; cDNA; 1904 BP.

DE Human PRO polynucleotide #50.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 226
ID ADE04411 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 227
ID ADE92540 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 228
ID ADG21249 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 229
ID ADG22890 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 230
ID ADF97225 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 231
ID ADG80289 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 232
ID ADG79737 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 233
ID ADH55029 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 234
ID ADH55581 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003087353-A1.

PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 235
ID ADI63800 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 236
ID ADI64749 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 237
ID ADI63248 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 238
ID ADH81662 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 239
ID ADH81110 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 240
ID ACD23902 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 241
ID ACA67043 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 10; Length 1904;
Query Match Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 242
ID ADM82279 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 11; Length 1904;
Query Match Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 243
ID ADNI5678 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003087353-A1.

PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 253
ID ADE23628 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 254
ID ADE24271 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 255
ID ADD87096 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 256
ID ADE88962 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 257
ID ADE18101 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 258
ID ADE88410 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 259
ID ADE94430 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 260
ID ADE90841 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 261
ID ADE94982 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.

Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 271
ID ADG23994 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 272
ID ADF98348 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 273
ID ADG03179 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 274
ID ADF98900 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 275
ID ADG16485 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 276
ID ADG04944 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 277
ID ADG19211 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 278
ID ADG13048 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 279
ID ADG08105 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 60; DB 12; Length 1904;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;

RESULT 280
ID ADG15275 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 12; Length 1904;
Query Match Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 281
ID ADF96673 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 12; Length 1904;
Query Match Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 282
ID ADG05858 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 12; Length 1904;
Query Match Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 283
ID ADG23442 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 12; Length 1904;
Query Match Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 284
ID ADG03731 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 12; Length 1904;
Query Match Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 285
ID ADG34632 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 12; Length 1904;
Query Match Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 286
ID ADG06929 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 12; Length 1904;
Query Match Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 287
ID ADG07481 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 12; Length 1904;
Query Match Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 288
ID ADG54976 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 12; Length 1904;
Query Match Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 289

ID ADG60640 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 12; Length 1904;
Query Match Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 290
ID ADG61744 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 12; Length 1904;
Query Match Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 291
ID ADG81945 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 12; Length 1904;
Query Match Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 292
ID ADG57184 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 12; Length 1904;
Query Match Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 293
ID ADG56632 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 12; Length 1904;
Query Match Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 294
ID ADG55528 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 12; Length 1904;
Query Match Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 295
ID ADG58288 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 12; Length 1904;
Query Match Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 296
ID ADG70654 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 12; Length 1904;
Query Match Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 297
ID ADG57736 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 12; Length 1904;
Query Match Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 298
ID ADG53320 standard; cDNA; 1904 BP.

DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 12; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 299
ID ADG11206 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 12; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 300
ID ADG81393 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003207805-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 12; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 301
ID ADH30355 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US200307723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 12; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 302
ID ADH11722 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 12; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 303
ID ADG52144 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 12; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 304
ID ADG53872 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 12; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 305
ID ADG80841 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 12; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 306
ID ADG56080 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 12; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 307
ID ADH12346 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207378-A1.

PD 06-NOV-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 12; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 308
ID ADG61192 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 12; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 309
ID ADH28279 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 12; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 310
ID ADG54424 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 12; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 311
ID ADG59464 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 12; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 312
ID ADI80888 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 12; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 313
ID ADG09631 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 12; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 314
ID ADI15102 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 12; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 315
ID ADG08979 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 12; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 316
ID ADI14434 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207383-A1.
PD 06-NOV-2003.

PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 12; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 317
ID ADI18029 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 12; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 318
ID ADJ63310 standard; cDNA; 1904 BP.
DE Novel human secreted and transmembrane protein PRO4403 cDNA.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 12; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 319
ID ADJ77205 standard; cDNA; 1904 BP.
DE Human PRO polynucleotide #50.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 12; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 320
ID ADJ55327 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 12; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 321
ID ADM27463 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 12; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 322
ID ADM42187 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 12; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 323
ID ADM28049 standard; cDNA; 1904 BP.
DE cDNA encoding human PRO polypeptide #50.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH) GENENTECH INC. 2.7%; Score 60; DB 12; Length 1904;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
RESULT 324
ID ABL39593 standard; cDNA; 1964 BP.
DE Human cancer suppressing gene PP928 encoding cDNA SEQ ID NO:30.
PN CN131318-A.
PD 19-SEP-2001.
PA (SHAN-) SHANGHAI INST ONCOLOGY. 2.7%; Score 60; DB 6; Length 1964;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.5e-11;
RESULT 325
ID ADQ21276 standard; DNA; 2072 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 4096.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC. 2.7%; Score 60; DB 10; Length 4096;

Query Match
Best Local Similarity 100.0%; Pred. No. 4.5e-11;
RESULT 326
ID ADI57346 standard; cDNA; 2169 BP.
DE Human pyruvate kinase, liver cDNA SEQ ID NO:30.
PN WO2003066086-A2.
PD 14-AUG-2003.
PA (DEVE-) DEVELOPMENTAL BIOLOGICALS INC. 2.7%; Score 60; DB 10; Length 2169;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.4e-11;
RESULT 327
ID AAD07661 standard; cDNA; 2329 BP.
DE Human secreted protein-encoding gene 7 cDNA clone HNTDL21, SEQ ID NO:17.
PN WO200134644-A1.
PD 17-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC. 2.7%; Score 60; DB 5; Length 2329;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.4e-11;
RESULT 328
ID ADQ24017 standard; DNA; 3554 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6837.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC. 2.7%; Score 60; DB 12; Length 3554;
Query Match
Best Local Similarity 100.0%; Pred. No. 4e-11;
RESULT 329
ID AAL16677 standard; cDNA; 4086 BP.
DE Human secreted protein clone kv10.8 nucleotide sequence SEQ ID NO:119.
PN WO200009552-A1.
PD 24-FEB-2000.
PA (GENY) GENETICS INST INC. 2.7%; Score 60; DB 3; Length 4086;
Query Match
Best Local Similarity 100.0%; Pred. No. 3.8e-11;
RESULT 330
ID ABK39753 standard; cDNA; 4086 BP.
DE cDNA encoding clone #50560 (L987P) of lung tumour protein.
PN WO200204514-A2.
PD 17-JAN-2002.
PA (CORI-) CORIAX CORP. 2.7%; Score 60; DB 6; Length 4086;
Query Match
Best Local Similarity 100.0%; Pred. No. 3.8e-11;
RESULT 331
ID ACA12082 standard; cDNA; 4086 BP.
DE Human lung cancer-associated cDNA L987P extended sequence.
PN US2002197669-A1.
PD 26-DEC-2002.
PA (BANG/) BANGUR C S.
PA (FANG/) FANGER G R.
PA (WANG/) WANG A.
PA (WANG/) WANG T.
PA (SWIT/) SWITZER A P.
PA (MCNE/) MCNEILL P D.
PA (CLAP/) CLAPPER J D.
Query Match
Best Local Similarity 100.0%; Pred. No. 3.8e-11;
RESULT 332
ID ACA03268 standard; cDNA; 4086 BP.
DE Lung cancer therapy and diagnosis associated cDNA #1755.
PN US2002172952-A1.
PD 21-NOV-2002.
PA (CORI-) CORIAX CORP. 2.7%; Score 60; DB 8; Length 4086;
Query Match
Best Local Similarity 100.0%; Pred. No. 3.8e-11;
RESULT 333
ID ADH47320 standard; cDNA; 4086 BP.
DE Human lung tumour cDNA clone, SEQ ID No 1801.
PN WO2003037267-A2.
PD 08-MAY-2003.
PA (CORI-) CORIAX CORP. 2.7%; Score 60; DB 10; Length 4086;
Query Match
Best Local Similarity 100.0%; Pred. No. 3.8e-11;
RESULT 334

Query Match
Best Local Similarity 2.6%; Score 59; DB 10; Length 115;
DE Human prostate expression marker cDNA 30279.
PN WO200160860-A2.

RESULT 342

ID AAD56370 standard; DNA; 169 BP.
DE Human secreted protein-encoding gene 8 CDNA clone HDMSA74, SEQ ID NO:30.
PN WO2003038038-A2.
PD 08-MAY-2003.

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 2.6%; Score 59; DB 9; Length 169;
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5191.
PN WO2004048938-A2.
PD 10-JUN-2004.

PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match
Best Local Similarity 2.7%; Score 60; DB 12; Length 4824;
DE Human cell adhesion and extracellular matrix protein, CAECM-7, DNA.
PN WO2003027230-A2.
PD 03-APR-2003.

PA (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 2.7%; Score 60; DB 8; Length 10569;
DE Human colon cancer-associated cDNA, SEQ ID No 749.
PN WO200212280-A2.
PD 14-FEB-2002.

PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 2.6%; Score 59; DB 6; Length 81;
DE Human colon cancer-associated cDNA, SEQ ID No 157.
PN WO200212280-A2.
PD 14-FEB-2002.

PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 2.6%; Score 59; DB 6; Length 90;
DE Human colon cancer-associated cDNA, SEQ ID No 106 BP.
PN WO9740069-A2.

PA (GEMY) GENETICS INST INC.
Query Match
Best Local Similarity 2.6%; Score 59; DB 2; Length 106;
DE Mouse mitochondrial DNA sequence SEQ ID NO:1326.
PN WO2003020220-A2.
PD 13-MAR-2003.

PA (UYEM-) UNIV EMORY.
Query Match
Best Local Similarity 2.6%; Score 59; DB 10; Length 111;
DE Arabidopsis thaliana polynucleotide #743.
PN US2002142319-A1.
PD 03-OCT-2002.

PA (GORL/) GORLACH J.
PA (ANYV/) AN Y.
PA (HAMJ/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (HARG/) HARGISS T R.
PA (YUYU/) YU Y.
PA (PAGE/) PAGE A.
PA (RAME/) RAMEAKA J G.
PA (MATH/) MATHEW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.

Query Match
Best Local Similarity 2.6%; Score 59; DB 5; Length 244; Length 244;
DE Nucleotide sequence of a human ribosomal protein L18a.
PN WO20015324-A2.
PD 26-JUL-2001.

PA (UYNO-) UNIV NOTTINGHAM TRENT.
Query Match
Best Local Similarity 2.6%; Score 59; DB 5; Length 244;

Best Local Similarity 100.0%; Pred. No. 1.6e-10;
RESULT 351
ID ADI72681 standard; DNA; 246 BP.
DE Human ovarian cancer DNA marker #5423.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
RESULT 352
ID ADL37820 standard; DNA; 246 BP.
DE Human ovarian cancer DNA marker #11710.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
RESULT 353
ID ABV3658 standard; cDNA; 254 BP.
DE Human breast specific gene SEQ ID NO 101.
PN WO200266605-A2.
PD 29-AUG-2002.
PA (DIAD-) DIADEXUS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
RESULT 354
ID ABV37898 standard; cDNA; 257 BP.
DE Human prostate expression marker cDNA 37889.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
RESULT 355
ID ABV49125 standard; cDNA; 270 BP.
DE Human prostate expression marker cDNA 49116.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
RESULT 356
ID ABV61841 standard; cDNA; 281 BP.
DE Human prostate expression marker cDNA 61832.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
RESULT 357
ID ABZ08427 standard; cDNA; 290 BP.
DE Human leukocyte derived cDNA SEQ ID NO 8418.
PN WO200257414-A2.
PD 25-JUL-2002.
PA (BIOC-) BIOCARDIA INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
RESULT 358
ID ABV61015 standard; cDNA; 294 BP.
DE Human prostate expression marker cDNA 61006.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
RESULT 359
ID ABX48782 standard; cDNA; 299 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #13947.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT-) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.

PA (WARR/) WARREN W C.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
RESULT 360
ID ABV19334 standard; cDNA; 305 BP.
DE Human prostate expression marker cDNA 19325.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
RESULT 361
ID ABV49426 standard; cDNA; 308 BP.
DE Human prostate expression marker cDNA 49417.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
RESULT 362
ID ADK60878 standard; DNA; 308 BP.
DE Ovarian cancer-related DNA #33 with altered ovarian cancer expression.
PN WO2003068054-A2.
PD 21-AUG-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
RESULT 363
ID AAH70139 standard; cDNA; 309 BP.
DE Human cervical cancer marker nucleic acid 1413.
PN WO200142467-A2.
PD 14-JUN-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
RESULT 364
ID AAL25957 standard; cDNA; 313 BP.
DE Human breast cancer expressed polynucleotide 18414.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
RESULT 365
ID ADL43989 standard; DNA; 324 BP.
DE Human ovarian cancer DNA marker #17879.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
RESULT 366
ID ABV19659 standard; cDNA; 333 BP.
DE Human prostate expression marker cDNA 19650.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
RESULT 367
ID AAI83209 standard; cDNA; 356 BP.
DE Human polynucleotide SEQ ID NO 3269.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
RESULT 368
ID ABL87200 standard; cDNA; 359 BP.
DE Human ovarian cancer related cDNA clone SEQ ID NO:10178.
PN WO200192581-A2.
PD 06-DEC-2001.

PA (CORI-) CORIXA CORP.
 Query Match 2.6%; Score 59; DB 6; Length 359;
 Best Local Similarity 100.0%; Pred. No. 1.5e-10;
 RESULT 369
 ID ABV60981 standard; cDNA; 360 BP.
 DE Human prostate expression marker cDNA 60972.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 2.6%; Score 59; DB 5; Length 360;
 Best Local Similarity 100.0%; Pred. No. 1.5e-10;
 RESULT 370
 ID ADK61648 standard; DNA; 360 BP.
 DE Ovarian cancer-related DNA #803 with altered ovarian cancer expression.
 PN WO2003068054-A2.
 PD 21-AUG-2003.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA (SLOK) SLOAN KETTERING INST CANCER RES.
 Query Match 2.6%; Score 59; DB 10; Length 360;
 Best Local Similarity 100.0%; Pred. No. 1.5e-10;
 RESULT 371
 ID AAI83219 standard; cDNA; 362 BP.
 DE Human polynucleotide SEQ ID NO 3279.
 PN WO200164835-A2.
 PD 07-SEP-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 2.6%; Score 59; DB 4; Length 362;
 Best Local Similarity 100.0%; Pred. No. 1.5e-10;
 RESULT 372
 ID ABX42829 standard; cDNA; 373 BP.
 DE Bovine EST associated with lactation/muscle/fat deposition #7994.
 PN US2002137139-A1.
 PD 26-SEP-2002.
 PA (BYAT/) BYATT J C.
 PA (MATH/) MATHIALAGAN N.
 PA (TAON/) TAO N.
 PA (WARF/) WARREN W C.
 Query Match 2.6%; Score 59; DB 8; Length 373;
 Best Local Similarity 100.0%; Pred. No. 1.5e-10;
 RESULT 373
 ID ABV14963 standard; cDNA; 374 BP.
 DE Human prostate expression marker cDNA 14954.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 2.8%; Score 59; DB 5; Length 374;
 Best Local Similarity 100.0%; Pred. No. 1.5e-10;
 RESULT 374
 ID AAI88772 standard; cDNA; 375 BP.
 DE Human polynucleotide SEQ ID NO 8832.
 PN WO200164835-A2.
 PD 07-SEP-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 2.6%; Score 59; DB 4; Length 375;
 Best Local Similarity 100.0%; Pred. No. 1.5e-10;
 RESULT 375
 ID ABV05794 standard; cDNA; 375 BP.
 DE Human prostate expression marker cDNA 5785.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 2.6%; Score 59; DB 5; Length 375;
 Best Local Similarity 100.0%; Pred. No. 1.5e-10;
 RESULT 376
 ID ABV57992 standard; cDNA; 376 BP.
 DE Human prostate expression marker cDNA 57983.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 2.8%; Score 59; DB 5; Length 376;
 Best Local Similarity 100.0%; Pred. No. 1.5e-10;
 RESULT 377
 ID ABV56400 standard; cDNA; 376 BP.

DE Human prostate expression marker cDNA 56391.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 2.6%; Score 59; DB 5; Length 376;
 Best Local Similarity 100.0%; Pred. No. 1.5e-10;
 RESULT 378
 ID ABT22632 standard; DNA; 378 BP.
 DE Breast cancer marker gene SEQ ID NO 1005.
 PN WO200285298-A2.
 PD 31-OCT-2002.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 2.6%; Score 59; DB 10; Length 378;
 Best Local Similarity 100.0%; Pred. No. 1.5e-10;
 RESULT 379
 ID ABZ08196 standard; cDNA; 384 BP.
 DE Human leukocyte derived cDNA SEQ ID NO 8187.
 PN WO200257414-A2.
 PD 25-JUL-2002.
 PA (BIOC-) BIOCARDIA INC.
 Query Match 2.6%; Score 59; DB 6; Length 384;
 Best Local Similarity 100.0%; Pred. No. 1.4e-10;
 RESULT 380
 ID AAI90569 standard; cDNA; 393 BP.
 DE Human polynucleotide SEQ ID NO 10629.
 PN WO200164835-A2.
 PD 07-SEP-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 2.6%; Score 59; DB 4; Length 393;
 Best Local Similarity 100.0%; Pred. No. 1.4e-10;
 RESULT 381
 ID ADL44065 standard; DNA; 394 BP.
 DE Human ovarian cancer DNA marker #17955.
 PN WO200170979-A2.
 PD 27-SEP-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 2.6%; Score 59; DB 5; Length 394;
 Best Local Similarity 100.0%; Pred. No. 1.4e-10;
 RESULT 382
 ID AAI83099 standard; cDNA; 395 BP.
 DE Human polynucleotide SEQ ID NO 3159.
 PN WO200164835-A2.
 PD 07-SEP-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 2.6%; Score 59; DB 4; Length 395;
 Best Local Similarity 100.0%; Pred. No. 1.4e-10;
 RESULT 383
 ID AAI88643 standard; cDNA; 396 BP.
 DE Human polynucleotide SEQ ID NO 8703.
 PN WO200164835-A2.
 PD 07-SEP-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 2.6%; Score 59; DB 4; Length 396;
 Best Local Similarity 100.0%; Pred. No. 1.4e-10;
 RESULT 384
 ID ABV13524 standard; cDNA; 396 BP.
 DE Human prostate expression marker cDNA 13515.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 2.6%; Score 59; DB 5; Length 396;
 Best Local Similarity 100.0%; Pred. No. 1.4e-10;
 RESULT 385
 ID AAI87808 standard; cDNA; 399 BP.
 DE Human polynucleotide SEQ ID NO 7868.
 PN WO200164835-A2.
 PD 07-SEP-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 2.6%; Score 59; DB 4; Length 399;
 Best Local Similarity 100.0%; Pred. No. 1.4e-10;
 RESULT 386
 ID ABX47608 standard; cDNA; 399 BP.
 DE Bovine EST associated with lactation/muscle/fat deposition #12773.

PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 2.6%; Score 59; DB 8; Length 399;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 387
ID AAS44813 standard; DNA; 400 BP.
DE Mouse contig polynucleotide sequence #66.
PN WO200164834-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 59; DB 4; Length 400;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 388
ID ABV14838 standard; cDNA; 400 BP.
DE Human prostate expression marker cDNA 14829.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 400;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 389
ID ADL44204 standard; DNA; 402 BP.
DE Human ovarian cancer DNA marker #18094.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 402;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 390
ID AAI87975 standard; cDNA; 403 BP.
DE Human polynucleotide SEQ ID NO 8035.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 59; DB 4; Length 403;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 391
ID AAI83327 standard; cDNA; 405 BP.
DE Human polynucleotide SEQ ID NO 3387.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 59; DB 4; Length 405;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 392
ID AAI93716 standard; cDNA; 411 BP.
DE Human polynucleotide SEQ ID NO 13776.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 59; DB 4; Length 411;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 393
ID AAI88867 standard; cDNA; 416 BP.
DE Human polynucleotide SEQ ID NO 8927.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 59; DB 4; Length 416;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 394
ID AAL25912 standard; cDNA; 417 BP.
DE Human breast cancer expressed polynucleotide 18369.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 4; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 395
ID ABX45215 standard; cDNA; 435 BP.
ID AAI85189 standard; cDNA; 417 BP.
DE Human polynucleotide SEQ ID NO 5249.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 59; DB 4; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 396
ID AAI90979 standard; cDNA; 417 BP.
DE Human polynucleotide SEQ ID NO 11039.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 59; DB 4; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 397
ID AAI82925 standard; cDNA; 417 BP.
DE Human polynucleotide SEQ ID NO 2985.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 59; DB 4; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 398
ID AAI80556 standard; cDNA; 420 BP.
DE Human polynucleotide SEQ ID NO 616.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 59; DB 4; Length 420;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 399
ID ABV56528 standard; cDNA; 421 BP.
DE Human prostate expression marker cDNA 56519.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 421;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 400
ID AAI82066 standard; cDNA; 422 BP.
DE Human polynucleotide SEQ ID NO 2126.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 59; DB 4; Length 422;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 401
ID ADL41653 standard; DNA; 425 BP.
DE Human ovarian cancer DNA marker #15543.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 425;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 402
ID ABV60871 standard; cDNA; 426 BP.
DE Human prostate expression marker cDNA 60862.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 426;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 403
ID ABV44832 standard; cDNA; 433 BP.
DE Human prostate expression marker cDNA 44823.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 433;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 404
ID ABX45215 standard; cDNA; 435 BP.

DE Bovine EST associated with lactation/muscle/fat deposition #10380.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 2.6%; Score 59; DB 8; Length 435;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 405
ID ABV35046 standard; cDNA; 436 BP.
DE Human prostate expression marker cDNA 39037.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 436;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 406
ID ABV38926 standard; cDNA; 436 BP.
DE Human prostate expression marker cDNA 38917.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 436;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 407
ID ABV44714 standard; cDNA; 436 BP.
DE Human prostate expression marker cDNA 44705.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.8%; Score 59; DB 5; Length 436;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 408
ID ABV34639 standard; cDNA; 442 BP.
DE Human prostate expression marker cDNA 34630.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 442;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 409
ID ABV43495 standard; cDNA; 442 BP.
DE Human prostate expression marker cDNA 43486.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 442;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 410
ID AAI83052 standard; cDNA; 452 BP.
DE Human polynucleotide SEQ ID NO 3112.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 59; DB 4; Length 452;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 411
ID ABX35770 standard; cDNA; 452 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #935.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 2.6%; Score 59; DB 8; Length 452;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 412
ID AAS60714 standard; cDNA; 456 BP.
DE Human cancer agent-resistance marker #469.
PN WO200179556-A2.
PD 25-OCT-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 4; Length 456;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 413
ID ABV36028 standard; cDNA; 459 BP.
DE Human prostate expression marker cDNA 36019.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 459;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 414
ID ABV37900 standard; cDNA; 459 BP.
DE Human prostate expression marker cDNA 37891.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 459;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 415
ID AAH64924 standard; cDNA; 462 BP.
DE Human secreted protein cDNA, SEQ ID NO: 200.
PN WO200142451-A2.
PD 14-JUN-2001.
PA (GEST) GENSET.
Query Match 2.6%; Score 59; DB 5; Length 462;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 416
ID AAL19122 standard; cDNA; 472 BP.
DE Human breast cancer expressed polynucleotide 11579.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 4; Length 472;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 417
ID ADL43530 standard; DNA; 476 BP.
DE Human ovarian cancer DNA marker #17420.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 476;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 418
ID ABV61013 standard; cDNA; 478 BP.
DE Human prostate expression marker cDNA 61004.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 478;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 419
ID AAL19077 standard; cDNA; 486 BP.
DE Human breast cancer expressed polynucleotide 11534.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 4; Length 486;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 420
ID ADL44998 standard; DNA; 501 BP.
DE Human ovarian cancer DNA marker #18888.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 501;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 421
ID ABV5765 standard; cDNA; 502 BP.
DE Human prostate expression marker cDNA 57756.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Query Match 2.6%; Score 59; DB 5; Length 502;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 422
ID ABV35805 standard; cDNA; 503 BP.
DE Human prostate expression marker cDNA 35796.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 423
ID ABV4605 standard; cDNA; 503 BP.
DE Human prostate expression marker cDNA 44596.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 424
ID ABV56784 standard; cDNA; 505 BP.
DE Human prostate expression marker cDNA 56775.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 505;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 425
ID ACH23748 standard; cDNA; 506 BP.
DE Human adult ovary cDNA #2128.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 2.6%; Score 59; DB 9; Length 506;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 426
ID ABL87166 standard; cDNA; 508 BP.
DE Human ovarian cancer related cDNA clone SEQ ID NO:10144.
PN WO200192581-A2.
PD 06-DEC-2001.
PA (CORI-) CORIXA CORP.
Query Match 2.6%; Score 59; DB 6; Length 508;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 427
ID ABV49485 standard; cDNA; 516 BP.
DE Human prostate expression marker cDNA 49476.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 516;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
RESULT 428
ID ADL43674 standard; DNA; 526 BP.
DE Human ovarian cancer DNA marker #17564.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 526;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
RESULT 429
ID AAS60111 standard; cDNA; 530 BP.
DE Human cancer agent-sensitive marker #112.
PN WO200179556-A2.
PD 25-OCT-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 4; Length 530;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
RESULT 430
ID ABV56384 standard; cDNA; 535 BP.
DE Human prostate expression marker cDNA 56375.

PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 535;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
RESULT 431
ID AAH34620 standard; cDNA; 545 BP.
DE Human colon cancer antigen encoding cDNA SEQ ID NO:1702.
PN WO200122920-A2.
PD 05-APR-2001.
PA (HUNA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 59; DB 4; Length 545;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
RESULT 432
ID ABV56662 standard; cDNA; 549 BP.
DE Human prostate expression marker cDNA 56653.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 549;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
RESULT 433
ID ABV56468 standard; cDNA; 549 BP.
DE Human prostate expression marker cDNA 56459.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 549;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
RESULT 434
ID ABV14728 standard; cDNA; 555 BP.
DE Human prostate expression marker cDNA 14719.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 555;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
RESULT 435
ID AAS29149 standard; cDNA; 565 BP.
DE cDNA encoding for human DNA-binding protein #120.
PN WO200155162-A1.
PD 02-AUG-2001.
PA (HUNA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 59; DB 5; Length 565;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
RESULT 436
ID ABS68289 standard; cDNA; 565 BP.
DE cDNA encoding human DNA-binding protein #120.
PN US2002102638-A1.
PD 01-AUG-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 2.6%; Score 59; DB 6; Length 565;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
RESULT 437
ID ADC25283 standard; cDNA; 565 BP.
DE Human cDNA from extracellular matrix gene 120.
PN US2003049650-A1.
PD 13-MAR-2003.
PA (HUNA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 59; DB 10; Length 565;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
RESULT 438
ID ADL43620 standard; DNA; 566 BP.
DE Human ovarian cancer DNA marker #17510.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 566;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
RESULT 439
ID ABL87230 standard; cDNA; 585 BP.

DE Human ovarian cancer related cDNA clone SEQ ID NO:10208.
 PN WO200192581-A2.
 PD 06-DEC-2001.
 PA (CORI-) CORIXA CORP.
 Query Match 2.6%; Score 59; DB 6; Length 585;
 Best Local Similarity 100.0%; Pred. No. 1.3e-10;
 RESULT 440
 ID ADL37504 standard; DNA; 610 BP.
 DE Human ovarian cancer DNA marker #11394.
 PN WO200170979-A2.
 PD 27-SEP-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 2.8%; Score 59; DB 5; Length 610;
 Best Local Similarity 100.0%; Pred. No. 1.3e-10;
 RESULT 441
 ID ADI72360 standard; DNA; 610 BP.
 DE Human ovarian cancer DNA marker #5102.
 PN WO200170979-A2.
 PD 27-SEP-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 2.6%; Score 59; DB 5; Length 610;
 Best Local Similarity 100.0%; Pred. No. 1.3e-10;
 RESULT 442
 ID AHT71564 standard; cDNA; 611 BP.
 DE Human cervical cancer marker nucleic acid 2838.
 PN WO200142467-A2.
 PD 14-JUN-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 2.6%; Score 59; DB 4; Length 611;
 Best Local Similarity 100.0%; Pred. No. 1.3e-10;
 RESULT 443
 ID AHT22374 standard; DNA; 620 BP.
 DE Breast cancer marker gene SEQ ID No 747.
 PN WO200282598-A2.
 PD 31-OCT-2002.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 2.6%; Score 59; DB 10; Length 620;
 Best Local Similarity 100.0%; Pred. No. 1.3e-10;
 RESULT 444
 ID ADK61473 standard; DNA; 631 BP.
 DE Ovarian cancer-related DNA #628 with altered ovarian cancer expression.
 PN WO2003068054-A2.
 PD 21-AUG-2003.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA (SLOK) SLOAN KETTERING INST CANCER RES.
 Query Match 2.6%; Score 59; DB 10; Length 631;
 Best Local Similarity 100.0%; Pred. No. 1.3e-10;
 RESULT 445
 ID AA298055 standard; cDNA; 639 BP.
 DE Human secreted protein encoding nucleotide sequence SEQ ID NO:49.
 PN WO200004140-A1.
 PD 27-JAN-2000.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.6%; Score 59; DB 3; Length 639;
 Best Local Similarity 100.0%; Pred. No. 1.3e-10;
 RESULT 446
 ID AAD11668 standard; cDNA; 639 BP.
 DE Human secreted protein-encoding gene 39 cDNA clone HE2DY70, SEQ ID NO:49.
 PN WO200151504-A1.
 PD 19-JUL-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.6%; Score 59; DB 4; Length 639;
 Best Local Similarity 100.0%; Pred. No. 1.3e-10;
 RESULT 447
 ID ABK69764 standard; cDNA; 639 BP.
 DE Human secreted protein gene 39.
 PN WO200226931-A2.
 PD 04-APR-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.6%; Score 59; DB 6; Length 639;
 Best Local Similarity 100.0%; Pred. No. 1.3e-10;
 RESULT 448
 ID ADA39770 standard; cDNA; 639 BP.
 DE Human secreted protein encoding cDNA.
 PN WO2002102993-A2.
 PD 27-DEC-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.6%; Score 59; DB 8; Length 639;
 Best Local Similarity 100.0%; Pred. No. 1.3e-10;
 RESULT 449
 ID ADA55961 standard; DNA; 639 BP.
 DE Gene encoding human secreted protein #140.
 PN WO2002102994-A2.
 PD 27-DEC-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.6%; Score 59; DB 10; Length 639;
 Best Local Similarity 100.0%; Pred. No. 1.3e-10;
 RESULT 450
 ID ADI71997 standard; DNA; 664 BP.
 DE Human ovarian cancer DNA marker #4739.
 PN WO200170979-A2.
 PD 27-SEP-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 2.6%; Score 59; DB 5; Length 664;
 Best Local Similarity 100.0%; Pred. No. 1.3e-10;
 RESULT 451
 ID ADL37146 standard; DNA; 664 BP.
 DE Human ovarian cancer DNA marker #11036.
 PN WO200170979-A2.
 PD 27-SEP-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 2.6%; Score 59; DB 5; Length 664;
 Best Local Similarity 100.0%; Pred. No. 1.3e-10;
 RESULT 452
 ID AAS62239 standard; cDNA; 681 BP.
 DE cDNA sequence #26 encoding novel human secreted protein.
 PN WO200177291-A2.
 PD 18-OCT-2001.
 PA (GEMY) GENETICS INST INC.
 Query Match 2.6%; Score 59; DB 6; Length 681;
 Best Local Similarity 100.0%; Pred. No. 1.3e-10;
 RESULT 453
 ID ABA06495 standard; cDNA; 758 BP.
 DE Human cDNA SEQ ID NO: 161.
 PN WO200154474-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.6%; Score 59; DB 4; Length 758;
 Best Local Similarity 100.0%; Pred. No. 1.2e-10;
 RESULT 454
 ID ABV83832 standard; cDNA; 758 BP.
 DE Human polynucleotide SEQ ID NO 161.
 PN US2002090672-A1.
 PD 11-JUL-2002.
 PA (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 PA (BARA/) BARASH S C.
 Query Match 2.6%; Score 59; DB 6; Length 758;
 Best Local Similarity 100.0%; Pred. No. 1.2e-10;
 RESULT 455
 ID AAI95164 standard; cDNA; 771 BP.
 DE Human neuroblastoma expressed polynucleotide SEQ ID NO 1239.
 PN WO200166719-A1.
 PD 13-SEP-2001.
 PA (CHIB-) CHIBA PREFECTURE.
 PA (HISM) HISAMITSU PHARM CO LTD.
 Query Match 2.6%; Score 59; DB 4; Length 771;
 Best Local Similarity 100.0%; Pred. No. 1.2e-10;
 RESULT 456
 ID ADL38237 standard; DNA; 810 BP.
 DE Human ovarian cancer DNA marker #12127.
 PN WO200170979-A2.
 PD 27-SEP-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 2.6%; Score 59; DB 5; Length 810;
 Best Local Similarity 100.0%; Pred. No. 1.2e-10;

RESULT 457
ID ADI73104 standard; DNA; 810 BP.
DE Human ovarian cancer DNA marker #5946.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 59; DB 5; Length 810;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
RESULT 458
ID ABK34898 standard; cDNA; 811 BP.
DE Human cDNA encoding secreted protein #36.
PN WO200177288-A2.
PD 18-OCT-2001.
PA (GEMY) GENETICS INST INC.
Query Match 2.6%; Score 59; DB 6; Length 811;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
RESULT 459
ID AAC78094 standard; cDNA; 827 BP.
DE Human cancer associated gene sequence SEQ ID NO:488.
PN WO200055350-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 59; DB 3; Length 827;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
RESULT 460
ID AAX89609 standard; cDNA; 831 BP.
DE Human secreted protein clone bg570_1 encoding cDNA.
PN WO9935253-A1.
PD 15-JUL-1999.
PA (GEMY) GENETICS INST INC.
Query Match 2.6%; Score 59; DB 2; Length 831;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
RESULT 461
ID AAS59240 standard; cDNA; 831 BP.
DE Human cDNA encoding a secreted protein bg570_1.
PN WO200175068-A2.
PD 11-OCT-2001.
PA (GEMY) GENETICS INST INC.
Query Match 2.6%; Score 59; DB 4; Length 831;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
RESULT 462
ID ABA90909 standard; cDNA; 831 BP.
DE Human polynucleotide SEQ ID NO 67.
PN US2001039335-A1.
PD 08-NOV-2001.
PA (JACO/) JACOBS K.
PA (MCCO/) MCCOY J M.
PA (LAVA/) LAVALLIE E R.
PA (COLL/) COLLINS-RACIE L A.
PA (EVAN/) EVANS C.
PA (MERB/) MERBERG D.
PA (TREA/) TREACY M.
PA (AGOS/) AGOSTINO M J.
PA (STEI/) STEININGER R J.
PA (SPAU/) SPAULDING V.
PA (WONG/) WONG G G.
PA (CLAR/) CLARK H.
PA (FECH/) FECHTEL K.
Query Match 2.6%; Score 59; DB 6; Length 831;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
RESULT 463
ID ADC78824 standard; DNA; 835 BP.
DE Human PRO protein coding sequence #27.
PN WO2003034984-A2.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 10; Length 835;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
RESULT 464
ID AAS25860 standard; cDNA; 836 BP.
DE Human cDNA encoding a novel secreted protein, Seq ID 39.
PN WO200155322-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 59; DB 4; Length 836;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
RESULT 465
ID ABX73201 standard; DNA; 836 BP.
DE Human novel polynucleotide #29.
PN US2002132753-A1.
PD 19-SEP-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 2.6%; Score 59; DB 9; Length 836;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
RESULT 466
ID ABZ78019 standard; cDNA; 841 BP.
DE Human breast specific nucleic acid #33.
PN WO200268645-A2.
PD 06-SEP-2002.
PA (DIAD-) DIADEXUS INC.
Query Match 2.6%; Score 59; DB 6; Length 841;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
RESULT 467
ID ADK67944 standard; cDNA; 860 BP.
DE Mouse cDNA clone F38, related to serine/threonine kinase.
PN WO2004013289-A2.
PD 12-FEB-2004.
PA (UYOH-) UNIV OHIO.
Query Match 2.6%; Score 59; DB 12; Length 860;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
RESULT 468
ID ABA06476 standard; cDNA; 912 BP.
DE Human cDNA SEQ ID NO: 142.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 59; DB 4; Length 912;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
RESULT 469
ID ABV83813 standard; cDNA; 912 BP.
DE Human polynucleotide SEQ ID NO 142.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 2.6%; Score 59; DB 6; Length 912;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
RESULT 470
ID AAS40889 standard; cDNA; 913 BP.
DE cDNA encoding novel human enzyme polypeptide #105.
PN WO200155301-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 59; DB 4; Length 913;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
RESULT 471
ID ABA06682 standard; cDNA; 913 BP.
DE Human cDNA SEQ ID NO: 348.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 59; DB 4; Length 913;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
RESULT 472
ID AAS29696 standard; cDNA; 913 BP.
DE Human endocrine polypeptide encoding cDNA SEQ ID NO 196.
PN WO200155364-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 59; DB 5; Length 913;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
RESULT 473
ID ABV84019 standard; cDNA; 913 BP.

DE Human polynucleotide SEQ ID NO 348.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 2.6%; Score 59; DB 6; Length 913;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
RESULT 474
ID ABQ80003 standard; cDNA; 925 BP.
DE Secreted human protein cDNA.
PN WO2003002138-A1.
PD 09-JAN-2003.
PA (PEKE) PE CORP NY.
Query Match 2.6%; Score 59; DB 8; Length 925;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
RESULT 475
ID AAA78431 standard; cDNA; 952 BP.
DE Human secreted protein gene 46 SEQ ID NO:61.
PN WO200035937-A1.
PD 22-JUN-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 59; DB 3; Length 952;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
RESULT 476
ID AAC69107 standard; DNA; 995 BP.
DE Human secreted protein gene 24 clone HAMFL84.
PN WO200053371-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 59; DB 3; Length 995;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
RESULT 477
ID ABK35340 standard; cDNA; 995 BP.
DE Human cDNA encoding secreted protein #478.
PN WO200177288-A2.
PD 18-OCT-2001.
PA (GEMY) GENETICS INST INC.
Query Match 2.6%; Score 59; DB 6; Length 995;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
RESULT 478
ID AAX20414 standard; DNA; 1071 BP.
DE Human secreted protein gene 3.
PN WO9906423-A1.
PD 11-FEB-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 59; DB 2; Length 1071;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
RESULT 479
ID AD90198 standard; cDNA; 1071 BP.
DE Novel human secreted protein cDNA seq id 13.
PN US2003199683-A1.
PD 23-OCT-2003.
PA (RUBE/) RUBEN S M.
PA (FENG/) FENG P.
PA (LAF/) LAFLEUR D W.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (KYAW/) KYAW H.
PA (LIYV/) LI Y.
PA (ZENG/) ZENG Z.
PA (CART/) CARTER K C.
PA (ENDR/) ENDRESS G A.
PA (WEIY/) WEI Y.
PA (FANP/) FAN P.
PA (ROSE/) ROSEN C A.
Query Match 2.6%; Score 59; DB 10; Length 1071;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
RESULT 480
ID ADG90017 standard; cDNA; 1071 BP.
DE Human cDNA from secreted protein gene 3.
PN US2003166541-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 59; DB 10; Length 1071;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
RESULT 481
ID ADO62876 standard; DNA; 1091 BP.
DE Transcription factor G3055 orthologous sequence, SEQ ID 1343.
PN WO2004031349-A2.
PD 15-APR-2004.
PA (MENDEL-) MENDEL BIOTECHNOLOGY INC.
Query Match 2.6%; Score 59; DB 12; Length 1091;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
RESULT 482
ID AAA29167 standard; cDNA; 1106 BP.
DE Rice 4-hydroxyphenylpyruvate dioxygenase partial cDNA.
PN WO200032757-A2.
PD 08-JUN-2000.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 2.6%; Score 59; DB 3; Length 1106;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
RESULT 483
ID ABT02999 standard; DNA; 1107 BP.
DE Human breast specific coding sequence SEQ ID NO: 4.
PN WO200240672-A2.
PD 23-MAY-2002.
PA (DIAD-) DIADEXUS INC.
Query Match 2.6%; Score 59; DB 6; Length 1107;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
RESULT 484
ID AAS28831 standard; cDNA; 1125 BP.
DE Human immunoglobulin encoding cDNA SEQ ID NO 77.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 59; DB 4; Length 1125;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
RESULT 485
ID ADB31556 standard; cDNA; 1125 BP.
DE Human cDNA encoding a novel protein SEQ ID NO 77.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 59; DB 10; Length 1125;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
RESULT 486
ID RAV84347 standard; cDNA; 1180 BP.
DE Human Apo-2DCR cDNA clone DNA33085.
PN WO9858062-A1.
PD 23-DEC-1998.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 2; Length 1180;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
RESULT 487
ID ABS53571 standard; cDNA; 1180 BP.
DE cDNA encoding native human Apo-2DCR #2.
PN US2002102706-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 6; Length 1180;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
RESULT 488
ID ABS53570 standard; cDNA; 1180 BP.
DE cDNA encoding native human Apo-2DCR #1.
PN US2002102706-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 6; Length 1180;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
RESULT 489
ID RAD64037 standard; cDNA; 1180 BP.
DE Human Apo-2DCR cDNA #1.
PN US2003138915-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.

Query Match 2.6%; Score 59; DB 10; Length 1180;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
RESULT 490
ID AAD64038 standard; cDNA; 1180 BP.
DE Human Apo-2DCR cDNA #2.
PN US2003138915-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 10; Length 1180;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
RESULT 491
ID ACC00704 standard; cDNA; 1249 BP.
DE Zea mays oil trait related cDNA sequence SEQ ID NO:157.
PN WO2003002751-A2.
PD 09-JAN-2003.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 2.8%; Score 59; DB 8; Length 1249;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
RESULT 492
ID AAA93129 standard; cDNA; 1293 BP.
DE Human secreted protein coding sequence SEQ ID NO: 57.
PN WO200049134-A1.
PD 24-AUG-2000.
PA (ALPH-) ALPHAGEN INC.
Query Match 2.6%; Score 59; DB 3; Length 1293;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
RESULT 493
ID ACC00651 standard; cDNA; 1307 BP.
DE Zea mays oil trait related cDNA sequence SEQ ID NO:51.
PN WO2003002751-A2.
PD 09-JAN-2003.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 2.8%; Score 59; DB 8; Length 1307;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
RESULT 494
ID ADC23530 standard; cDNA; 1307 BP.
DE cDNA encodes protein involved in altering plant oil phenotype (SeqID 35).
PN WO2003001902-A2.
PD 09-JAN-2003.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 2.6%; Score 59; DB 10; Length 1307;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
RESULT 495
ID ADQ23192 standard; DNA; 1383 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6012.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.6%; Score 59; DB 12; Length 1383;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
RESULT 496
ID ADQ24215 standard; DNA; 1469 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7035.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.6%; Score 59; DB 12; Length 1469;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
RESULT 497
ID ADI16785 standard; cDNA; 1513 BP.
DE Human NOVX cDNA to treat human pathological conditions SeqID321.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 2.6%; Score 59; DB 6; Length 1513;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
RESULT 498
ID ADN42439 standard; cDNA; 1513 BP.
DE Human cDNA encoding NOV 99.
PN US2004033493-A1.

19-FEB-2004.
PA (TCHE/) TCHERNEV V T.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PATI/) PATTURAJAN M.
PA (SHIM/) SHIMKETS R A.
PA (LILL/) LI L.
PA (GANG/) GANGOLLI E A.
PA (PADI/) PADIGARU M.
PA (ANDE/) ANDERSON D W.
PA (RASI/) RASTELLI L.
PA (MILL/) MILLER C E.
PA (GERL/) GERLACH V.
PA (TAUP/) TAUPIER R J.
PA (GUSE/) GUSEV V Y.
PA (COLM/) COLMAN S D.
PA (WOLE/) WOLENC A R.
PA (PENA/) PENNA C E A.
PA (FURT/) FURTAK K.
PA (GROS/) GROSSE W M.
PA (ALSO/) ALSOBROOK J P.
PA (LEPL/) LEPLEY D M.
PA (RIEG/) RIEGER D K.
PA (BURG/) BURGESS C E.
Query Match 2.6%; Score 59; DB 12; Length 1513;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
RESULT 499
ID AAX16675 standard; DNA; 1554 BP.
DE Xenopus WA545 protein encoding DNA.
PN WO9902678-A1.
PD 21-JAN-1999.
PA (GEMY) GENETICS INST INC.
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
Query Match 2.6%; Score 59; DB 2; Length 1554;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 500
ID ABK35953 standard; cDNA; 1554 BP.
DE cDNA sequence #344 encoding novel human secreted protein.
PN WO200177289-A2.
PD 18-OCT-2001.
PA (GEMY) GENETICS INST INC.
Query Match 2.6%; Score 59; DB 6; Length 1554;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 501
ID AAF21791 standard; DNA; 1614 BP.
DE Human breast and ovarian cancer associated antigen gene SEQ ID 178.
PN WO200055173-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 59; DB 3; Length 1614;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 502
ID AAA15694 standard; cDNA; 1651 BP.
DE Cancer suppressor gene down-regulated in large intestine cancer.
PN WO200018911-A1.
PD 06-APR-2000.
PA (ZHEN/) ZHENG S.
Query Match 2.6%; Score 59; DB 3; Length 1651;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 503
ID AAF97914 standard; cDNA; 1651 BP.
DE Human secreted protein cDNA, SEQ ID NO: 41.
PN WO200121658-A1.
PD 29-MAR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 59; DB 4; Length 1651;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 504
ID AAD07360 standard; DNA; 1651 BP.
DE Human DNA encoding SNC73 protein (marker 11).
PN WO200136674-A2.
PD 25-MAY-2001.
PA (ASTR) ASTRAZENECA AB.

PA (ASTR) ASTRAZENECA UK LTD.
 Query Match 2.6%; Score 59; DB 4; Length 1651;
 Best Local Similarity 100.0%; Pred. No. 1e-10;
 RESULT 505
 ID ADI82272 standard; DNA; 1683 BP.
 DE Human DNA differentially expressed in embryonic stem cells #2.
 PN US2003224411-A1.
 PD 04-DEC-2003.
 PA (STAN/) STANTON L W.
 PA (IRAN/) BRANDENBERGER R.
 PA (GOLD/) GOLD J D.
 PA (IRVI/) IRVING J M.
 PA (NAND/) MANDALAM R.
 PA (MOKM/) MOK M.
 PA (SHEL/) SHELTON D.
 Query Match 2.6%; Score 59; DB 12; Length 1683;
 Best Local Similarity 100.0%; Pred. No. 1e-10;
 RESULT 506
 ID ADP10415 standard; DNA; 1705 BP.
 DE Reference mRNA sequences for marker probe #92.
 PN WO2004042346-A2.
 PD 21-MAY-2004.
 PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
 Query Match 2.6%; Score 59; DB 12; Length 1705;
 Best Local Similarity 100.0%; Pred. No. 1e-10;
 RESULT 507
 ID ABK98825 standard; cDNA; 1724 BP.
 DE Babesia cDNA sequence for clone 60s.2.
 PN WO200253016-A2.
 PD 11-JUL-2002.
 PA (CORI-) CORIXA CORP.
 Query Match 2.6%; Score 59; DB 6; Length 1724;
 Best Local Similarity 100.0%; Pred. No. 1e-10;
 RESULT 508
 ID ABK33338 standard; cDNA; 1759 BP.
 DE cDNA encoding human PRO protein, Seq ID No 5.
 PN WO200208288-A2.
 PD 31-JAN-2002.
 PA (GETH) GENENTECH INC.
 Query Match 2.6%; Score 59; DB 6; Length 1759;
 Best Local Similarity 100.0%; Pred. No. 1e-10;
 RESULT 509
 ID ACA6499 standard; cDNA; 1759 BP.
 DE Novel human secreted and transmembrane protein PRO7174 cDNA.
 PN US200308063-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 2.6%; Score 59; DB 8; Length 1759;
 Best Local Similarity 100.0%; Pred. No. 1e-10;
 RESULT 510
 ID ABT44228 standard; cDNA; 1759 BP.
 DE Human PRO7174 cDNA.
 PN US2003050448-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 2.6%; Score 59; DB 9; Length 1759;
 Best Local Similarity 100.0%; Pred. No. 1e-10;
 RESULT 511
 ID ABT44511 standard; cDNA; 1759 BP.
 DE Human PRO7174 cDNA.
 PN US2003027988-A1.
 PD 06-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 2.6%; Score 59; DB 9; Length 1759;
 Best Local Similarity 100.0%; Pred. No. 1e-10;
 RESULT 512
 ID AC082178 standard; cDNA; 1759 BP.
 DE Human secreted/transmembrane polypeptide PRO 7174 cDNA.
 PN US2003044934-A1.
 PD 06-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 2.6%; Score 59; DB 9; Length 1759;
 Best Local Similarity 100.0%; Pred. No. 1e-10;

RESULT 513
 ID ABT43884 standard; cDNA; 1759 BP.
 DE Human membrane bound receptor/protein PRO7174 cDNA sequence.
 PN US2003065147-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 2.6%; Score 59; DB 9; Length 1759;
 Best Local Similarity 100.0%; Pred. No. 1e-10;
 RESULT 514
 ID ADB83495 standard; cDNA; 1759 BP.
 DE Novel human secreted and transmembrane protein PRO7174 cDNA.
 PN US2003073814-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 2.6%; Score 59; DB 9; Length 1759;
 Best Local Similarity 100.0%; Pred. No. 1e-10;
 RESULT 515
 ID ADB80601 standard; cDNA; 1759 BP.
 DE Novel human secreted and transmembrane protein PRO7174 cDNA.
 PN US2003088068-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 2.6%; Score 59; DB 9; Length 1759;
 Best Local Similarity 100.0%; Pred. No. 1e-10;
 RESULT 516
 ID ADB73142 standard; cDNA; 1759 BP.
 DE Novel human secreted and transmembrane protein PRO7174 cDNA.
 PN US2003096968-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 2.6%; Score 59; DB 9; Length 1759;
 Best Local Similarity 100.0%; Pred. No. 1e-10;
 RESULT 517
 ID ADB78224 standard; cDNA; 1759 BP.
 DE Novel human secreted and transmembrane protein PRO7174 cDNA.
 PN US2003092889-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 2.6%; Score 59; DB 9; Length 1759;
 Best Local Similarity 100.0%; Pred. No. 1e-10;
 RESULT 518
 ID ADB84872 standard; cDNA; 1759 BP.
 DE Human PRO polynucleotide #3.
 PN US2003073817-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 2.6%; Score 59; DB 10; Length 1759;
 Best Local Similarity 100.0%; Pred. No. 1e-10;
 RESULT 519
 ID ADB77978 standard; cDNA; 1759 BP.
 DE Novel human secreted and transmembrane protein PRO7174 cDNA.
 PN US2003092886-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 2.6%; Score 59; DB 10; Length 1759;
 Best Local Similarity 100.0%; Pred. No. 1e-10;
 RESULT 520
 ID ADB87044 standard; cDNA; 1759 BP.
 DE Human PRO polynucleotide #3.
 PN US2003088067-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 2.6%; Score 59; DB 10; Length 1759;
 Best Local Similarity 100.0%; Pred. No. 1e-10;
 RESULT 521
 ID ADB84626 standard; cDNA; 1759 BP.
 DE Human PRO polynucleotide #3.
 PN US2003092890-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 2.6%; Score 59; DB 10; Length 1759;
 Best Local Similarity 100.0%; Pred. No. 1e-10;
 RESULT 522
 ID ADB84626 standard; cDNA; 1759 BP.
 DE Human PRO polynucleotide #3.
 PN US2003092890-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 2.6%; Score 59; DB 10; Length 1759;
 Best Local Similarity 100.0%; Pred. No. 1e-10;

ID ADB83741 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003069397-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 59; DB 10; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
Query Match
RESULT 523
ID ADB72896 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003092887-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 59; DB 10; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
Query Match
RESULT 524
ID ADC36734 standard; cDNA; 1759 BP.
DE Human PRO polynucleotide #3.
PN US2003088065-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 59; DB 10; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
Query Match
RESULT 525
ID ADC21724 standard; cDNA; 1759 BP.
DE Human PRO polynucleotide #3.
PN US2003096969-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 59; DB 10; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
Query Match
RESULT 526
ID ADC49755 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003088064-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 59; DB 10; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
Query Match
RESULT 527
ID ADC48954 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003088070-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 59; DB 10; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
Query Match
RESULT 528
ID ADC49471 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003088071-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 59; DB 10; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
Query Match
RESULT 529
ID ADC47332 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003088072-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 59; DB 10; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
Query Match
RESULT 530
ID ADC47077 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003105288-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 59; DB 10; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
Query Match
RESULT 531
ID ADC77952 standard; cDNA; 1759 BP.

DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003096972-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 59; DB 10; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
Query Match
RESULT 532
ID ADD06187 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003073816-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 59; DB 10; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
Query Match
RESULT 533
ID ADC77706 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003088066-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 59; DB 10; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
Query Match
RESULT 534
ID ADD50669 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003105291-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 59; DB 10; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
Query Match
RESULT 535
ID ADD50915 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003105290-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 59; DB 10; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
Query Match
RESULT 536
ID ADD50396 standard; cDNA; 1759 BP.
DE Human PRO polynucleotide #3.
PN US2003096971-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 59; DB 10; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
Query Match
RESULT 537
ID ADD50150 standard; cDNA; 1759 BP.
DE Human PRO polynucleotide #3.
PN US2003096970-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 59; DB 10; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
Query Match
RESULT 538
ID ADD51161 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003105289-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 59; DB 10; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
Query Match
RESULT 539
ID ACA66843 standard; cDNA; 1759 BP.
DE cDNA encoding human PRO polypeptide #3.
PN US2003036635-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 59; DB 10; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
Query Match
RESULT 540
ID ACD68595 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.

PN US2003045687-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 59; DB 10; Length 1759;
Query Match Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 541
ID ADC48708 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003032888-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 59; DB 12; Length 1759;
Query Match Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 542
ID ADE20879 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003100735-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 59; DB 12; Length 1759;
Query Match Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 543
ID ADE05723 standard; cDNA; 1759 BP.
DE Human PRO polynucleotide #3.
PN US2003100728-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 59; DB 12; Length 1759;
Query Match Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 544
ID ADD74952 standard; cDNA; 1759 BP.
DE Human PRO polynucleotide #3.
PN US2003100712-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 59; DB 12; Length 1759;
Query Match Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 545
ID ADD75698 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003100717-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 59; DB 12; Length 1759;
Query Match Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 546
ID ADD84930 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003100722-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 59; DB 12; Length 1759;
Query Match Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 547
ID ADD86756 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003100738-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 59; DB 12; Length 1759;
Query Match Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 548
ID ADE20633 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003100734-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 59; DB 12; Length 1759;
Query Match Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 549
ID ADE38930 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003096362-A1.

PD 22-MAY-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 59; DB 12; Length 1759;
Query Match Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 550
ID ADE05477 standard; cDNA; 1759 BP.
DE Human PRO polynucleotide #3.
PN US2003100727-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 59; DB 12; Length 1759;
Query Match Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 551
ID ADD73462 standard; cDNA; 1759 BP.
DE Human PRO polynucleotide #3.
PN US2003100711-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 59; DB 12; Length 1759;
Query Match Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 552
ID ADD78302 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003100737-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 59; DB 12; Length 1759;
Query Match Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 553
ID ADE21125 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003100736-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 59; DB 12; Length 1759;
Query Match Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 554
ID ADD77240 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003100732-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 59; DB 12; Length 1759;
Query Match Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 555
ID ADE20387 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003100733-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 59; DB 12; Length 1759;
Query Match Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 556
ID ADD75452 standard; cDNA; 1759 BP.
DE Human PRO polynucleotide #3.
PN US2003100064-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 59; DB 12; Length 1759;
Query Match Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 557
ID ADD73968 standard; cDNA; 1759 BP.
DE Human PRO polynucleotide #3.
PN US2003100708-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 59; DB 12; Length 1759;
Query Match Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 558
ID ADD74214 standard; cDNA; 1759 BP.
DE Human PRO polynucleotide #3.
PN US2003100709-A1.
PD 29-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 559
ID ADD75944 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003100718-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 560
ID ADD85436 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003100721-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 561
ID ADE04985 standard; cDNA; 1759 BP.
DE Human PRO polynucleotide #3.
PN US2003100726-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 562
ID ADD75198 standard; cDNA; 1759 BP.
DE Human PRO polynucleotide #3.
PN US2003100714-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 563
ID ADD76742 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003100715-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 564
ID ADD86510 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003100719-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 565
ID ADD77978 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003100731-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 566
ID ADD77486 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003100729-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 567
ID ADD7732 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003100730-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 568
ID ADD85190 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003100725-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 569
ID ADD73722 standard; cDNA; 1759 BP.
DE Human PRO polynucleotide #3.
PN US2003100710-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 570
ID ADD74460 standard; cDNA; 1759 BP.
DE Human PRO polynucleotide #3.
PN US2003100713-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 571
ID ADD76988 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003100716-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 572
ID ADD85682 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003100720-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 573
ID ADE05231 standard; cDNA; 1759 BP.
DE Human PRO polynucleotide #3.
PN US2003100723-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 574
ID ADD74706 standard; cDNA; 1759 BP.
DE Human PRO polynucleotide #3.
PN US2003100724-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 575
ID ADG05518 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003096959-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 576
ID ADG27072 standard; cDNA; 1759 BP.
DE Human PRO polynucleotide #3.
PN US2003096962-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 577
ID ADG27072 standard; cDNA; 1759 BP.
DE Human PRO polynucleotide #3.
PN US2003100730-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 578
ID ADG27072 standard; cDNA; 1759 BP.
DE Human PRO polynucleotide #3.
PN US2003100730-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.

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Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 577
ID ADG1135 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003096967-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 578
ID ADG11914 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003096963-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 579
ID ADP94471 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003096964-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 580
ID ADG06567 standard; cDNA; 1759 BP.
DE Human PRO polynucleotide #3.
PN US2003096966-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 581
ID ADH38911 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003096965-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 582
ID ADG34001 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2004006206-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 583
ID ADI33471 standard; cDNA; 1759 BP.
DE Human PRO polynucleotide #3.
PN US2003096960-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 584
ID ADH69565 standard; cDNA; 1759 BP.
DE Human PRO polynucleotide #3.
PN US2004019183-A1.
PD 29-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 585
ID ADI29726 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003096961-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 586
ID ADI29726 standard; cDNA; 1759 BP.
DE Novel human secreted and transmembrane protein PRO7174 cDNA.
PN US2003096961-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 587
ID ADK66481 standard; cDNA; 1759 BP.
DE Human PRO polynucleotide #3.
PN US2004044180-A1.
PD 04-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 59; DB 12; Length 1759;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 588
ID ADC77664 standard; cDNA; 1764 BP.
DE Human 27410 protein encoding cDNA SEQ ID NO:27.
PN WO2003073983-A2.
PD 12-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 2.6%; Score 59; DB 10; Length 1764;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 589
ID ABK99853 standard; cDNA; 1769 BP.
DE Babesia cDNA sequence for clone 60s.55.
PN WO200253016-A2.
PD 11-JUL-2002.
PA (CORI-) CORIXA CORP.
Query Match 2.6%; Score 59; DB 6; Length 1769;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 590
ID ADI42816 standard; DNA; 1803 BP.
DE Plant transcription factor polynucleotide #820.
PN US2004019927-A1.
PD 29-JAN-2004.
PA (SHER-) SHERMAN B K.
PA (RIEC-) RIECHMANN J L.
PA (JIAN-) JIANG C.
PA (HEAR-) HEARD J E.
PA (HAAR-) HAAKE V.
PA (CREE-) CREELMAN R A.
PA (RATC-) RATCLIFFE O.
PA (ADAM-) ADAM L J.
PA (REUB-) REUBER T L.
PA (KEDD-) KEDDIE J.
PA (BROU-) BROUN P E.
PA (PILG-) PILGRIM M L.
PA (DUBE-) DUBELL A N.
PA (PINE-) PINEDA O.
PA (YUGG-) YU G.
Query Match 2.6%; Score 59; DB 12; Length 1803;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 591
ID ADO3025 standard; cDNA; 1803 BP.
DE Corn orthologue of Thalecress transcription factor, cDNA #126.
PN US2004045049-A1.
PD 04-MAR-2004.
PA (ZHAN-) ZHANG J.
PA (FROM-) FROMM M E.
PA (HEAR-) HEARD J E.
PA (RIEC-) RIECHMANN J L.
PA (ADAM-) ADAM L J.
PA (BROU-) BROUN P E.
PA (PINE-) PINEDA O.
PA (REUB-) REUBER T L.
PA (KEDD-) KEDDIE J S.
PA (YUGG-) YU G.
PA (JIAN-) JIANG C.
PA (SAMA-) SAMAHA R S.
PA (PILG-) PILGRIM M L.
PA (CREE-) CREELMAN R A.
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PA (DUBE/) DUBELL A N.
 PA (RATC/) RATCLIFFE O.
 PA (KUMI/) KUMIMOTO R.
 PA (SHER/) SHERMAN B K.
 Query Match 2.6%; Score 59; DB 12; Length 1803;
 Best Local Similarity 100.0%; Pred. No. 1e-10;
 RESULT 592
 ID AAF98705 standard; DNA; 1815 BP.
 DE Human ovarian cancer cell expressed sequence 10805.
 PN WO200118542-A2.
 PD 15-MAR-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 2.6%; Score 59; DB 5; Length 1815;
 Best Local Similarity 100.0%; Pred. No. 1e-10;
 RESULT 593
 ID AAD33245 standard; cDNA; 1817 BP.
 DE Human secreted protein-encoding gene 9 cDNA clone HDABU01, SEQ ID NO:19.
 PN WO200218435-A1.
 PD 07-MAR-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.6%; Score 59; DB 6; Length 1817;
 Best Local Similarity 100.0%; Pred. No. 1e-10;
 RESULT 594
 ID AAS41019 standard; cDNA; 1854 BP.
 DE cDNA encoding novel human enzyme polypeptide #235.
 PN WO200153301-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.6%; Score 59; DB 4; Length 1854;
 Best Local Similarity 100.0%; Pred. No. 1e-10;
 RESULT 595
 ID ABK97609 standard; cDNA; 1868 BP.
 DE cDNA encoding novel extracellular signal-regulated kinase.
 PN US2001053844-A1.
 PD 20-DEC-2001.
 PA (YANC/) YAN C.
 PA (ABUT/) ABU-THREIDEH J.
 PA (SHAO/) SHAO W.
 PA (MERK/) MERKULOV G V.
 PA (DFRA/) DI FRANCESCO V.
 PA (BEAS/) BEASLEY E M.
 Query Match 2.6%; Score 59; DB 6; Length 1868;
 Best Local Similarity 100.0%; Pred. No. 1e-10;
 RESULT 596
 ID ADH00897 standard; cDNA; 1868 BP.
 DE Human kinase cDNA.
 PN US2003166219-A1.
 PD 04-SEP-2003.
 PA (PEKE) PE CORP NY.
 Query Match 2.6%; Score 59; DB 10; Length 1868;
 Best Local Similarity 100.0%; Pred. No. 1e-10;
 RESULT 597
 ID AAK98915 standard; cDNA; 1878 BP.
 DE cDNA of a human WAP/extracellular signal-regulated kinase subfamily.
 PN US2001051360-A1.
 PD 13-DEC-2001.
 PA (WEIM/) WEI M.
 PA (GUG/) GUEGLER K.
 PA (KETC/) KETCHUM K A.
 PA (MERK/) MERKULOV G V.
 PA (WOOD/) WOODAGE T.
 PA (DFRA/) DI FRANCESCO V.
 PA (BEAS/) BEASLEY E M.
 Query Match 2.6%; Score 59; DB 6; Length 1878;
 Best Local Similarity 100.0%; Pred. No. 1e-10;
 RESULT 598
 ID ADG90363 standard; cDNA; 1878 BP.
 DE Human kinase cDNA.
 PN US2003166218-A1.
 PD 04-SEP-2003.
 PA (PEKE) PE CORP NY.
 Query Match 2.6%; Score 59; DB 10; Length 1878;
 Best Local Similarity 100.0%; Pred. No. 1e-10;

RESULT 599.
 ID ADL45481 standard; DNA; 1885 BP.
 DE Human ovarian cancer DNA marker #19371.
 PN WO200170979-A2.
 PD 27-SEP-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 2.6%; Score 59; DB 5; Length 1885;
 Best Local Similarity 100.0%; Pred. No. 1e-10;
 RESULT 600
 ID ABQ54288 standard; cDNA; 2054 BP.
 DE Human ovarian antigen HSPSY43 cDNA, SEQ ID NO:168.
 PN WO200200677-A1.
 PD 03-JAN-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.6%; Score 59; DB 6; Length 2054;
 Best Local Similarity 100.0%; Pred. No. 9.8e-11;
 RESULT 601
 ID AAZ10670 standard; cDNA; 2083 BP.
 DE cDNA encoding a human secreted protein.
 PN WO9943693-A1.
 PD 02-SEP-1999.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.6%; Score 59; DB 2; Length 2083;
 Best Local Similarity 100.0%; Pred. No. 9.8e-11;
 RESULT 602
 ID ADL45474 standard; DNA; 2236 BP.
 DE Human ovarian cancer DNA marker #19364.
 PN WO200170979-A2.
 PD 27-SEP-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 2.6%; Score 59; DB 5; Length 2236;
 Best Local Similarity 100.0%; Pred. No. 9.6e-11;
 RESULT 603
 ID ADC38669 standard; cDNA; 2238 BP.
 DE Human cDNA encoding a secreted protein #14.
 PN US2002193567-A1.
 PD 19-DEC-2002.
 PA (GEMY) GENETICS INST INC.
 Query Match 2.6%; Score 59; DB 10; Length 2238;
 Best Local Similarity 100.0%; Pred. No. 9.6e-11;
 RESULT 604
 ID ABV22595 standard; cDNA; 2242 BP.
 DE Human prostate expression marker cDNA 22586.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 2.6%; Score 59; DB 5; Length 2242;
 Best Local Similarity 100.0%; Pred. No. 9.6e-11;
 RESULT 605
 ID ABV28416 standard; cDNA; 2242 BP.
 DE Human prostate expression marker cDNA 28407.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 2.6%; Score 59; DB 5; Length 2242;
 Best Local Similarity 100.0%; Pred. No. 9.6e-11;
 RESULT 606
 ID AAC75666 standard; cDNA; 2244 BP.
 DE Human ORFX ORF1221 polynucleotide sequence SEQ ID NO:2441.
 PN WO200058473-A2.
 PD 05-OCT-2000.
 PA (CURA-) CURAGEN CORP.
 Query Match 2.6%; Score 59; DB 3; Length 2244;
 Best Local Similarity 100.0%; Pred. No. 9.6e-11;
 RESULT 607
 ID ABX92071 standard; cDNA; 2269 BP.
 DE lung specific nucleic acid (LSNA) #113.
 PN WO200268633-A2.
 PD 06-SEP-2002.
 PA (DIAD-) DIADEXUS INC.
 Query Match 2.6%; Score 59; DB 6; Length 2269;
 Best Local Similarity 100.0%; Pred. No. 9.6e-11;
 RESULT 608

ID AAX99856 standard; DNA; 2504 BP.
DE Human secreted protein coding sequence clone bn69_15.
PN WO9938959-A1.
PD 05-AUG-1999.
PA (GEM) GENETICS INST INC.
Query Match 2.6%; Score 59; DB 2; Length 2504;
Best Local Similarity 100.0%; Pred. No. 9.4e-11;
RESULT 609
ID AAS59280 standard; cDNA; 2504 BP.
DE Human cDNA encoding a secreted protein bn69_15.
PN WO200175068-A2.
PD 11-OCT-2001.
PA (GEM) GENETICS INST INC.
Query Match 2.8%; Score 59; DB 4; Length 2504;
Best Local Similarity 100.0%; Pred. No. 9.4e-11;
RESULT 610
ID ABA90949 standard; cDNA; 2504 BP.
DE Human polynucleotide SEQ ID NO 147.
PN US2001039335-A1.
PD 08-NOV-2001.
PA (JACO) JACOBS K.
PA (MCCO) MCCOY J M.
PA (LAVA) LAVALLIE E R.
PA (COLL) COLLINS-RACIE L A.
PA (EVAN) EVANS C.
PA (MERB) MERBERG D.
PA (TREA) TREACY M.
PA (AGOS) AGOSTINO M J.
PA (STEI) STEININGER R J.
PA (SPAU) SPAULDING V.
PA (WONG) WONG G G.
PA (CLAR) CLARK H.
PA (FECH) FECHTEL K.
Query Match 2.6%; Score 59; DB 6; Length 2504;
Best Local Similarity 100.0%; Pred. No. 9.4e-11;
RESULT 611
ID ABA55051 standard; cDNA; 3036 BP.
DE Human ovarian antigen HOCQ58 cDNA, SEQ ID NO:931.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 59; DB 6; Length 3036;
Best Local Similarity 100.0%; Pred. No. 9e-11;
RESULT 612
ID AAF2384 standard; cDNA; 3268 BP.
DE Human secreted protein Gene 12 SEQ ID NO:22.
PN WO200061629-A1.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE) ROSEN C A.
Query Match 2.6%; Score 59; DB 3; Length 3268;
Best Local Similarity 100.0%; Pred. No. 8.8e-11;
RESULT 613
ID ADI36904 standard; cDNA; 3719 BP.
DE Human HLRRNS-3 cDNA.
PN US2003220263-A1.
PD 27-NOV-2003.
PA (FEDE) FEDER J N.
PA (MINT) MINTIER G.
PA (RAMA) RAMANATHAN C S.
Query Match 2.6%; Score 59; DB 12; Length 3719;
Best Local Similarity 100.0%; Pred. No. 8.6e-11;
RESULT 614
ID AAL38913 standard; cDNA; 3832 BP.
DE Human mitochondrial RNA polymerase cDNA.
PN WO200238759-A2.
PD 16-MAY-2002.
PA (MITO-) MITOTECH AB.
Query Match 2.6%; Score 59; DB 6; Length 3832;
Best Local Similarity 100.0%; Pred. No. 8.5e-11;
RESULT 615
ID ADQ24393 standard; DNA; 4522 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7213.

PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.6%; Score 59; DB 12; Length 4522;
Best Local Similarity 100.0%; Pred. No. 8.2e-11;
RESULT 616
ID ADQ24286 standard; DNA; 4522 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7106.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.6%; Score 59; DB 12; Length 4522;
Best Local Similarity 100.0%; Pred. No. 8.2e-11;
RESULT 617
ID ADQ24340 standard; DNA; 4696 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7160.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.6%; Score 59; DB 12; Length 4696;
Best Local Similarity 100.0%; Pred. No. 8.1e-11;
RESULT 618
ID ABK87749 standard; cDNA; 5344 BP.
DE Human cDNA encoding metalloprotease of the ADAMTS family 53014 #2.
PN WO200251995-A1.
PD 04-JUL-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 2.6%; Score 59; DB 6; Length 5344;
Best Local Similarity 100.0%; Pred. No. 7.9e-11;
RESULT 619
ID ABK87748 standard; cDNA; 5701 BP.
DE Human cDNA encoding metalloprotease of the ADAMTS family 53014 #1.
PN WO200251995-A1.
PD 04-JUL-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 2.6%; Score 59; DB 6; Length 5701;
Best Local Similarity 100.0%; Pred. No. 7.8e-11;
RESULT 620
ID ADQ22539 standard; DNA; 7047 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5359.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.6%; Score 59; DB 12; Length 7047;
Best Local Similarity 100.0%; Pred. No. 7.4e-11;
RESULT 621
ID AAS32492 standard; DNA; 32191 BP.
DE Human genomic DNA for novel endocrine antigen, SEQ ID No 446.
PN WO200155319-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 59; DB 4; Length 32191;
Best Local Similarity 100.0%; Pred. No. 5.2e-11;
RESULT 622
ID AEQ94562 standard; DNA; 101 BP.
DE Tumour suppression-related oligonucleotide #213.
PN PR2819824-A1.
PD 26-JUL-2002.
PA (MOLE-) MOLECULAR ENGINES LAB SA.
Query Match 2.6%; Score 58; DB 6; Length 101;
Best Local Similarity 100.0%; Pred. No. 4.3e-10;
RESULT 623
ID AAS07787 standard; DNA; 153 BP.
DE Cervical cancer pre-malignant condition DNA marker #86.
PN WO200142792-A2.
PD 14-JUN-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 58; DB 4; Length 153;
Best Local Similarity 100.0%; Pred. No. 3.9e-10;
RESULT 624
ID AAS29047 standard; cDNA; 155 BP.
DE cDNA encoding for human DNA-binding protein #18.
PN WO200155162-A1.

PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 58; DB 5; Length 155;
Best Local Similarity 100.0%; Pred. No. 3.9e-10;
RESULT 625
ID ABS68187 standard; cDNA; 155 BP.
DE cDNA encoding human DNA-binding protein #18.
PN US2002102638-A1.
PD 01-AUG-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 2.6%; Score 58; DB 6; Length 155;
Best Local Similarity 100.0%; Pred. No. 3.9e-10;
RESULT 626
ID ADC25181 standard; cDNA; 155 BP.
DE Human cDNA from extracellular matrix gene 18.
PN US2003049650-A1.
PD 13-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 58; DB 10; Length 155;
Best Local Similarity 100.0%; Pred. No. 3.9e-10;
RESULT 627
ID ABX45893 standard; cDNA; 160 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #11058.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 2.6%; Score 58; DB 8; Length 160;
Best Local Similarity 100.0%; Pred. No. 3.9e-10;
RESULT 628
ID ABV05796 standard; cDNA; 177 BP.
DE Human prostate expression marker cDNA 5787.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 58; DB 5; Length 177;
Best Local Similarity 100.0%; Pred. No. 3.8e-10;
RESULT 629
ID ABX49026 standard; cDNA; 179 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #14191.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 2.6%; Score 58; DB 8; Length 179;
Best Local Similarity 100.0%; Pred. No. 3.8e-10;
RESULT 630
ID ABX36136 standard; cDNA; 181 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #1301.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 2.6%; Score 58; DB 8; Length 181;
Best Local Similarity 100.0%; Pred. No. 3.8e-10;
RESULT 631
ID AAZ21523 standard; DNA; 196 BP.
DE Progression suppressed gene 28 (PGSen28).
PN WO9943844-A1.
PD 02-SEP-1999.
PA (UYCO) UNIV COLUMBIA NEW YORK.
Query Match 2.6%; Score 58; DB 2; Length 196;
Best Local Similarity 100.0%; Pred. No. 3.7e-10;
RESULT 632
ID ABV58264 standard; cDNA; 201 BP.

DE Human prostate expression marker cDNA 58255.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 58; DB 5; Length 201;
Best Local Similarity 100.0%; Pred. No. 3.7e-10;
RESULT 633
ID ABV57413 standard; cDNA; 206 BP.
DE Human prostate expression marker cDNA 57404.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 58; DB 5; Length 206;
Best Local Similarity 100.0%; Pred. No. 3.7e-10;
RESULT 634
ID ABX38781 standard; cDNA; 207 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #3946.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 2.6%; Score 58; DB 8; Length 207;
Best Local Similarity 100.0%; Pred. No. 3.7e-10;
RESULT 635
ID ABV57409 standard; cDNA; 234 BP.
DE Human prostate expression marker cDNA 57400.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 58; DB 5; Length 234;
Best Local Similarity 100.0%; Pred. No. 3.5e-10;
RESULT 636
ID ABX47018 standard; cDNA; 236 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #12183.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 2.6%; Score 58; DB 8; Length 236;
Best Local Similarity 100.0%; Pred. No. 3.5e-10;
RESULT 637
ID ABV56779 standard; cDNA; 247 BP.
DE Human prostate expression marker cDNA 56770.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 58; DB 5; Length 247;
Best Local Similarity 100.0%; Pred. No. 3.5e-10;
RESULT 638
ID ABV19470 standard; cDNA; 254 BP.
DE Human prostate expression marker cDNA 19461.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 58; DB 5; Length 254;
Best Local Similarity 100.0%; Pred. No. 3.5e-10;
RESULT 639
ID ABV49446 standard; cDNA; 254 BP.
DE Human prostate expression marker cDNA 49437.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 58; DB 5; Length 254;
Best Local Similarity 100.0%; Pred. No. 3.5e-10;
RESULT 640
ID AAV00423 standard; cDNA; 259 BP.
DE 3' fragment of clone H1075_1.
PN WO9740069-A2.
PD 30-OCT-1997.

PA (GEMV) GENETICS INST INC.
 Query Match 2.6%; Score 58; DB 2; Length 259;
 Best Local Similarity 100.0%; Pred. No. 3.5e-10;
 RESULT 641
 ID AAT85891 standard; cDNA to mRNA; 263 BP.
 DE Malassezia fungus MF-3 antigenic protein PCR amplification fragment.
 PN WO9721817-A1.
 PD 19-JUN-1997.
 PA (TAKI) TAKARA SHUZO CO LTD.
 Query Match 2.6%; Score 58; DB 2; Length 263;
 Best Local Similarity 100.0%; Pred. No. 3.5e-10;
 RESULT 642
 ID AAS29061 standard; cDNA; 266 BP.
 DE cDNA encoding for human DNA-binding protein #32.
 PN WO200155162-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.6%; Score 58; DB 5; Length 266;
 Best Local Similarity 100.0%; Pred. No. 3.4e-10;
 RESULT 643
 ID ABS68201 standard; cDNA; 266 BP.
 DE cDNA encoding human DNA-binding protein #32.
 PN US2002102638-A1.
 PD 01-AUG-2002.
 PA (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 PA (BARA/) BARASH S C.
 Query Match 2.6%; Score 58; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 3.4e-10;
 RESULT 644
 ID ADC25195 standard; cDNA; 266 BP.
 DE Human cDNA from extracellular matrix gene 32.
 PN US2003049650-A1.
 PD 13-MAR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.6%; Score 58; DB 10; Length 266;
 Best Local Similarity 100.0%; Pred. No. 3.4e-10;
 RESULT 645
 ID ABV49555 standard; cDNA; 278 BP.
 DE Human prostate expression marker cDNA 49946.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 2.6%; Score 58; DB 5; Length 278;
 Best Local Similarity 100.0%; Pred. No. 3.4e-10;
 RESULT 646
 ID AAL20269 standard; cDNA; 282 BP.
 DE Human breast cancer expressed polynucleotide 12726.
 PN WO200151628-A2.
 PD 19-JUL-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 2.6%; Score 58; DB 4; Length 282;
 Best Local Similarity 100.0%; Pred. No. 3.4e-10;
 RESULT 647
 ID AAS60667 standard; cDNA; 285 BP.
 DE Human cancer agent-resistance marker #422.
 PN WO200179556-A2.
 PD 25-OCT-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 2.6%; Score 58; DB 4; Length 285;
 Best Local Similarity 100.0%; Pred. No. 3.4e-10;
 RESULT 648
 ID ABL87534 standard; cDNA; 294 BP.
 DE Human ovarian cancer related cDNA clone SEQ ID NO:10512.
 PN WO200192581-A2.
 PD 06-DEC-2001.
 PA (CORI-) CORIXA CORP.
 Query Match 2.6%; Score 58; DB 6; Length 294;
 Best Local Similarity 100.0%; Pred. No. 3.4e-10;
 RESULT 649
 ID ABX37743 standard; cDNA; 316 BP.
 DE Bovine EST associated with lactation/muscle/fat deposition #2908.
 PN US2002137139-A1.

PD 26-SEP-2002.
 PA (BYAT/) BYATT J C.
 PA (MATH/) MATHIALAGAN N.
 PA (TAON/) TAO N.
 PA (WARR/) WARREN W C.
 Query Match 2.6%; Score 58; DB 8; Length 316;
 Best Local Similarity 100.0%; Pred. No. 3.3e-10;
 RESULT 650
 ID ABL93053 standard; cDNA; 321 BP.
 DE Rat metastatic tumour cell related cDNA SEQ ID NO 107.
 PN WO200208456-A2.
 PD 31-JAN-2002.
 PA (GESL) FORSCHUNGSZENTRUM KARLSRUHE GMBH.
 Query Match 2.6%; Score 58; DB 6; Length 321;
 Best Local Similarity 100.0%; Pred. No. 3.3e-10;
 RESULT 651
 ID ADN07844 standard; cDNA; 321 BP.
 DE Human mammary carcinoma MLSSH cDNA library sequence #107.
 PN DE10229391-A1.
 PD 29-JAN-2004.
 PA (GESL) FORSCHUNGSZENTRUM KARLSRUHE GMBH.
 Query Match 2.6%; Score 58; DB 12; Length 321;
 Best Local Similarity 100.0%; Pred. No. 3.3e-10;
 RESULT 652
 ID ABV59017 standard; cDNA; 325 BP.
 DE Human prostate expression marker cDNA 59008.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 2.6%; Score 58; DB 5; Length 325;
 Best Local Similarity 100.0%; Pred. No. 3.3e-10;
 RESULT 653
 ID ABX47256 standard; cDNA; 329 BP.
 DE Bovine EST associated with lactation/muscle/fat deposition #12421.
 PN US2002137139-A1.
 PD 26-SEP-2002.
 PA (BYAT/) BYATT J C.
 PA (MATH/) MATHIALAGAN N.
 PA (TAON/) TAO N.
 PA (WARR/) WARREN W C.
 Query Match 2.6%; Score 58; DB 8; Length 329;
 Best Local Similarity 100.0%; Pred. No. 3.3e-10;
 RESULT 654
 ID ABK54903 standard; cDNA; 342 BP.
 DE Human colon cancer-associated cDNA, SEQ ID NO 373.
 PN WO200212280-A2.
 PD 14-FEB-2002.
 PA (CORI-) CORIXA CORP.
 Query Match 2.6%; Score 58; DB 6; Length 342;
 Best Local Similarity 100.0%; Pred. No. 3.3e-10;
 RESULT 655
 ID RAI88527 standard; cDNA; 352 BP.
 DE Human polynucleotide SEQ ID NO 8587.
 PN WO200164835-A2.
 PD 07-SEP-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 2.6%; Score 58; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 3.2e-10;
 RESULT 656
 ID AAC77649 standard; cDNA; 353 BP.
 DE Human cancer associated gene sequence SEQ ID NO:43.
 PN WO200055350-A1.
 PD 21-SEP-2000.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.6%; Score 58; DB 3; Length 353;
 Best Local Similarity 100.0%; Pred. No. 3.2e-10;
 RESULT 657
 ID AEX43971 standard; cDNA; 357 BP.
 DE Bovine EST associated with lactation/muscle/fat deposition #9136.
 PN US2002137139-A1.
 PD 26-SEP-2002.
 PA (BYAT/) BYATT J C.
 PA (MATH/) MATHIALAGAN N.

PA (TAON/) TAO N.
 PA (WARR/) WARREN W C.
 Query Match 2.6%; Score 58; DB 8; Length 357;
 Best Local Similarity 100.0%; Pred. No. 3.2e-10;
 RESULT 658
 ID ABV14871 standard; cDNA; 360 BP.
 DE Human prostate expression marker cDNA 14862.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 2.6%; Score 58; DB 5; Length 360;
 Best Local Similarity 100.0%; Pred. No. 3.2e-10;
 RESULT 659
 ID AAI88707 standard; cDNA; 363 BP.
 DE Human polynucleotide SEQ ID NO 8767.
 PN WO200164835-A2.
 PD 07-SEP-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 2.6%; Score 58; DB 4; Length 363;
 Best Local Similarity 100.0%; Pred. No. 3.2e-10;
 RESULT 660
 ID AAI84802 standard; cDNA; 364 BP.
 DE Human polynucleotide SEQ ID NO 4862.
 PN WO200164835-A2.
 PD 07-SEP-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 2.6%; Score 58; DB 4; Length 364;
 Best Local Similarity 100.0%; Pred. No. 3.2e-10;
 RESULT 661
 ID AAI84912 standard; cDNA; 364 BP.
 DE Human polynucleotide SEQ ID NO 4972.
 PN WO200164835-A2.
 PD 07-SEP-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 2.6%; Score 58; DB 4; Length 364;
 Best Local Similarity 100.0%; Pred. No. 3.2e-10;
 RESULT 662
 ID AAI84900 standard; cDNA; 364 BP.
 DE Human polynucleotide SEQ ID NO 4960.
 PN WO200164835-A2.
 PD 07-SEP-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 2.6%; Score 58; DB 4; Length 364;
 Best Local Similarity 100.0%; Pred. No. 3.2e-10;
 RESULT 663
 ID ACH30766 standard; cDNA; 364 BP.
 DE Human bone marrow cDNA #57.
 PN US2003073623-A1.
 PD 17-APR-2003.
 PA (DRMA/) DRMANAC R T.
 PA (LABA/) LABAT I.
 PA (STAC/) STACHE-CRAIN B.
 PA (DICK/) DICKSON M C.
 PA (JONE/) JONES L W.
 Query Match 2.6%; Score 58; DB 9; Length 364;
 Best Local Similarity 100.0%; Pred. No. 3.2e-10;
 RESULT 664
 ID AAI87540 standard; cDNA; 366 BP.
 DE Human polynucleotide SEQ ID NO 7600.
 PN WO200164835-A2.
 PD 07-SEP-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 2.6%; Score 58; DB 4; Length 366;
 Best Local Similarity 100.0%; Pred. No. 3.2e-10;
 RESULT 665
 ID ABV55687 standard; cDNA; 367 BP.
 DE Human prostate expression marker cDNA 55678.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 2.6%; Score 58; DB 5; Length 367;
 Best Local Similarity 100.0%; Pred. No. 3.2e-10;
 RESULT 666

ID ABX37863 standard; cDNA; 369 BP.
 DE Bovine EST associated with lactation/muscle/fat deposition #3028.
 PN US2002137139-A1.
 PD 26-SEP-2002.
 PA (BYAT/) BYATT J C.
 PA (MATH/) MATHIALAGAN N.
 PA (TAON/) TAO N.
 PA (WARR/) WARREN W C.
 Query Match 2.6%; Score 58; DB 8; Length 369;
 Best Local Similarity 100.0%; Pred. No. 3.2e-10;
 RESULT 667
 ID ABV58076 standard; cDNA; 373 BP.
 DE Human prostate expression marker cDNA 58067.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 2.6%; Score 58; DB 5; Length 373;
 Best Local Similarity 100.0%; Pred. No. 3.2e-10;
 RESULT 668
 ID AAI87907 standard; cDNA; 374 BP.
 DE Human polynucleotide SEQ ID NO 7967.
 PN WO200164835-A2.
 PD 07-SEP-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 2.6%; Score 58; DB 4; Length 374;
 Best Local Similarity 100.0%; Pred. No. 3.2e-10;
 RESULT 669
 ID ABV49242 standard; cDNA; 377 BP.
 DE Human prostate expression marker cDNA 49233.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 2.6%; Score 58; DB 5; Length 377;
 Best Local Similarity 100.0%; Pred. No. 3.2e-10;
 RESULT 670
 ID ABQ56755 standard; cDNA; 377 BP.
 DE Human colon cancer related nucleotide sequence SEQ ID NO:450.
 PN WO200229086-A2.
 PD 11-APR-2002.
 PA (FARB) BAYER CORP.
 Query Match 2.6%; Score 58; DB 6; Length 377;
 Best Local Similarity 100.0%; Pred. No. 3.2e-10;
 RESULT 671
 ID AAI82118 standard; cDNA; 385 BP.
 DE Human polynucleotide SEQ ID NO 2178.
 PN WO200164835-A2.
 PD 07-SEP-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 2.6%; Score 58; DB 4; Length 385;
 Best Local Similarity 100.0%; Pred. No. 3.2e-10;
 RESULT 672
 ID AAI84785 standard; cDNA; 388 BP.
 DE Human polynucleotide SEQ ID NO 4845.
 PN WO200164835-A2.
 PD 07-SEP-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 2.6%; Score 58; DB 4; Length 388;
 Best Local Similarity 100.0%; Pred. No. 3.2e-10;
 RESULT 673
 ID AAI88514 standard; cDNA; 389 BP.
 DE Human polynucleotide SEQ ID NO 8574.
 PN WO200164835-A2.
 PD 07-SEP-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 2.6%; Score 58; DB 4; Length 389;
 Best Local Similarity 100.0%; Pred. No. 3.2e-10;
 RESULT 674
 ID AAI85202 standard; cDNA; 390 BP.
 DE Human polynucleotide SEQ ID NO 5262.
 PN WO200164835-A2.
 PD 07-SEP-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 2.6%; Score 58; DB 4; Length 390;

Best Local Similarity 100.0%; Pred. No. 3.2e-10;
RESULT 675
ID ABV39048 standard; cDNA; 392 BP.
DE Human prostate expression marker cDNA 39039.
PN WO200160860-A2.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 58; DB 5; Length 392;
Best Local Similarity 100.0%; Pred. No. 3.2e-10;
RESULT 676
ID AAI83459 standard; cDNA; 394 BP.
DE Human polynucleotide SEQ ID NO 3519.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 58; DB 4; Length 394;
Best Local Similarity 100.0%; Pred. No. 3.1e-10;
RESULT 677
ID ABZ53884 standard; cDNA; 394 BP.
DE Aspergillus oryzae polynucleotide SEQ ID NO 2997.
PN WO200279476-A1.
PD 10-OCT-2002.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (NARE-) NAT RES INST BREWING.
PA (NORO) NAT FOOD RES INST MIN AGRIC.
Query Match 2.6%; Score 58; DB 8; Length 394;
Best Local Similarity 100.0%; Pred. No. 3.1e-10;
RESULT 678
ID ABV57596 standard; cDNA; 396 BP.
DE Human prostate expression marker cDNA 57587.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 58; DB 5; Length 396;
Best Local Similarity 100.0%; Pred. No. 3.1e-10;
RESULT 679
ID ABV14965 standard; cDNA; 400 BP.
DE Human prostate expression marker cDNA 14956.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 58; DB 5; Length 400;
Best Local Similarity 100.0%; Pred. No. 3.1e-10;
RESULT 680
ID ADF50926 standard; cDNA; 400 BP.
DE Human cysteine rich intestinal protein 1 cDNA (SeqID 25).
PN WO2003060164-A1.
PD 24-JUL-2003.
PA (ARCT-) ARCTURUS ENG INC.
PA (GEO) GEN HOSPITAL CORP.
Query Match 2.6%; Score 58; DB 10; Length 400;
Best Local Similarity 100.0%; Pred. No. 3.1e-10;
RESULT 681
ID ABV38958 standard; cDNA; 404 BP.
DE Human prostate expression marker cDNA 38949.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 58; DB 5; Length 404;
Best Local Similarity 100.0%; Pred. No. 3.1e-10;
RESULT 682
ID AAI83837 standard; cDNA; 405 BP.
DE Human polynucleotide SEQ ID NO 3897.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 58; DB 4; Length 405;
Best Local Similarity 100.0%; Pred. No. 3.1e-10;
RESULT 683
ID AAI88562 standard; cDNA; 406 BP.
DE Human polynucleotide SEQ ID NO 8622.
PN WO200164835-A2.
PD 07-SEP-2001.

PA (HYSE-) HYSEQ INC. 2.6%; Score 58; DB 4; Length 406;
Best Local Similarity 100.0%; Pred. No. 3.1e-10;
RESULT 684
ID ADG32960 standard; DNA; 406 BP.
DE Human DNA differentially expressed in patients with SLE SeqID284.
PN WO2003090694-A2.
PD 06-NOV-2003.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Query Match 2.6%; Score 58; DB 10; Length 406;
Best Local Similarity 100.0%; Pred. No. 3.1e-10;
RESULT 685
ID AAI84733 standard; cDNA; 407 BP.
DE Human polynucleotide SEQ ID NO 4793.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 58; DB 4; Length 407;
Best Local Similarity 100.0%; Pred. No. 3.1e-10;
RESULT 686
ID AAI88682 standard; cDNA; 407 BP.
DE Human polynucleotide SEQ ID NO 8742.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 58; DB 4; Length 407;
Best Local Similarity 100.0%; Pred. No. 3.1e-10;
RESULT 687
ID ABK34899 standard; cDNA; 409 BP.
DE Human cDNA encoding secreted protein #37.
PN WO200177288-A2.
PD 18-OCT-2001.
PA (GEMY) GENETICS INST INC.
Query Match 2.6%; Score 58; DB 6; Length 409;
Best Local Similarity 100.0%; Pred. No. 3.1e-10;
RESULT 688
ID AAI84650 standard; cDNA; 410 BP.
DE Human polynucleotide SEQ ID NO 4710.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 58; DB 4; Length 410;
Best Local Similarity 100.0%; Pred. No. 3.1e-10;
RESULT 689
ID AAI81190 standard; cDNA; 410 BP.
DE Human polynucleotide SEQ ID NO 1250.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 58; DB 4; Length 410;
Best Local Similarity 100.0%; Pred. No. 3.1e-10;
RESULT 690
ID AAI80427 standard; cDNA; 412 BP.
DE Human polynucleotide SEQ ID NO 487.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 58; DB 4; Length 412;
Best Local Similarity 100.0%; Pred. No. 3.1e-10;
RESULT 691
ID AAI19684 standard; cDNA; 413 BP.
DE Human breast cancer expressed polynucleotide 12141.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 58; DB 4; Length 413;
Best Local Similarity 100.0%; Pred. No. 3.1e-10;
RESULT 692
ID AAI85194 standard; cDNA; 414 BP.
DE Human polynucleotide SEQ ID NO 5254.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.

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Query Match
Best Local Similarity 2.6%; Score 58; DB 4; Length 414;
RESULT 693
ID ABX40997 standard; cDNA; 414 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #6162.
PN US2002137139-A1.
PA (ANY/) GORLACH J.
PA (HAM/) AN Y.
PA (PRIC/) PRICE J L.
PA (RAIN/) RAINES T M.
PA (YUY/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
PA (KRIC/) KRICKER M.
PA (SLAT/) SLATER T.
PA (DAVI/) DAVIS K R.
PA (ALLE/) ALLEN K.
PA (HOFF/) HOFFMAN N.
PA (HURB/) HURBAN P.
Query Match
Best Local Similarity 2.6%; Score 58; DB 8; Length 422;
RESULT 694
ID ABX41704 standard; cDNA; 415 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #6869.
PN US2002137139-A1.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match
Best Local Similarity 2.6%; Score 58; DB 8; Length 414;
RESULT 695
ID ABX41704 standard; cDNA; 415 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #6869.
PN US2002137139-A1.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match
Best Local Similarity 2.6%; Score 58; DB 8; Length 415;
RESULT 696
ID AAI89032 standard; cDNA; 416 BP.
DE Human polynucleotide SEQ ID NO 9092.
PN WO200164835-A2.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 2.6%; Score 58; DB 4; Length 416;
RESULT 697
ID AAI83898 standard; cDNA; 417 BP.
DE Human polynucleotide SEQ ID NO 3958.
PN WO200164835-A2.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 2.6%; Score 58; DB 4; Length 417;
RESULT 698
ID AAI88586 standard; cDNA; 419 BP.
DE Human adult lung cDNA #283.
PN US2003073623-A1.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match
Best Local Similarity 2.6%; Score 58; DB 9; Length 419;
RESULT 699
ID AAI88586 standard; cDNA; 420 BP.
DE Human polynucleotide SEQ ID NO 8646.
PN WO200164835-A2.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 2.6%; Score 58; DB 4; Length 420;
RESULT 700
ID AAI89084 standard; cDNA; 421 BP.
DE Human polynucleotide SEQ ID NO 9144.
PN WO200164835-A2.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 2.6%; Score 58; DB 4; Length 421;
RESULT 701
ID ABX38360 standard; cDNA; 423 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #3525.
PN US2002137139-A1.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match
Best Local Similarity 2.6%; Score 58; DB 8; Length 434;
RESULT 702
ID ADL45796 standard; DNA; 423 BP.
DE Human ovarian cancer DNA marker #19686.
PN WO200170979-A2.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 2.6%; Score 58; DB 5; Length 423;
RESULT 703
ID ACH24941 standard; cDNA; 424 BP.
DE Human adult ovary cDNA #3321.
PN US2003073623-A1.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match
Best Local Similarity 2.6%; Score 58; DB 9; Length 424;
RESULT 704
ID ABV05669 standard; cDNA; 429 BP.
DE Human prostate expression marker cDNA 5660.
PN WO200160860-A2.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 2.6%; Score 58; DB 5; Length 429;
RESULT 705
ID ABX38360 standard; cDNA; 434 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #3525.
PN US2002137139-A1.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match
Best Local Similarity 2.6%; Score 58; DB 8; Length 434;
RESULT 706
ID AAI93088 standard; cDNA; 438 BP.
DE Human polynucleotide SEQ ID NO 13148.
PN WO200164835-A2.
PA (HYSE-) HYSEQ INC.

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PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 58; DB 4; Length 438;
Best Local Similarity 100.0%; Pred. No. 3.1e-10;
RESULT 707
ID AAZ09474 standard; DNA; 441 BP.
DE p135-NT3 construct DNA.
PN WO9941390-A2.
PD 19-AUG-1999.
PA (AVET-) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.
Query Match 2.6%; Score 58; DB 2; Length 441;
Best Local Similarity 100.0%; Pred. No. 3.1e-10;
RESULT 708
ID ABL94108 standard; cDNA; 442 BP.
DE Arabidopsis thaliana nucleic acid sequence Ref:2027873 SEQ ID NO:873.
PN US200203280-A1.
PD 21-FEB-2002.
PA (GORL-) GORLACH J.
PA (ANYV-) AN Y.
PA (HAMI-) HAMILTON C M.
PA (PRIC-) PRICE J L.
PA (RAIN-) RAINES T M.
PA (YUYV-) YU Y.
PA (RAME-) RAMEAKA J G.
PA (PAGE-) PAGE A.
PA (MATH-) MATHIEU A V.
PA (LEDF-) LEDFORD B L.
PA (WOES-) WOESSNER J P.
PA (HAAS-) HAAS W D.
PA (GARC-) GARCIA C A.
PA (KRIC-) KRICKER M.
PA (SLAT-) SLATER T.
PA (DAVI-) DAVIS K R.
PA (ALLE-) ALLEN K.
PA (HOFF-) HOFFMAN N.
PA (HURB-) HURBAN P.
Query Match 2.6%; Score 58; DB 6; Length 442;
Best Local Similarity 100.0%; Pred. No. 3.1e-10;
RESULT 709
ID AAA75749 standard; cDNA; 443 BP.
DE cDNA encoding a dermaseptin precursor polypeptide.
PN WO200005337-A1.
PD 21-SEP-2000.
PA (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP.
Query Match 2.6%; Score 58; DB 3; Length 443;
Best Local Similarity 100.0%; Pred. No. 3.1e-10;
RESULT 710
ID ABV19606 standard; cDNA; 446 BP.
DE Human prostate expression marker cDNA 19597.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 58; DB 5; Length 446;
Best Local Similarity 100.0%; Pred. No. 3.1e-10;
RESULT 711
ID AA182904 standard; cDNA; 448 BP.
DE Human polynucleotide SEQ ID NO 2964.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 58; DB 4; Length 448;
Best Local Similarity 100.0%; Pred. No. 3.1e-10;
RESULT 712
ID ABV56778 standard; cDNA; 451 BP.
DE Human prostate expression marker cDNA 56769.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 58; DB 5; Length 451;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 713
ID ABV49374 standard; cDNA; 453 BP.
DE Human prostate expression marker cDNA 49365.
PN WO200160860-A2.

PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 58; DB 5; Length 453;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 714
ID AAK87910 standard; cDNA; 456 BP.
DE Human digestive system antigen coding sequence SEQ ID NO: 226.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 58; DB 4; Length 456;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 715
ID AAS60044 standard; cDNA; 461 BP.
DE Human cancer agent-sensitve marker #45.
PN WO200179556-A2.
PD 25-OCT-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 58; DB 4; Length 461;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 716
ID ACH24394 standard; cDNA; 461 BP.
DE Human adult ovary cDNA #2774.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA-) DRMANAC R T.
PA (LAER-) LABAT I.
PA (STAC-) STACHE-CRAIN B.
PA (DICK-) DICKSON M C.
PA (JONE-) JONES L W.
Query Match 2.6%; Score 58; DB 9; Length 461;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 717
ID AAV58579 standard; cDNA; 470 BP.
DE Prostate tumour specific gene clone ID-4288.
PN WO9837418-A2.
PD 27-AUG-1998.
PA (CORI-) CORIXA CORP.
Query Match 2.6%; Score 58; DB 2; Length 470;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 718
ID AAV61312 standard; cDNA; 470 BP.
DE cDNA sequence of prostate tumour clone ID-4288.
PN WO9837093-A2.
PD 27-AUG-1998.
PA (CORI-) CORIXA CORP.
Query Match 2.6%; Score 58; DB 2; Length 470;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 719
ID AAA06342 standard; cDNA; 470 BP.
DE Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:102.
PN WO200004149-A2.
PD 27-JAN-2000.
PA (CORI-) CORIXA CORP.
Query Match 2.6%; Score 58; DB 3; Length 470;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 720
ID ABS71247 standard; cDNA; 470 BP.
DE Human prostate tumour protein partial DNA sequence #102.
PN US2002090372-A1.
PD 11-JUL-2002.
PA (XUJJ-) XU J.
PA (DILL-) DILLON D C.
Query Match 2.6%; Score 58; DB 3; Length 470;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 721
ID AAH93458 standard; cDNA; 470 BP.
DE Human prostate-specific cDNA sequence ID-4288.
PN WO200151633-A2.
PD 19-JUL-2001.
PA (CORI-) CORIXA CORP.
Query Match 2.6%; Score 58; DB 4; Length 470;
Best Local Similarity 100.0%; Pred. No. 3e-10;

RESULT 722
 ID AAS63550 standard; cDNA; 470 BP.
 DE Human prostate cDNA sequence #102.
 PN WO200173032-A2.
 PD 04-OCT-2001.
 PA (CORI-) CORIXA CORP.
 Query Match 2.6%; Score 58; DB 4; Length 470;
 Best Local Similarity 100.0%; Pred. No. 3e-10;
 RESULT 723
 ID AAH02523 standard; cDNA; 470 BP.
 DE Prostate tumour antigen determined cDNA sequence for ID-4288.
 PN WO200125272-A2.
 PD 12-APR-2001.
 PA (CORI-) CORIXA CORP.
 Query Match 2.6%; Score 58; DB 4; Length 470;
 Best Local Similarity 100.0%; Pred. No. 3e-10;
 RESULT 724
 ID AAH84772 standard; cDNA; 470 BP.
 DE Human prostate-specific cDNA sequence ID-4288.
 PN WO200134802-A2.
 PD 17-MAY-2001.
 PA (CORI-) CORIXA CORP.
 Query Match 2.6%; Score 58; DB 4; Length 470;
 Best Local Similarity 100.0%; Pred. No. 3e-10;
 RESULT 725
 ID ACAS9359 standard; cDNA; 470 BP.
 DE Prostate cancer therapy associated cDNA #102.
 PN US2002192763-A1.
 PD 19-DEC-2002.
 PA (XUJ/) XU J.
 PA (DILL/) DILLON D C.
 PA (MITC/) MITCHAM J L.
 PA (HARL/) HARLOCKER S L.
 PA (JIAN/) JIANG Y.
 PA (KALO/) KALOS M D.
 PA (FANG/) FANGER G R.
 PA (RETT/) RETTER M W.
 PA (STOL/) STOLK J A.
 PA (DAYC/) DAY C H.
 PA (VEDV/) VEDVICK T S.
 PA (CART/) CARTER D.
 PA (LISK/) LI S X.
 PA (WANG/) WANG A.
 PA (SKEI/) SKEIKY Y A W.
 PA (HEPL/) HEPLER W T.
 PA (HEND/) HENDERSON R A.
 Query Match 2.6%; Score 58; DB 4; Length 470;
 Best Local Similarity 100.0%; Pred. No. 3e-10;
 RESULT 726
 ID AAS10101 standard; cDNA; 470 BP.
 DE Human prostate tumour cDNA ID-4288.
 PN US6262245-B1.
 PD 17-JUL-2001.
 PA (CORI-) CORIXA CORP.
 Query Match 2.6%; Score 58; DB 5; Length 470;
 Best Local Similarity 100.0%; Pred. No. 3e-10;
 RESULT 727
 ID ABL94922 standard; cDNA; 470 BP.
 DE Human ID-4288 cDNA sequence SEQ ID NO 102.
 PN US2002022248-A1.
 PD 21-FEB-2002.
 PA (XUJ/) XU J.
 PA (DILL/) DILLON D C.
 PA (MITC/) MITCHAM J L.
 PA (HARL/) HARLOCKER S L.
 PA (JIAN/) JIANG Y.
 PA (KALO/) KALOS M D.
 PA (FANG/) FANGER G R.

PA (RETT/) RETTER M W.
 PA (STOL/) STOLK J A.
 PA (DAYC/) DAY C H.
 PA (VEDV/) VEDVICK T S.
 PA (CART/) CARTER D.
 PA (LISK/) LI S X.
 PA (WANG/) WANG A.
 PA (SKEI/) SKEIKY Y A W.
 PA (HEPL/) HEPLER W T.
 PA (HEND/) HENDERSON R A.
 Query Match 2.6%; Score 58; DB 6; Length 470;
 Best Local Similarity 100.0%; Pred. No. 3e-10;
 RESULT 728
 ID ABS58631 standard; cDNA; 470 BP.
 DE Prostate tumour cDNA #102.
 PN US2002081580-A1.
 PD 27-JUN-2002.
 PA (XUJ/) XU J.
 PA (DILL/) DILLON D C.
 Query Match 2.6%; Score 58; DB 6; Length 470;
 Best Local Similarity 100.0%; Pred. No. 3e-10;
 RESULT 729
 ID ACC95086 standard; cDNA; 470 BP.
 DE Prostate tumour specific cDNA sequence SEQ ID 102.
 PN WO200289747-A2.
 PD 14-NOV-2002.
 PA (CORI-) CORIXA CORP.
 Query Match 2.6%; Score 58; DB 8; Length 470;
 Best Local Similarity 100.0%; Pred. No. 3e-10;
 RESULT 730
 ID ADB13552 standard; cDNA; 470 BP.
 DE Human prostate specific cDNA ID-4288.
 PN US2003185830-A1.
 PD 02-OCT-2003.
 PA (CORI-) CORIXA CORP.
 Query Match 2.6%; Score 58; DB 10; Length 470;
 Best Local Similarity 100.0%; Pred. No. 3e-10;
 RESULT 731
 ID ADG26968 standard; cDNA; 470 BP.
 DE Human prostate-specific cDNA #102.
 PN US2003157089-A1.
 PD 21-AUG-2003.
 PA (CORI-) CORIXA CORP.
 Query Match 2.6%; Score 58; DB 10; Length 470;
 Best Local Similarity 100.0%; Pred. No. 3e-10;
 RESULT 732
 ID ABV47755 standard; cDNA; 471 BP.
 DE Human prostate expression marker cDNA 47746.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 2.6%; Score 58; DB 5; Length 471;
 Best Local Similarity 100.0%; Pred. No. 3e-10;
 RESULT 733
 ID ABX41242 standard; cDNA; 473 BP.
 DE Bovine EST associated with lactation/muscle/fat deposition #6407.
 PN US2002137139-A1.
 PD 26-SEP-2002.
 PA (BYAT/) BYATT J C.
 PA (MATH/) MATHIALAGAN N.
 PA (TAON/) TAO N.
 PA (WARR/) WARREN W C.
 Query Match 2.6%; Score 58; DB 8; Length 473;
 Best Local Similarity 100.0%; Pred. No. 3e-10;
 RESULT 734
 ID AAI83554 standard; cDNA; 480 BP.
 DE Human polynucleotide SEQ ID NO 3614.
 PN WO200164835-A2.
 PD 07-SEP-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 2.6%; Score 58; DB 4; Length 480;
 Best Local Similarity 100.0%; Pred. No. 3e-10;
 RESULT 735

DE cDNA encoding human PRO polypeptide #93.
FN US2003036141-A1.
PD 20-FEB-2003.

Query Match
Best Local Similarity 2.6%; Score 58; DB 8; Length 485;
Pred. No. 3e-10;

RESULT 744

ID ACA73477 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
FN US2003036146-A1.
PD 20-FEB-2003.

Query Match
Best Local Similarity 2.6%; Score 58; DB 8; Length 485;
Pred. No. 3e-10;

RESULT 745

ID ACA05792 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
FN US2003036162-A1.
PD 20-FEB-2003.

Query Match
Best Local Similarity 2.6%; Score 58; DB 8; Length 485;
Pred. No. 3e-10;

RESULT 746

ID ACA66626 standard; cDNA; 485 BP.
DE cDNA encoding human PRO protein #93.
FN US2003036137-A1.
PD 20-FEB-2003.

Query Match
Best Local Similarity 2.6%; Score 58; DB 8; Length 485;
Pred. No. 3e-10;

RESULT 747

ID ACA64328 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cdNA.
FN US2003003531-A1.
PD 02-JAN-2003.

Query Match
Best Local Similarity 2.6%; Score 58; DB 8; Length 485;
Pred. No. 3e-10;

RESULT 748

ID ACA91185 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cdNA.
FN US2003018173-A1.
PD 23-JAN-2003.

Query Match
Best Local Similarity 2.6%; Score 58; DB 8; Length 485;
Pred. No. 3e-10;

RESULT 749

ID ACD81562 standard; cDNA; 485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1003.
FN US2003009013-A1.
PD 09-JAN-2003.

Query Match
Best Local Similarity 2.6%; Score 58; DB 8; Length 485;
Pred. No. 3e-10;

RESULT 750

ID ACF20201 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cdNA, SEQ ID NO:185.
FN US2003040063-A1.
PD 27-FEB-2003.

Query Match
Best Local Similarity 2.6%; Score 58; DB 8; Length 485;
Pred. No. 3e-10;

RESULT 751

ID ACF19587 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cdNA, SEQ ID NO:185.
FN US2003040064-A1.
PD 27-FEB-2003.

Query Match
Best Local Similarity 2.6%; Score 58; DB 8; Length 485;
Pred. No. 3e-10;

RESULT 752

ID ACD1875 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
FN US2003027267-A1.
PD 06-FEB-2003.

Query Match
Best Local Similarity 2.6%; Score 58; DB 8; Length 485;
Pred. No. 3e-10;

DE ACH16280 standard; cDNA; 480 BP.
FN US2003073623-A1.
PD 17-APR-2003.

Query Match
Best Local Similarity 2.6%; Score 58; DB 9; Length 480;
Pred. No. 3e-10;

RESULT 735

ID ACH40652 standard; cDNA; 480 BP.
DE Human foetal brain cDNA #2019.
FN US2003073623-A1.
PD 17-APR-2003.

Query Match
Best Local Similarity 2.6%; Score 58; DB 9; Length 480;
Pred. No. 3e-10;

RESULT 736

ID ABEV4907 standard; cDNA; 483 BP.
DE Human prostate expression marker cDNA 48898.
FN WO200160860-A2.
PD 23-AUG-2001.

Query Match
Best Local Similarity 2.6%; Score 58; DB 5; Length 483;
Pred. No. 3e-10;

RESULT 737

ID AAZ65037 standard; cDNA; 485 BP.
DE Membrane-bound protein PRO1003 encoding cdNA.
FN WO9963088-A2.
PD 09-DEC-1999.

Query Match
Best Local Similarity 2.6%; Score 58; DB 3; Length 485;
Pred. No. 3e-10;

RESULT 738

ID AAZ65037 standard; cDNA; 485 BP.
DE Membrane-bound protein PRO1003 encoding cdNA.
FN WO9963088-A2.
PD 09-DEC-1999.

Query Match
Best Local Similarity 2.6%; Score 58; DB 3; Length 485;
Pred. No. 3e-10;

RESULT 739

ID AAF92079 standard; cDNA; 485 BP.
DE Human DNA encoding PRO polypeptide sequence #93.
FN WO200168848-A2.
PD 20-SEP-2001.

Query Match
Best Local Similarity 2.6%; Score 58; DB 4; Length 485;
Pred. No. 3e-10;

RESULT 740

ID AAF92079 standard; cDNA; 485 BP.
DE Human DNA encoding PRO polypeptide sequence #93.
FN WO200168848-A2.
PD 20-SEP-2001.

Query Match
Best Local Similarity 2.6%; Score 58; DB 4; Length 485;
Pred. No. 3e-10;

RESULT 741

ID AAF44183 standard; cDNA; 485 BP.
DE Human PRO1003 (UNQ487) nucleotide sequence SEQ ID NO:245.
FN WO200073454-A1.
PD 07-DEC-2000.

Query Match
Best Local Similarity 2.6%; Score 58; DB 4; Length 485;
Pred. No. 3e-10;

RESULT 742

ID ABS74399 standard; cDNA; 485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1003.
FN US2002119130-A1.
PD 29-AUG-2002.

Query Match
Best Local Similarity 2.6%; Score 58; DB 6; Length 485;
Pred. No. 3e-10;

RESULT 743

ID ACS89467 standard; cDNA; 485 BP.
DE Human cDNA encoding secreted/transmembrane protein (PRO) cDNA #93.
FN US2003027267-A1.
PD 06-FEB-2003.

Query Match
Best Local Similarity 2.6%; Score 58; DB 8; Length 485;
Pred. No. 3e-10;

Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 753
ID ACF13040 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 754
ID ACD25143 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 755
ID ACF00192 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 756
ID ACA50384 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 757
ID ACA72249 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 758
ID ACD04773 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 759
ID ACD18234 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 760
ID ACD08241 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 761
ID ACA88675 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 762
ID ACA70117 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;

RESULT 763
ID ACD12339 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 764
ID ACC74254 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 765
ID ACD15882 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 766
ID ACD25450 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 767
ID ACD17927 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 768
ID ACC88214 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 769
ID ACD21568 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 770
ID ACD18635 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 771
ID ACA58831 standard; cDNA; 485 BP.
DE cDNA encoding human secreted polypeptide PRO1003.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 772
ID ABX98245 standard; cDNA; 485 BP.
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 185.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 773

ID ACD13996 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #93.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 774
ID ACD09776 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 775
ID ACC88521 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 776
ID ACD21261 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 777
ID ABX75633 standard; cDNA; 485 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1003.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 778
ID ACA64007 standard; cDNA; 485 BP.
DE cDNA encoding human PRO polypeptide #22.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 779
ID ABX97836 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #93.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 780
ID ACA97312 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 781
ID ACA57775 standard; cDNA; 485 BP.
DE Human PRO1003 cDNA.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 782
ID ACD14303 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #93.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 783
ID ACC91086 standard; cDNA; 485 BP.

DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 784
ID ACC88828 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 785
ID ACD07025 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #93.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 786
ID ACA67476 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #93.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 787
ID ACC81531 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 788
ID ACA91271 standard; cDNA; 485 BP.
DE cDNA encoding human PRO polypeptide #22.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 789
ID ACC89135 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 790
ID ACC86491 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 791
ID ACC89749 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 792
ID ACC92928 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 793
ID ACC91086 standard; cDNA; 485 BP.

ID ABX80787 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein cDNA, #97.
PN US2003027162-A1.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 794
ID ACA72556 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #93.
PN US2003022295-A1.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 795
ID ACA89074 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003022297-A1.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 796
ID ACA69810 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003032105-A1.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 797
ID ACA96953 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003032123-A1.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 798
ID ACA90949 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003032108-A1.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 799
ID ACA70731 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003032111-A1.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 800
ID ACA95241 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003032119-A1.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 801
ID ACD44296 standard; cDNA; 485 BP.
DE cDNA encoding human PRO1003 polypeptide.
PN US2002127576-A1.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 802
ID ACC86184 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003027263-A1.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 803
ID ACD45170 standard; cDNA; 485 BP.

DE Human secreted/transmembrane polypeptide PRO1003 cDNA.
PN US2003009012-A1.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 804
ID ACC90056 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003027271-A1.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 805
ID ACD12664 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003036125-A1.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 806
ID ACF19894 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003040068-A1.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 807
ID ABX76838 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #93.
PN US2003027280-A1.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 808
ID ACA73170 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003022300-A1.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 809
ID ACA68713 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003036136-A1.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 810
ID ACA74557 standard; cDNA; 485 BP.
DE cDNA encoding human PRO polypeptide #93.
PN US2003036138-A1.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 811
ID ACA70424 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003032109-A1.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 812
ID ACD14610 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #93.
PN US2003040066-A1.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 813
ID ACA93718 standard; cDNA; 485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1003.
PN US2003045684-A1.

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PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 814
ID ACA6282 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 815
ID ABX98747 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 816
ID ACA67292 standard; cDNA; 485 BP.
DE cDNA encoding human secreted polypeptide PRO1003.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 817
ID ACC81224 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 818
ID ACA95548 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 819
ID ACD04466 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 820
ID ACC87507 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 821
ID ACF12569 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 822
ID ACH66265 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 823
ID ABX79467 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein cDNA, #97.
PN US2003036155-A1.
PD 20-FEB-2003.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 824
ID ACA96284 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #93.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 825
ID ACA65058 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #93.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 826
ID ACA73784 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 827
ID ACA74196 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 828
ID ACA96591 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #93.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 829
ID ACD10697 standard; cDNA; 485 BP.
DE cDNA encoding human PRO polypeptide #93.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 830
ID ACC91393 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 831
ID ACA93488 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003022187-A1.
PD 30-JAN-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 832
ID ACD02728 standard; cDNA; 485 BP.
DE cDNA encoding human PRO polypeptide #93.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 833
ID ACC87293 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003036155-A1.
PD 20-FEB-2003.
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PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 834
ID ACC85877 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 835
ID ABX81170 standard; DNA; 485 BP.
DE Novel human secreted or transmembrane protein PRO1108 DNA.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 836
ID ACA65365 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #93.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 837
ID ACA94182 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 838
ID ACA57926 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #93.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 839
ID ACA31428 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 840
ID ACA90642 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 841
ID ACD16189 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 842
ID ACD17350 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 843
ID ACC92007 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;

RESULT 844
ID ACD02319 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 845
ID ACA74864 standard; cDNA; 485 BP.
DE cDNA encoding human PRO polypeptide #93.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 846
ID ACA91735 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #93.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 847
ID ACA89310 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 848
ID ACA71379 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 849
ID ACC90779 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 850
ID ACA85789 standard; cDNA; 485 BP.
DE cDNA encoding human PRO protein #93.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 851
ID ACA68947 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 852
ID ACA92986 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003017476-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 853
ID ACA94934 standard; cDNA; 485 BP.
DE cDNA encoding human PRO polypeptide #93.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;

RESULT 854
ID ACD16496 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 855
ID ACD15575 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 856
ID ACA98469 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #22.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 857
ID ABX17070 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #68.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 858
ID ABX16678 standard; cDNA; 485 BP.
DE Human cDNA encoding secreted/transmembrane protein #93.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 859
ID ACA67925 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 860
ID ACA63394 standard; cDNA; 485 BP.
DE cDNA encoding human PRO polypeptide #22.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 861
ID ACA97619 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #93.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 862
ID ACA99068 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 863
ID ACC91700 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003040076-A1.
PD 27-FEB-2003.

PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 864
ID ACD11111 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 865
ID ACD14961 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 866
ID ACA88374 standard; cDNA; 485 BP.
DE Human secreted and transmembrane polypeptide PRO1003 cDNA.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 867
ID ACD81881 standard; cDNA; 485 BP.
DE cDNA encoding human PRO1003 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 868
ID ACD11725 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003032118-A1.
PD 13-FEB-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 869
ID ACC95854 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003036135-A1.
PD 20-FEB-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 870
ID ACF16417 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 871
ID ACF02535 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 872
ID ACF02842 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 873
ID ACF21429 standard; cDNA; 485 BP.

DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Query Match Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 874
ID ACF10113 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Query Match Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 875
ID ACF78006 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Query Match Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 876
ID ACD46711 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Query Match Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 877
ID ACD49474 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Query Match Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 878
ID ACF28241 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Query Match Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 879
ID ACD88931 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Query Match Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 880
ID ACD84326 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #93.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Query Match Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 881
ID ACD99100 standard; cDNA; 485 BP.
DE cDNA encoding human PRO polypeptide #93.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Query Match Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 882
ID ADA77937 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.

PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Query Match Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 883
ID ACF48842 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003104539-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Query Match Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 884
ID ACD09162 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003036131-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Query Match Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 885
ID ACF11955 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003040075-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Query Match Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 886
ID ACF41189 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Query Match Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 887
ID ACF15803 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003044930-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Query Match Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 888
ID ACF16110 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Query Match Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 889
ID ADB17100 standard; cDNA; 485 BP.
DE Human cDNA clone (SeqID 43) encoding the transmembrane PRO protein.
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Query Match Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 890
ID ACD31937 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Query Match Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 891
ID ACF18745 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Query Match Best Local Similarity 100.0%; Pred. No. 3e-10;

RESULT 892
ID ACF09192 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 893
ID ACF78313 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 894
ID ACF51912 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003064440-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 895
ID ACF26399 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003086704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 896
ID ACF24192 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 897
ID ACF63503 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 898
ID ACF50377 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 899
ID ACH07848 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 900
ID ACF13654 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 901
ID ACD41580 standard; cDNA; 485 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003055159-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 902
ID ADA37756 standard; cDNA; 485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1003.
PN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 903
ID ACF31993 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 904
ID ACF23271 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 905
ID ACF39961 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 906
ID ACD45483 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 907
ID ACF53140 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 908
ID ACF27320 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 909
ID ACF45158 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 910
ID ACF29776 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.

PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 911
ID ACD89852 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 912
ID ACD84633 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #93.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 913
ID ACD98793 standard; cDNA; 485 BP.
DE cDNA encoding human PRO polypeptide #93.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 914
ID ACF77085 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003082717-A1.
PD 01-MAY-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 915
ID ACF76778 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003104538-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 916
ID ACF49763 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003104542-A1.
PD 05-JUN-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 917
ID ACF50070 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003104543-A1.
PD 05-JUN-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 918
ID ADA21442 standard; cDNA; 485 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO1003.
PN US2003054404-A1.
PD 20-MAR-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 919
ID ACD09469 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003036127-A1.
PD 20-FEB-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 920

ID ACD08548 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003040061-A1.
PD 27-FEB-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 921
ID ACH03597 standard; cDNA; 485 BP.
DE Human secreted/transmembrane polypeptide PRO 1003 cDNA.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 922
ID ACF12262 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003036130-A1.
PD 20-FEB-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 923
ID ACC94770 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 924
ID ACD22489 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 925
ID ACF15189 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003044917-A1.
PD 06-MAR-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 926
ID ACC97284 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003044929-A1.
PD 06-MAR-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 927
ID ACC92314 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 928
ID ACF13961 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 929
ID ACF14268 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 930
ID ADA10229 standard; cDNA; 485 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1003.
PN US2003059831-A1.
PD 27-MAR-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 931
ID ACF09499 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 932
ID ACD45790 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003084454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 933
ID ACD47939 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US200306461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 934
ID ACD67670 standard; cDNA; 485 BP.
DE cDNA encoding human PRO polypeptide #93.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 935
ID ACF25478 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003088727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 936
ID ACF29162 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 937
ID ACD84940 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 938
ID ACD84019 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #93.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;

RESULT 939
ID ACD88010 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003088776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 940
ID ACF30697 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 941
ID ACF32300 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 942
ID ACH11960 standard; cDNA; 485 BP.
DE cDNA encoding human PRO polypeptide #93.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 943
ID ACH12267 standard; cDNA; 485 BP.
DE cDNA encoding human PRO polypeptide #93.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 944
ID ADA19905 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 945
ID ACD40659 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003032134-A1.
PD 13-FEB-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 946
ID ADB17288 standard; cDNA; 485 BP.
DE Human cDNA clone (seqid 43) encoding the transmembrane PRO protein.
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 947
ID ADA17773 standard; cDNA; 485 BP.
DE cDNA encoding human PRO1003 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 948
ID ACF18131 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.

PD US2003054481-A1.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
Query Match
RESULT 949
ID ACF08578 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
Query Match
RESULT 950
ID ACF31379 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
Query Match
RESULT 951
ID ACF52219 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
Query Match
RESULT 952
ID ACD50088 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
Query Match
RESULT 953
ID ACF38791 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
Query Match
RESULT 954
ID ACF26706 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
Query Match
RESULT 955
ID ACF24806 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
Query Match
RESULT 956
ID ACF46386 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
Query Match
RESULT 957
ID ACF27934 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068751-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
Query Match
RESULT 958
ID ACD89238 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
Query Match
RESULT 959
ID ACF63810 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
Query Match
RESULT 960
ID ACF60450 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003087374-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
Query Match
RESULT 961
ID ACHI2574 standard; cDNA; 485 BP.
DE cDNA encoding human PRO polypeptide #93.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
Query Match
RESULT 962
ID ACH09997 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
Query Match
RESULT 963
ID ACD03852 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003040055-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
Query Match
RESULT 964
ID ACD10390 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003036164-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
Query Match
RESULT 965
ID ACD12032 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003040074-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
Query Match
RESULT 966
ID ACF42417 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
Query Match
RESULT 967

ID ADA27881 standard; cDNA; 485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1003.
PN US2003054359-A1.
PD 20-MAR-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 968
ID ACF18438 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 969
ID ACF02228 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 970
ID ACF21736 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 971
ID ACF10420 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003073169-A1.
PD 17-APR-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 972
ID ACF33872 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 973
ID ACF44834 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 974
ID ACD90466 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 975
ID ACD91079 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 976
ID ACF30390 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003067478-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 977
ID ACD87089 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003088773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 978
ID ACF60143 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 979
ID ACF46693 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003087373-A1.
PD 08-MAY-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 980
ID ACF75550 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003096353-A1.
PD 22-MAY-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 981
ID ADA79729 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003073173-A1.
PD 17-APR-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 982
ID ACF17210 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003054458-A1.
PD 20-MAR-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 983
ID ACF22964 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 984
ID ACF07964 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 985
ID ACF08271 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 986
ID ACF30390 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003067478-A1.

ID ACF40575 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 987
ID ACF53754 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 988
ID ACF47018 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 989
ID ACF47921 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 990
ID ACF47307 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 991
ID ACF46079 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 992
ID ACD86168 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 993
ID ACF52526 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003082715-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 994
ID ACF52833 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003082716-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 995
ID ACF64826 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068737-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 996
ID ACF76471 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 997
ID ACF61371 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 998
ID ACF61678 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 999
ID ACD30709 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003032125-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1000
ID ACD31630 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003054454-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1001
ID ACD32551 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1002
ID ADA20077 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1003
ID ACD82111 standard; cDNA; 485 BP.
DE Human secreted/transmembrane polypeptide PRO 1003 cDNA.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1004
ID ACF17517 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1005
ID ACF64826 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068737-A1.

Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1005
ID ADA94461 standard; cDNA; 485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1003.
PN US2003059832-A1.
PD 27-MAR-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1006
ID ACF07350 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1007
ID ACF20508 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1008
ID ACF21122 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1009
ID ACF20815 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1010
ID ACD47632 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1011
ID ACF47614 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1012
ID ACF5347 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003086679-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1013
ID ACD86782 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1014
ID ACH05030 standard; cDNA; 485 BP.
DE cDNA encoding human PRO polypeptide #93.

PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1015
ID ACF44527 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1016
ID ADA81456 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1017
ID ACD22182 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003027276-A1.
PD 06-FEB-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1018
ID ACD24529 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003044920-A1.
PD 06-MAR-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1019
ID ACD39732 standard; cDNA; 485 BP.
DE cDNA encoding human PRO polypeptide #93.
PN US2003027265-A1.
PD 06-FEB-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1020
ID ACD40039 standard; cDNA; 485 BP.
DE cDNA encoding human PRO polypeptide #93.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1021
ID ACF13347 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1022
ID ACF03149 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1023
ID ACF78620 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;

Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1024
ID ACF11341 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003073171-A1.
PD 17-APR-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1025
ID ACF50684 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003032121-A1.
PD 13-FEB-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1026
ID ACF34179 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1027
ID ACD46404 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1028
ID ACD48246 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1029
ID ACF27627 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1030
ID ACF24499 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1031
ID ACD85554 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1032
ID ACD90159 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1033
ID ACD83712 standard; cDNA; 485 BP.

DE Human PRO polynucleotide #93.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1034
ID ACF49149 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003104540-A1.
PD 05-JUN-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1035
ID ACH07234 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1036
ID ACH07541 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1037
ID ACH08155 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1038
ID ACH11346 standard; cDNA; 485 BP.
DE cDNA encoding human PRO polypeptide #93.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1039
ID ACH11653 standard; cDNA; 485 BP.
DE cDNA encoding human PRO polypeptide #93.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1040
ID ACH10304 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1041
ID ACF01307 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003040059-A1.
PD 27-FEB-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1042
ID ACF40882 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003040078-A1.
PD 27-FEB-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 58; DB 9; Length 485;
RESULT 1043
ID ACD24222 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003044918-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 58; DB 9; Length 485;
RESULT 1044
ID ACD31323 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003032132-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 58; DB 9; Length 485;
RESULT 1045
ID ACF17824 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 58; DB 9; Length 485;
RESULT 1046
ID ADA38686 standard; cDNA; 485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1003.
PN US2003059780-A1.
PD 27-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 58; DB 9; Length 485;
RESULT 1047
ID ACF32607 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 58; DB 9; Length 485;
RESULT 1048
ID ACF40268 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 58; DB 9; Length 485;
RESULT 1049
ID ACF48228 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003064441-A1.
PD 03-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 58; DB 9; Length 485;
RESULT 1050
ID ACF38177 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 58; DB 9; Length 485;
RESULT 1051
ID ACF25113 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 58; DB 9; Length 485;
RESULT 1052
ID ACF27013 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003032133-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 58; DB 9; Length 485;
RESULT 1053
ID ACF29469 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003073174-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 58; DB 9; Length 485;
RESULT 1054
ID ACD87703 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 58; DB 9; Length 485;
RESULT 1055
ID ACF76164 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 58; DB 9; Length 485;
RESULT 1056
ID ACF49456 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003104541-A1.
PD 05-JUN-2003.
Query Match
Best Local Similarity 100.0%; Score 58; DB 9; Length 485;
RESULT 1057
ID ACF43913 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 58; DB 9; Length 485;
RESULT 1058
ID ACH06258 standard; cDNA; 485 BP.
DE cDNA encoding human PRO polypeptide #93.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 58; DB 9; Length 485;
RESULT 1059
ID ACH06565 standard; cDNA; 485 BP.
DE cDNA encoding human PRO polypeptide #93.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 58; DB 9; Length 485;
RESULT 1060
ID ADA83254 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 58; DB 9; Length 485;
RESULT 1061
ID ACC92621 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003032133-A1.
PD 13-FEB-2003.

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Query Match      2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1062
ID ACC93235 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003032136-A1.
PD 13-FEB-2003.
Query Match      2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1063
ID ACF19280 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003036129-A1.
PD 20-FEB-2003.
Query Match      2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1064
ID ACD12971 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003040053-A1.
PD 27-FEB-2003.
Query Match      2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1065
ID ACF06429 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003040057-A1.
PD 27-FEB-2003.
Query Match      2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1066
ID ACC94463 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003054467-A1.
PD 20-MAR-2003.
Query Match      2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1067
ID ACC97891 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003044932-A1.
PD 06-MAR-2003.
Query Match      2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1068
ID ACC94156 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003027270-A1.
PD 06-FEB-2003.
Query Match      2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1069
ID ACF42110 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003054469-A1.
PD 20-MAR-2003.
Query Match      2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1070
ID ACD31016 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003032126-A1.
PD 13-FEB-2003.
Query Match      2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1071
ID ACD43045 standard; cDNA; 485 BP.
DE cDNA encoding human PRO polypeptide #93.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.

Query Match      2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1072
ID ACD43352 standard; cDNA; 485 BP.
DE cDNA encoding human PRO polypeptide #93.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.

Query Match      2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1073
ID ACF14882 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.

Query Match      2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1074
ID ADA92807 standard; cDNA; 485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1003.
PN US2003060407-A1.
PD 27-MAR-2003.
Query Match      2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1075
ID ACF01614 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003049738-A1.
PD 13-MAR-2003.
Query Match      2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1076
ID ACF31686 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.

Query Match      2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1077
ID ACD67363 standard; cDNA; 485 BP.
DE cDNA encoding human PRO polypeptide #93.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.

Query Match      2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1078
ID ACD48553 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.

Query Match      2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1079
ID ACD4860 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003054468-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.

Query Match      2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1080
ID ACF51298 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.

Query Match      2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1081
ID ACD43045 standard; cDNA; 485 BP.
DE cDNA encoding human PRO polypeptide #93.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
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ID ACF54061 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1082
Query Match
ID ACF25785 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1083
Query Match
ID ACF39098 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1084
Query Match
ID ACF28855 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1085
Query Match
ID ACD90772 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1086
Query Match
ID ACD86475 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1087
Query Match
ID ACH05337 standard; cDNA; 485 BP.
DE cDNA encoding human PRO polypeptide #93.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1088
Query Match
ID ACF65133 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1089
Query Match
ID ADB20297 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003082767-A1.
PD 01-MAY-2003.
Query Match
ID ACF43606 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.

PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1091
ID ACH09076 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1092
ID ACH09383 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1093
ID ADA78549 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1094
ID ACF09806 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003088720-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1095
ID ADA00374 standard; cDNA; 485 BP.
DE Human secreted/transmembrane polypeptide PRO 1003 cDNA.
PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1096
ID ACF50991 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1097
ID ACF23885 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1098
ID ACD88317 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1099
ID ACD88317 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1099
ID ACH09690 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003049776-A1.

PD 13-MAR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1100
ID ACH10611 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1101
ID ACD11418 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003036126-A1.
PD 20-FEB-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1102
ID ACC96468 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003044924-A1.
PD 06-MAR-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1103
ID ACC98498 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003044927-A1.
PD 06-MAR-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1104
ID ACF41803 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003040072-A1.
PD 27-FEB-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1105
ID ACF16724 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003040073-A1.
PD 27-FEB-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1106
ID ACD32244 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1107
ID ACD30402 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003032124-A1.
PD 13-FEB-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1108
ID ACD41273 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1109
ID ACF07657 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.

PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1110
ID ACF31072 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1111
ID ACF77392 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1112
ID ACF11034 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003073170-A1.
PD 17-APR-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1113
ID ACF32914 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1114
ID ACF26092 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1115
ID ACD83405 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #93.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1116
ID ACF23578 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1117
ID ACF42992 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 485;
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1118
ID ACF43299 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003104551-A1.
PD 05-JUN-2003.

PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1119
ID ACH05951 standard; cDNA; 485 BP.
DE cDNA encoding human PRO polypeptide #93.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1120
ID ACH09769 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1121
ID ACC90363 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003027273-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1122
ID ACF10727 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003036119-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1123
ID ACC93542 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003036120-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1124
ID ACC96161 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1125
ID ACD24836 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003044921-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1126
ID ACF01921 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1127
ID ACF22043 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1128
ID ACF22657 standard; cDNA; 485 BP.

DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1129
ID ACF08885 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1130
ID ACF33221 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1131
ID ACF54675 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1132
ID ACF48535 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003084444-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1133
ID ACD47325 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1134
ID ACD49167 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1135
ID ACF37870 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1136
ID ACF30083 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1137
ID ACD87396 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.

PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1138
ID ACF61985 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003104538-A1.
PD 05-JUN-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1139
ID ACH10918 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1140
ID ACD10083 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003036158-A1.
PD 20-FEB-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1141
ID ACD16808 standard; cDNA; 485 BP.
DE cDNA encoding human PRO polypeptide #93.
PN US2003036151-A1.
PD 20-FEB-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1142
ID ACH65442 standard; cDNA; 485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1003.
PN US2003044806-A1.
PD 06-MAR-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1143
ID ACC99105 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003040067-A1.
PD 27-FEB-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1144
ID ACF00499 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003054456-A1.
PD 20-MAR-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1145
ID ACD40966 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1146
ID ACF14575 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1147
ID ACF22350 standard; cDNA; 485 BP.

DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1148
ID ACF78927 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003049764-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1149
ID ACF11648 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003073177-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1150
ID ADA22368 standard; cDNA; 485 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO1003.
PN US2003040473-A1.
PD 27-FEB-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1151
ID ACF51605 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1152
ID ACF33528 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1153
ID ACD49781 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003068731-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1154
ID ACF37563 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068683-A1.
PD 10-APR-2003.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1155
ID ACF28548 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1156
ID ACD88624 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003068681-A1.
PD 10-APR-2003.

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Query Match
Best Local Similarity 2.6%; Score 58; DB 9; Length 485;
RESULT 1157
ID ACF75243 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.6%; Score 58; DB 9; Length 485;
RESULT 1158
ID ACF61064 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.6%; Score 58; DB 9; Length 485;
RESULT 1159
ID ACF44220 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003104556-A1.
PD 03-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.6%; Score 58; DB 9; Length 485;
RESULT 1160
ID ACH08462 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.6%; Score 58; DB 9; Length 485;
RESULT 1161
ID ACD39432 standard; cDNA; 485 BP.
DE Human cDNA encoding PRO1108.
PN US2003017982-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.6%; Score 58; DB 9; Length 485;
RESULT 1162
ID ACD39432 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003036122-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.6%; Score 58; DB 9; Length 485;
RESULT 1163
ID ACD20954 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.6%; Score 58; DB 9; Length 485;
RESULT 1164
ID ACF06736 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003040065-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.6%; Score 58; DB 9; Length 485;
RESULT 1165
ID ACD20647 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003044919-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.6%; Score 58; DB 9; Length 485;
RESULT 1166
ID ACD22796 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003040077-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.6%; Score 58; DB 9; Length 485;
RESULT 1167
ID ACF41496 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003044928-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.6%; Score 58; DB 9; Length 485;
RESULT 1168
ID ADA06534 standard; cDNA; 485 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #68.
PN US2003049638-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.6%; Score 58; DB 9; Length 485;
RESULT 1169
ID ADA39227 standard; cDNA; 485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1003.
PN US2003059782-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.6%; Score 58; DB 9; Length 485;
RESULT 1170
ID ACF07043 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.6%; Score 58; DB 9; Length 485;
RESULT 1171
ID ACF77699 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.6%; Score 58; DB 9; Length 485;
RESULT 1172
ID ACD46097 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.6%; Score 58; DB 9; Length 485;
RESULT 1173
ID ACF47000 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.6%; Score 58; DB 9; Length 485;
RESULT 1174
ID ACF54368 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.6%; Score 58; DB 9; Length 485;
RESULT 1175
ID ACF45772 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.6%; Score 58; DB 9; Length 485;
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RESULT 1176
ID ACF45465 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1177
ID ACF38484 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1178
ID ACD89545 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1179
ID ACD85247 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1180
ID ACD85861 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1181
ID ACF75857 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1182
ID ACF60757 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1183
ID ACH05644 standard; cDNA; 485 BP.
DE cDNA encoding human PRO polypeptide #93.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1184
ID ADA82620 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1185
ID ACF55596 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068761-A1.

ID ADB85616 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1186
ID ADB96253 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #68.
PN US2003054403-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1187
ID ACF55903 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068680-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1188
ID ACF55289 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1189
ID ADB85928 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1190
ID ACF56210 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1191
ID ACF56517 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1192
ID ADB68295 standard; cDNA; 485 BP.
DE Human PRO1003 cDNA.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1193
ID ADB68102 standard; cDNA; 485 BP.
DE Human PRO1003 cDNA.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1194
ID ACF55596 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068761-A1.

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PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1195
ID ACF54982 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1196
ID ADB90919 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1197
ID ADC57725 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #68.
PN US2003027754-A1.
PD 06-FEB-2003.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1198
ID ADC55089 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #68.
PN US2003045463-A1.
PD 06-MAR-2003.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1199
ID ADC11956 standard; cDNA; 485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1003.
PN US2003049681-A1.
PD 13-MAR-2003.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1200
ID ADC06999 standard; cDNA; 485 BP.
DE Human PRO1003 cDNA.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1201
ID ADC56378 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #68.
PN US2003064375-A1.
PD 03-APR-2003.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1202
ID ADC17178 standard; cDNA; 485 BP.
DE cDNA sequence encoding a PRO polypeptide (SeqID 43).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1203
ID ADC07433 standard; cDNA; 485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1003.
PN US2003068647-A1.
PD 10-APR-2003.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1204
ID ADC11423 standard; cDNA; 485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1003.
PN US2003068647-A1.
PD 10-APR-2003.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1205
ID ADC14876 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1206
ID ADC52371 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1207
ID ADC14545 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003082546-A1.
PD 01-MAY-2003.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1208
ID ADD08077 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003068623-A1.
PD 10-APR-2003.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1209
ID ADC81902 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #68.
PN US2003083461-A1.
PD 01-MAY-2003.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1210
ID ADD07544 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1211
ID ADC82435 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #68.
PN US2003059833-A1.
PD 27-MAR-2003.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1212
ID ADD05658 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1213
ID ADD08615 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003073090-A1.
PD 17-APR-2003.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1214

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ID ADD06864 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2002193300-A1.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1215
ID ADC83111 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #68.
PN US2003059783-A1.
PD 27-MAR-2003.
Query Match Best Local Similarity 100.0%; Score 58; DB 10; Length 485;
RESULT 1216
ID ADD55218 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #68.
PN US2003077593-A1.
PD 24-APR-2003.
Query Match Best Local Similarity 100.0%; Score 58; DB 10; Length 485;
RESULT 1217
ID ADD36047 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match Best Local Similarity 100.0%; Score 58; DB 10; Length 485;
RESULT 1218
ID ADD56176 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #68.
PN US2003077594-A1.
PD 24-APR-2003.
Query Match Best Local Similarity 100.0%; Score 58; DB 10; Length 485;
RESULT 1219
ID ADD54614 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #68.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match Best Local Similarity 100.0%; Score 58; DB 10; Length 485;
RESULT 1220
ID ADE26768 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003087304-A1.
PD 08-MAY-2003.
Query Match Best Local Similarity 100.0%; Score 58; DB 10; Length 485;
RESULT 1221
ID ADE26235 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003087305-A1.
PD 08-MAY-2003.
Query Match Best Local Similarity 100.0%; Score 58; DB 10; Length 485;
RESULT 1222
ID ADF67172 standard; cDNA; 485 BP.
DE Human PRO1003 nucleotide sequence SEQ ID NO:245.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match Best Local Similarity 100.0%; Score 58; DB 10; Length 485;
RESULT 1223
ID ADG01048 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003078387-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match Best Local Similarity 100.0%; Score 58; DB 10; Length 485;

Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1224
ID ADG08601 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match Best Local Similarity 100.0%; Score 58; DB 10; Length 485;
RESULT 1225
ID ADG02653 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match Best Local Similarity 100.0%; Score 58; DB 10; Length 485;
RESULT 1226
ID ADG01360 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match Best Local Similarity 100.0%; Score 58; DB 10; Length 485;
RESULT 1227
ID ADF95535 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match Best Local Similarity 100.0%; Score 58; DB 10; Length 485;
RESULT 1228
ID ADF95222 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match Best Local Similarity 100.0%; Score 58; DB 10; Length 485;
RESULT 1229
ID ADG12350 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003207392-A1.
PD 06-NOV-2003.
Query Match Best Local Similarity 100.0%; Score 58; DB 10; Length 485;
RESULT 1230
ID ADH24075 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match Best Local Similarity 100.0%; Score 58; DB 10; Length 485;
RESULT 1231
ID ADH34101 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match Best Local Similarity 100.0%; Score 58; DB 10; Length 485;
RESULT 1232
ID ADH29934 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match Best Local Similarity 100.0%; Score 58; DB 10; Length 485;
RESULT 1233
ID ADH29934 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match Best Local Similarity 100.0%; Score 58; DB 10; Length 485;

ID ADH23905 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1234
ID ADH09010 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #93.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1235
ID ADH85309 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1236
ID ADH24585 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1237
ID ADH37441 standard; cDNA; 485 BP.
DE Human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1238
ID ADH02030 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #22.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1239
ID ADH37611 standard; cDNA; 485 BP.
DE Human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1240
ID ADH85649 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1241
ID ADH24245 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1242
ID ADH38539 standard; cDNA; 485 BP.

DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1243
ID ADH83660 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #22.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1244
ID ADH29468 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1245
ID ADH27584 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1246
ID ADH37781 standard; cDNA; 485 BP.
DE Human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1247
ID ADH37958 standard; cDNA; 485 BP.
DE Human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1248
ID ADH57378 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1249
ID ADH53520 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1250
ID ADH53690 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1251
ID ADH52026 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.

PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1252
ID ADH99918 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1253
ID ADI25391 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1254
ID ADH90184 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1255
ID ADI25561 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1256
ID ADH97735 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1257
ID ADI35426 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #68.
PN US2003050457-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1258
ID ADI03583 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1259
ID ADI11940 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #22.
PN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1260
ID ADH90014 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181697-A1.
PD 25-SEP-2003.

PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1261
ID ADH99918 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003049682-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1262
ID ADH98415 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1263
ID ADI11090 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #22.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1264
ID ADI11600 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #22.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1265
ID ADH98245 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1266
ID ADH98585 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1267
ID ADH98075 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 10; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1268
ID ABX78620 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #93.
PN US2003027272-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1269
ID ACA75592 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003032127-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1270

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ID ACA71072 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003032112-A1.
PD 13-FEB-2003.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1271
ID ACC87600 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003027278-A1.
PD 06-FEB-2003.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1272
ID ACC86986 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003036159-A1.
PD 20-FEB-2003.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1273
ID ACD04159 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003040070-A1.
PD 27-FEB-2003.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1274
ID ABX77871 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #68.
PN US2003027163-A1.
PD 06-FEB-2003.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1275
ID ABX80283 standard; DNA; 485 BP.
DE Novel human secreted or transmembrane protein PRO1108 DNA.
PN US2002132252-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1276
ID ACA69189 standard; cDNA; 485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1003.
PN US2003032023-A1.
PD 13-FEB-2003.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1277
ID ACA69490 standard; cDNA; 485 BP.
DE cDNA encoding human PRO polypeptide #93.
PN US2003032113-A1.
PD 13-FEB-2003.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1278
ID ACA90335 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003036147-A1.
PD 20-FEB-2003.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1279
ID ACC89442 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1280
ID ABX90260 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein cDNA, #97.

PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1281
ID ACA98233 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1282
ID ACA93875 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1283
ID ACD15268 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1284
ID ACD08855 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1285
ID ACC96775 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1286
ID ACF15496 standard; cDNA; 485 BP.
DE Human secreted polypeptide PRO1003-encoding cDNA, SEQ ID NO:185.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1287
ID ABX64106 standard; cDNA; 485 BP.
DE cDNA encoding human PRO1003 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1288
ID ACA72863 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #93.
PN US2003036140-A1.
PD 20-FEB-2003.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1289
ID ACD03035 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003031353-A1.
PD 16-JAN-2003.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1290
ID ACD01850 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.

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PN US2003017544-A1.
Query Match
Best Local Similarity 2.6%; Score 58; DB 10; Length 485;
ID ADH97905 standard; cDNA; 485 BP.
RESULT 1291
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 2.6%; Score 58; DB 10; Length 485;
ID ADI05063 standard; cDNA; 485 BP.
RESULT 1292
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.6%; Score 58; DB 10; Length 485;
ID ADI03413 standard; cDNA; 485 BP.
RESULT 1293
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181654-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.6%; Score 58; DB 10; Length 485;
ID ADI04808 standard; cDNA; 485 BP.
RESULT 1294
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.6%; Score 58; DB 10; Length 485;
ID ADH78262 standard; cDNA; 485 BP.
RESULT 1295
DE Human PRO polynucleotide #22.
PN US2003181658-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.6%; Score 58; DB 10; Length 485;
ID ADI19606 standard; cDNA; 485 BP.
RESULT 1296
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.6%; Score 58; DB 10; Length 485;
ID ADH90354 standard; cDNA; 485 BP.
RESULT 1297
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.6%; Score 58; DB 10; Length 485;
ID ADI03073 standard; cDNA; 485 BP.
RESULT 1298
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.6%; Score 58; DB 10; Length 485;
ID ADH77922 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #22.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.6%; Score 58; DB 10; Length 485;
ID ADH79479 standard; cDNA; 485 BP.
RESULT 1308
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.6%; Score 58; DB 10; Length 485;
ID ADI05407 standard; cDNA; 485 BP.
RESULT 1307
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.6%; Score 58; DB 10; Length 485;
ID ADI11770 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #22.
PN US2003181685-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.6%; Score 58; DB 10; Length 485;
ID ADI02332 standard; cDNA; 485 BP.
RESULT 1305
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181650-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.6%; Score 58; DB 10; Length 485;
ID ADI11430 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #22.
PN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.6%; Score 58; DB 10; Length 485;
ID ADI03243 standard; cDNA; 485 BP.
RESULT 1303
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.6%; Score 58; DB 10; Length 485;
ID ADI01985 standard; cDNA; 485 BP.
RESULT 1302
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181652-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.6%; Score 58; DB 10; Length 485;
ID ADI01290 standard; cDNA; 485 BP.
RESULT 1301
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.6%; Score 58; DB 10; Length 485;
ID ADH97905 standard; cDNA; 485 BP.
RESULT 1300
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.6%; Score 58; DB 10; Length 485;
ID ADH97905 standard; cDNA; 485 BP.
RESULT 1300
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1309
ID ADI19436 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1310
ID ADI05237 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1311
ID ADH79649 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1312
ID ADI01475 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1313
ID ADI01645 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1314
ID ADI01815 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1315
ID ADH79819 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003191289-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1316
ID ADI04637 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1317
ID ADI02773 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181651-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1318
ID ADH78092 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #22.
PN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1319
ID ADI25731 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1320
ID ADI25901 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1321
ID ADK65413 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003073821-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1322
ID ADH98755 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1323
ID ADH79996 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 58; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1324
ID ADL32791 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 58; DB 11; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1325
ID ADM30325 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 58; DB 11; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1326
ID ADL93727 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 58; DB 11; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1327
ID ADL93727 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 58; DB 11; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;

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ID ADC52181 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003130483-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1328
ID ADE74322 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003211572-A1.
PD 13-NOV-2003.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1329
ID ADE74934 standard; cDNA; 485 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #93.
PN US2003211574-A1.
PD 13-NOV-2003.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1330
ID ADF35371 standard; cDNA; 485 BP.
DE cDNA encoding human PRO1003 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1331
ID ADG11621 standard; cDNA; 485 BP.
DE cDNA encoding human PRO1003 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1332
ID ADF96147 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003215909-A1.
PD 20-NOV-2003.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1333
ID ADG04418 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1334
ID ADG00578 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1335
ID ADH06613 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180852-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1336
ID ADH06443 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180853-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1337
ID ADG68864 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180855-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1338
ID ADH27754 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180912-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1339
ID ADH25095 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1340
ID ADH33727 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #22.
PN US2003181645-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1341
ID ADG82834 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #93.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1342
ID ADH02370 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #22.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1343
ID ADH07977 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1344
ID ADG69374 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1345
ID ADH39195 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1346
ID ADH39195 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180853-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

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Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1346
ID ADH26115 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1347
ID ADG83935 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #22.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1348
ID ADH19491 standard; cDNA; 485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1003.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1349
ID ADG85479 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003166848-A1.
PD 04-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1350
ID ADH06273 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1351
ID ADH30103 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1352
ID ADH24415 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1353
ID ADH33084 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #93.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1354
ID ADG69544 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1355
ID ADH07807 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1356
ID ADG85819 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1357
ID ADH39365 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1358
ID ADH33557 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #22.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1359
ID ADH33897 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #22.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1360
ID ADH01107 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #22.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1361
ID ADG69714 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1362
ID ADH20984 standard; cDNA; 485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1003.
PN US2003224358-A1.
PD 04-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1363
ID ADH02200 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #22.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1364
ID ADG69204 standard; cDNA; 485 BP.
```

DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
Query Match
RESULT 1365
ID ADG85989 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
Query Match
RESULT 1366
ID ADH24925 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
Query Match
RESULT 1367
ID ADH39542 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
Query Match
RESULT 1368
ID ADH20024 standard; cDNA; 485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1003.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
Query Match
RESULT 1369
ID ADH02540 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #22.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
Query Match
RESULT 1370
ID ADG69034 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
Query Match
RESULT 1371
ID ADH07637 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
Query Match
RESULT 1372
ID ADG86159 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
Query Match
RESULT 1373
ID ADH24755 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.

PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
Query Match
RESULT 1374
ID ADH25803 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
Query Match
RESULT 1375
ID ADH38369 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
Query Match
RESULT 1376
ID ADH57208 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
Query Match
RESULT 1377
ID ADH52196 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
Query Match
RESULT 1378
ID ADH49562 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
Query Match
RESULT 1379
ID ADH90524 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
Query Match
RESULT 1380
ID ADI11260 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #22.
PN US2003181683-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
Query Match
RESULT 1381
ID ADH98925 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003190698-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3e-10;
Query Match
RESULT 1382
ID ADI02155 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003190699-A1.

PD 09-OCT-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1383
ID ADK00928 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #22.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1393
ID ADK14449 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1394
ID ADJ64594 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #93.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1395
ID ADM31490 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1396
ID ADM36537 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1397
ID ADM40342 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1398
ID ADM80898 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #22.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1399
ID ADN37950 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1400
ID ABEV57059 standard; cDNA; 490 BP.
DE Human prostate expression marker cDNA 57050.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

PD 09-OCT-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1384
ID ADH90694 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1385
ID ADJ54823 standard; cDNA; 485 BP.
DE Human PRO polynucleotide #93.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1386
ID ADJ98739 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1387
ID ADH78898 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1388
ID ADJ99132 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1389
ID ADJ99302 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1390
ID ADJ98920 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 12; Length 485;
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 1391
ID ADH79068 standard; cDNA; 485 BP.
DE Novel human secreted and transmembrane protein PRO1003 cDNA.
PN US2003181702-A1.
PD 25-SEP-2003.

Query Match 2.6%; Score 58; DB 5; Length 490;
 Best Local Similarity 100.0%; Pred. No. 3e-10;
 RESULT 1401
 ID AAV58672 standard; cDNA; 509 BP.
 DE Prostate tumour specific gene clone 1D-4288.
 PN WO9837418-A2.
 PD 27-AUG-1998.
 PA (CORI-) CORIXA CORP.
 Query Match 2.6%; Score 58; DB 2; Length 509;
 Best Local Similarity 100.0%; Pred. No. 3e-10;
 RESULT 1402
 ID AAV61342 standard; cDNA; 509 BP.
 DE Extended cDNA sequence of prostate tumour clone 1D-4288.
 PN WO9837093-A2.
 PD 27-AUG-1998.
 PA (CORI-) CORIXA CORP.
 Query Match 2.6%; Score 58; DB 2; Length 509;
 Best Local Similarity 100.0%; Pred. No. 3e-10;
 RESULT 1403
 ID AAA06435 standard; cDNA; 509 BP.
 DE Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:202.
 PN WO200004149-A2.
 PD 27-JAN-2000.
 PA (CORI-) CORIXA CORP.
 Query Match 2.6%; Score 58; DB 3; Length 509;
 Best Local Similarity 100.0%; Pred. No. 3e-10;
 RESULT 1404
 ID ABS71340 standard; cDNA; 509 BP.
 DE Human prostate tumour protein partial DNA sequence #188.
 PN US2002090372-A1.
 PD 11-JUL-2002.
 PA (XUJJ/) XU J.
 PA (DILL/) DILLON D C.
 Query Match 2.6%; Score 58; DB 3; Length 509;
 Best Local Similarity 100.0%; Pred. No. 3e-10;
 RESULT 1405
 ID AAH93551 standard; cDNA; 509 BP.
 DE Human prostate-specific extended cDNA sequence 1D-4288.
 PN WO200151633-A2.
 PD 19-JUL-2001.
 PA (CORI-) CORIXA CORP.
 Query Match 2.6%; Score 58; DB 4; Length 509;
 Best Local Similarity 100.0%; Pred. No. 3e-10;
 RESULT 1406
 ID AAS63643 standard; cDNA; 509 BP.
 DE Human prostate cDNA sequence #195.
 PN WO200173032-A2.
 PD 04-OCT-2001.
 PA (CORI-) CORIXA CORP.
 Query Match 2.6%; Score 58; DB 4; Length 509;
 Best Local Similarity 100.0%; Pred. No. 3e-10;
 RESULT 1407
 ID AAH02616 standard; cDNA; 509 BP.
 DE Prostate tumour antigen determined extended cDNA for 1D-4288.
 PN WO200125272-A2.
 PD 12-APR-2001.
 PA (CORI-) CORIXA CORP.
 Query Match 2.6%; Score 58; DB 4; Length 509;
 Best Local Similarity 100.0%; Pred. No. 3e-10;
 RESULT 1408
 ID AAH84865 standard; cDNA; 509 BP.
 DE Human prostate-specific extended cDNA sequence 1D-4288.
 PN WO200134802-A2.
 PD 17-MAY-2001.
 PA (CORI-) CORIXA CORP.
 Query Match 2.6%; Score 58; DB 4; Length 509;
 Best Local Similarity 100.0%; Pred. No. 3e-10;
 RESULT 1409
 ID ACA59452 standard; cDNA; 509 BP.
 DE Prostate cancer therapy associated cDNA #195.
 PN US2002192763-A1.
 PD 19-DEC-2002.
 PA (XUJJ/) XU J.

(DILL/) DILLON D C.
 PA (MITC/) MITCHAM J L.
 PA (HARL/) HARLOCKER S L.
 PA (JIAN/) JIANG Y.
 PA (KALO/) KALOS M D.
 PA (FANG/) FANGER G R.
 PA (RETT/) RETTER M W.
 PA (STOL/) STOLK J A.
 PA (DAYC/) DAY C H.
 PA (VEDV/) VEDVICK T S.
 PA (CART/) CARTER D.
 PA (LISX/) LI S X.
 PA (WANG/) WANG A.
 PA (SKEI/) SKEIKY Y A W.
 PA (HEPL/) HEPLER W T.
 PA (HEND/) HENDERSON R A.
 PA (HURA/) HURAL J.
 PA (MCNE/) MCNEILL P D.
 PA (HOUG/) HOUGHTON R L.
 PA (DBAS/) Y DE BASSOLS C V.
 PA (FOYT/) FOY T M.
 Query Match 2.6%; Score 58; DB 5; Length 509;
 Best Local Similarity 100.0%; Pred. No. 3e-10;
 RESULT 1410
 ID AAS10194 standard; cDNA; 509 BP.
 DE Human prostate tumour cDNA 1D-4288 #2.
 PN US262245-B1.
 PD 17-JUL-2001.
 PA (CORI-) CORIXA CORP.
 Query Match 2.6%; Score 58; DB 5; Length 509;
 Best Local Similarity 100.0%; Pred. No. 3e-10;
 RESULT 1411
 ID ABL95015 standard; cDNA; 509 BP.
 DE Human 1D-4288 cDNA sequence SEQ ID NO 202.
 PN US200202248-A1.
 PD 21-FEB-2002.
 PA (XUJJ/) XU J.
 PA (DILL/) DILLON D C.
 PA (MITC/) MITCHAM J L.
 PA (HARL/) HARLOCKER S L.
 PA (JIAN/) JIANG Y.
 PA (KALO/) KALOS M D.
 PA (FANG/) FANGER G R.
 PA (RETT/) RETTER M W.
 PA (STOL/) STOLK J A.
 PA (DAYC/) DAY C H.
 PA (VEDV/) VEDVICK T S.
 PA (CART/) CARTER D.
 PA (LISX/) LI S X.
 PA (WANG/) WANG A.
 PA (SKEI/) SKEIKY Y A W.
 PA (HEPL/) HEPLER W T.
 PA (HEND/) HENDERSON R A.
 Query Match 2.6%; Score 58; DB 6; Length 509;
 Best Local Similarity 100.0%; Pred. No. 3e-10;
 RESULT 1412
 ID ABS8724 standard; cDNA; 509 BP.
 DE Prostate tumour cDNA #195.
 PN US2002081580-A1.
 PD 27-JUN-2002.
 PA (XUJJ/) XU J.
 PA (DILL/) DILLON D C.
 Query Match 2.6%; Score 58; DB 6; Length 509;
 Best Local Similarity 100.0%; Pred. No. 3e-10;
 RESULT 1413
 ID ACC95179 standard; cDNA; 509 BP.
 DE Prostate tumour specific cDNA sequence SEQ ID 202.
 PN WO200289747-A2.
 PD 14-NOV-2002.
 PA (CORI-) CORIXA CORP.
 Query Match 2.6%; Score 58; DB 8; Length 509;
 Best Local Similarity 100.0%; Pred. No. 3e-10;
 RESULT 1414

ID ADB13652 standard; cDNA; 509 BP.
 DE Human prostate specific extended cDNA 1D-4288.
 PN US2003185830-A1.
 PD 02-OCT-2003.
 PA (CORI-) CORIXA CORP.
 Query Match 2.6%; Score 58; DB 10; Length 509;
 Best Local Similarity 100.0%; Pred. No. 3e-10;
 RESULT 1415
 ID ADG26068 standard; cDNA; 509 BP.
 DE Human prostate-specific cDNA #195.
 PN US2003157089-A1.
 PD 10-JUN-2004.
 PA (CORI-) CORIXA CORP.
 Query Match 2.6%; Score 58; DB 10; Length 509;
 Best Local Similarity 100.0%; Pred. No. 3e-10;
 RESULT 1416
 ID ADQ21075 standard; DNA; 513 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 3895.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 2.6%; Score 58; DB 12; Length 513;
 Best Local Similarity 100.0%; Pred. No. 3e-10;
 RESULT 1417
 ID AAK63327 standard; cDNA; 519 BP.
 DE Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:8387.
 PN WO2001571182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.6%; Score 58; DB 4; Length 519;
 Best Local Similarity 100.0%; Pred. No. 3e-10;
 RESULT 1418
 ID AAS29134 standard; cDNA; 519 BP.
 DE cDNA encoding for human DNA-binding protein #105.
 PN WO200155162-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.6%; Score 58; DB 5; Length 519;
 Best Local Similarity 100.0%; Pred. No. 3e-10;
 RESULT 1419
 ID ABS68274 standard; cDNA; 519 BP.
 DE cDNA encoding human DNA-binding protein #105.
 PN US2002102638-A1.
 PD 01-AUG-2002.
 PA (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 PA (BARA/) BARASH S C.
 Query Match 2.6%; Score 58; DB 6; Length 519;
 Best Local Similarity 100.0%; Pred. No. 3e-10;
 RESULT 1420
 ID ADC25268 standard; cDNA; 519 BP.
 DE Human cDNA from extracellular matrix gene 105.
 PN US2003049650-A1.
 PD 13-MAR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.6%; Score 58; DB 10; Length 519;
 Best Local Similarity 100.0%; Pred. No. 3e-10;
 RESULT 1421
 ID ABV59169 standard; cDNA; 530 BP.
 DE Human prostate expression marker cDNA 59160.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 2.6%; Score 58; DB 5; Length 530;
 Best Local Similarity 100.0%; Pred. No. 2.9e-10;
 RESULT 1422
 ID ABV54230 standard; cDNA; 540 BP.
 DE Human prostate expression marker cDNA 54221.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 2.6%; Score 58; DB 5; Length 540;
 Best Local Similarity 100.0%; Pred. No. 2.9e-10;

RESULT 1423
 ID ACH43937 standard; cDNA; 550 BP.
 DE Human foetal brain cDNA #4662.
 PN US2003073623-A1.
 PD 17-APR-2003.
 PA (DRMA/) DRMANAC R T.
 PA (LABA/) LABAT I.
 PA (STAC/) STACHE-CRAIN B.
 PA (DICK/) DICKSON M C.
 PA (JONE/) JONES L W.
 Query Match 2.6%; Score 58; DB 9; Length 550;
 Best Local Similarity 100.0%; Pred. No. 2.9e-10;
 RESULT 1424
 ID ABX57018 standard; DNA; 564 BP.
 DE Arabidopsis thaliana polynucleotide #370.
 PN US2002040489-A1.
 PD 04-APR-2002.
 PA (GORL/) GORLACH J.
 PA (ANYV/) AN Y.
 PA (HAMI/) HAMILTON C M.
 PA (PRIC/) PRICE J L.
 PA (RAIN/) RAINES T M.
 PA (YUYI/) YU Y.
 PA (RAME/) RAMEAKA J G.
 PA (PAGE/) PAGE A.
 PA (MATH/) MATHEW A V.
 PA (LEDF/) LEDFORD B L.
 PA (WOES/) WOESSNER J P.
 PA (HAAS/) HAAS W D.
 PA (GARC/) GARCIA C A.
 PA (KRIC/) KRICKER M.
 PA (SLAT/) SLATER T.
 PA (DAVI/) DAVIS K R.
 PA (ALLE/) ALLEN K.
 PA (HOFF/) HOFFMAN N.
 PA (HURB/) HURBAN P.
 Query Match 2.6%; Score 58; DB 10; Length 564;
 Best Local Similarity 100.0%; Pred. No. 2.9e-10;
 RESULT 1425
 ID AAZ97052 standard; cDNA; 569 BP.
 DE Human secreted protein gene 34 cDNA clone HCHPF68, SEQ ID NO:44.
 PN WO9966041-A1.
 PD 23-DEC-1999.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.6%; Score 58; DB 3; Length 569;
 Best Local Similarity 100.0%; Pred. No. 2.9e-10;
 RESULT 1426
 ID ACH66681 standard; cDNA; 569 BP.
 DE Novel human secreted protein #34 cDNA.
 PN US2003065151-A1.
 PD 03-APR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.6%; Score 58; DB 9; Length 569;
 Best Local Similarity 100.0%; Pred. No. 2.9e-10;
 RESULT 1427
 ID ADP12881 standard; DNA; 575 BP.
 DE Reference mRNA sequence #95.
 PN WO2004042346-A2.
 PD 21-MAY-2004.
 PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
 Query Match 2.6%; Score 58; DB 12; Length 575;
 Best Local Similarity 100.0%; Pred. No. 2.9e-10;
 RESULT 1428
 ID ABL86809 standard; cDNA; 581 BP.
 DE Human ovarian cancer related cDNA clone SEQ ID NO:9787.
 PN WO200192581-A2.
 PD 06-DEC-2001.
 PA (CORI-) CORIXA CORP.
 Query Match 2.6%; Score 58; DB 6; Length 581;
 Best Local Similarity 100.0%; Pred. No. 2.9e-10;
 RESULT 1429
 ID ABV56190 standard; cDNA; 585 BP.
 DE Human prostate expression marker cDNA 56181.

PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 58; DB 5; Length 585;
Best Local Similarity 100.0%; Pred. No. 2.9e-10;
RESULT 1430
ID ABK5402 standard; cDNA; 586 BP.
DE Human colon cancer-associated cDNA, SEQ ID NO 872.
PN WO200212280-A2.
PD 14-FEB-2002.
PA (CORI-) CORIXA CORP.
Query Match 2.6%; Score 58; DB 6; Length 586;
Best Local Similarity 100.0%; Pred. No. 2.9e-10;
RESULT 1431
ID AAV84464 standard; DNA; 588 BP.
DE Human secreted protein gene 54 clone HE2AY71.
PN WO9854963-A2.
PD 10-DEC-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 58; DB 2; Length 588;
Best Local Similarity 100.0%; Pred. No. 2.9e-10;
RESULT 1432
ID ABA83247 standard; cDNA; 588 BP.
DE Human secreted protein gene 54 SEQ ID NO:64.
PN WO200162891-A2.
PD 30-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 58; DB 4; Length 588;
Best Local Similarity 100.0%; Pred. No. 2.9e-10;
RESULT 1433
ID ACH04748 standard; cDNA; 588 BP.
DE Novel human secreted protein #54 cDNA.
PN US2003065160-A1.
PD 03-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 58; DB 9; Length 588;
Best Local Similarity 100.0%; Pred. No. 2.9e-10;
RESULT 1434
ID ACD44558 standard; cDNA; 588 BP.
DE Human cDNA from novel secreted protein gene 54.
PN US6525174-B1.
PD 25-FEB-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 58; DB 9; Length 588;
Best Local Similarity 100.0%; Pred. No. 2.9e-10;
RESULT 1435
ID AAS25987 standard; cDNA; 600 BP.
DE Human cDNA encoding a novel secreted protein, Seq ID 166.
PN WO200153322-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 58; DB 4; Length 600;
Best Local Similarity 100.0%; Pred. No. 2.9e-10;
RESULT 1436
ID ABX73328 standard; DNA; 600 BP.
DE Human novel polynucleotide #156.
PN US2002132753-A1.
PD 19-SEP-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 2.6%; Score 58; DB 8; Length 600;
Best Local Similarity 100.0%; Pred. No. 2.9e-10;
RESULT 1437
ID AAC59787 standard; cDNA; 604 BP.
DE Human secreted protein gene 50 SEQ ID NO:60.
PN WO200056751-A1.
PD 28-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 58; DB 3; Length 604;
Best Local Similarity 100.0%; Pred. No. 2.9e-10;
RESULT 1438
ID ABV43916 standard; cDNA; 606 BP.

DE Human prostate expression marker cDNA 43907.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 58; DB 5; Length 606;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1439
ID ABV35070 standard; cDNA; 609 BP.
DE Human prostate expression marker cDNA 35061.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 58; DB 5; Length 609;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1440
ID AAZ06238 standard; DNA; 620 BP.
DE Human secreted protein gene No. 20.
PN WO9935158-A1.
PD 15-JUL-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 58; DB 2; Length 620;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1441
ID AAQ75445 standard; DNA; 635 BP.
DE Murine glycosylation inhibition factor (GIF).
PN WO9426923-A1.
PD 24-NOV-1994.
PA (LJOL-) LA JOLLA INST ALLERGY & IMMUNOLOGY.
PA (KIRI) KIRIN BEER KK.
Query Match 2.6%; Score 58; DB 2; Length 635;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1442
ID AAT38390 standard; cDNA; 635 BP.
DE Murine glycosylation inhibiting factor cDNA.
PN WO9631617-A1.
PD 10-OCT-1996.
PA (LJOL-) LA JOLLA INST ALLERGY & IMMUNOLOGY.
Query Match 2.6%; Score 58; DB 2; Length 635;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1443
ID AAA60768 standard; cDNA; 638 BP.
DE Pig SENS ligand nucleotide sequence SEQ ID NO:15.
PN WO200032627-A1.
PD 08-JUN-2000.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 2.6%; Score 58; DB 3; Length 638;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1444
ID ABK50021 standard; cDNA; 638 BP.
DE Pig sensory epithelium neurotrophin-like receptor (SENR) cDNA #1.
PN WO200214513-A1.
PD 21-FEB-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 2.6%; Score 58; DB 6; Length 638;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1445
ID AAK30410 standard; DNA; 687 BP.
DE DNA encoding a human secreted protein.
PN WO9907891-A1.
PD 18-FEB-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 58; DB 2; Length 687;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1446
ID ADB47824 standard; cDNA; 687 BP.
DE Novel human secreted protein cDNA #97.
PN US2003054443-A1.
PD 20-MAR-2003.
PA (RUBE/) RUBEN S M.
PA (SOPP/) SOPPET D R.
PA (EBNE/) EBNER R.
PA (OLSE/) OLSEN H S.
PA (YOUN/) YOUNG P E.

PA (GREG/) GREENE J M.
 PA (FERR/) FERRIE A M.
 PA (YUGG/) YU G.
 PA (NIJU/) NI J.
 PA (ROSE/) ROSEN C A.
 PA (BREW/) BREWER L A.
 PA (JANA/) JANAT F.
 PA (BIRS/) BIRSE C E.
 Query Match 2.6%; Score 58; DB 10; Length 687;
 Best Local Similarity 100.0%; Pred. No. 2.8e-10;
 RESULT 1447
 ID ADJ5379 standard; cDNA; 687 BP.
 DE Novel human secreted protein cDNA #97.
 PN US2004023283-A1.
 PD 05-FEB-2004.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.6%; Score 58; DB 12; Length 687;
 Best Local Similarity 100.0%; Pred. No. 2.8e-10;
 RESULT 1448
 ID AAT16856 standard; cDNA; 688 BP.
 DE Integrin subunit beta-3' cytoplasmic domain cDNA.
 PN US5498694-A.
 PD 12-MAR-1996.
 PA (LJOL-) LA JOLLA CANCER RES FOUND.
 Query Match 2.6%; Score 58; DB 2; Length 688;
 Best Local Similarity 100.0%; Pred. No. 2.8e-10;
 RESULT 1449
 ID AAK89424 standard; cDNA; 689 BP.
 DE Human digestive system antigen coding sequence SEQ ID NO: 740.
 PN WO200155314-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.6%; Score 58; DB 4; Length 689;
 Best Local Similarity 100.0%; Pred. No. 2.8e-10;
 RESULT 1450
 ID AAS39525 standard; cDNA; 689 BP.
 DE cDNA encoding novel human colon associated polypeptide #178.
 PN WO200155302-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.6%; Score 58; DB 5; Length 689;
 Best Local Similarity 100.0%; Pred. No. 2.8e-10;
 RESULT 1451
 ID ADB32251 standard; cDNA; 689 BP.
 DE Human novel colon related polypeptide cDNA SEQ ID NO 188.
 PN US2003050231-A1.
 PD 13-MAR-2003.
 PA (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 PA (BARA/) BARASH S C.
 Query Match 2.6%; Score 58; DB 9; Length 689;
 Best Local Similarity 100.0%; Pred. No. 2.8e-10;
 RESULT 1452
 ID AAA77669 standard; cDNA; 693 BP.
 DE Human PRO1286 cDNA sequence SEQ ID NO:198.
 PN WO200032221-A2.
 PD 08-JUN-2000.
 PA (GETH) GENENTECH INC.
 Query Match 2.6%; Score 58; DB 3; Length 693;
 Best Local Similarity 100.0%; Pred. No. 2.8e-10;
 RESULT 1453
 ID AAA37065 standard; cDNA; 693 BP.
 DE Human PRO1286 (UNQ655) cDNA sequence SEQ ID NO:143.
 PN WO200012708-A2.
 PD 09-MAR-2000.
 PA (GETH) GENENTECH INC.
 Query Match 2.6%; Score 58; DB 3; Length 693;
 Best Local Similarity 100.0%; Pred. No. 2.8e-10;
 RESULT 1454
 ID AAF54301 standard; DNA; 693 BP.
 DE DNA encoding protein of the invention #44.
 PN WO200078961-A1.
 PD 28-DEC-2000.

PA (GETH) GENENTECH INC.
 Query Match 2.6%; Score 58; DB 4; Length 693;
 Best Local Similarity 100.0%; Pred. No. 2.8e-10;
 RESULT 1455
 ID AAC91565 standard; cDNA; 693 BP.
 DE Human PRO1286 cDNA.
 PN WO200073348-A2.
 PD 07-DEC-2000.
 PA (GETH) GENENTECH INC.
 Query Match 2.6%; Score 58; DB 4; Length 693;
 Best Local Similarity 100.0%; Pred. No. 2.8e-10;
 RESULT 1456
 ID AAS21493 standard; cDNA; 693 BP.
 DE Human cDNA sequence encoding for PRO1286 polypeptide.
 PN WO200140466-A2.
 PD 07-JUN-2001.
 PA (GETH) GENENTECH INC.
 Query Match 2.6%; Score 58; DB 4; Length 693;
 Best Local Similarity 100.0%; Pred. No. 2.8e-10;
 RESULT 1457
 ID AAS15361 standard; cDNA; 693 BP.
 DE cDNA encoding human PRO1268 polypeptide.
 PN WO200166740-A2.
 PD 13-SEP-2001.
 PA (GETH) GENENTECH INC.
 Query Match 2.6%; Score 58; DB 4; Length 693;
 Best Local Similarity 100.0%; Pred. No. 2.8e-10;
 RESULT 1458
 ID ABK3623 standard; cDNA; 693 BP.
 DE cDNA encoding human PRO protein, Seq ID No 175.
 PN WO200208288-A2.
 PD 31-JAN-2002.
 PA (GETH) GENENTECH INC.
 Query Match 2.6%; Score 58; DB 6; Length 693;
 Best Local Similarity 100.0%; Pred. No. 2.8e-10;
 RESULT 1459
 ID ABL88171 standard; cDNA; 693 BP.
 DE Human PRO1286 cDNA sequence SEQ ID NO:199.
 PN WO200200690-A2.
 PD 03-JAN-2002.
 PA (GETH) GENENTECH INC.
 Query Match 2.6%; Score 58; DB 6; Length 693;
 Best Local Similarity 100.0%; Pred. No. 2.8e-10;
 RESULT 1460
 ID ABL95660 standard; cDNA; 693 BP.
 DE Human angiogenesis related cDNA PRO1286 SEQ ID NO: 199.
 PN WO200208284-A2.
 PD 31-JAN-2002.
 PA (GETH) GENENTECH INC.
 PA (BAKE/) BAKER K P.
 PA (FERR/) FERRARA N.
 PA (GERR/) GERBER H.
 PA (GERR/) GERRITSEN M E.
 PA (GODD/) GODDARD A.
 PA (GODO/) GODOWSKI P J.
 PA (GURN/) GURNEY A L.
 PA (HILL/) HILLAN K J.
 PA (MARS/) MARSTERS S A.
 PA (PANJ/) PAN J.
 PA (PAON/) PAONI N F.
 PA (STEP/) STEPHAN J F.
 PA (WATA/) WATANABE C K.
 PA (WILL/) WILLIAMS P M.
 PA (WOOD/) WOOD W I.
 Query Match 2.6%; Score 58; DB 6; Length 693;
 Best Local Similarity 100.0%; Pred. No. 2.8e-10;
 RESULT 1461
 ID ACA58002 standard; cDNA; 693 BP.
 DE cDNA encoding human neoplasia inhibiting PRO polypeptide PRO1286.
 PN US2002192209-A1.
 PD 19-DEC-2002.
 PA (GETH) GENENTECH INC.
 Query Match 2.6%; Score 58; DB 8; Length 693;

Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1462
ID ACA03852 standard; cDNA; 693 BP.
DE cDNA encoding human PRO polypeptide #250.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 693;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1463
ID ABX89390 standard; cDNA; 693 BP.
DE DNA encoding novel secreted and transmembrane protein PRO1286.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 693;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1464
ID ACDA2044 standard; cDNA; 693 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #250.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 693;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1465
ID ACA68584 standard; cDNA; 693 BP.
DE Novel human secreted and transmembrane protein PRO1286 cDNA.
PN US200308063-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 693;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1466
ID ACA04273 standard; cDNA; 693 BP.
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 499.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 8; Length 693;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1467
ID ADA46018 standard; cDNA; 693 BP.
DE Novel human secreted and transmembrane protein PRO1286 cDNA.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 693;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1468
ID ADA76449 standard; cDNA; 693 BP.
DE Human PRO polynucleotide #250.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 693;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1469
ID ABT44313 standard; cDNA; 693 BP.
DE Human PRO1286 cDNA.
PN US2003050448-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 693;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1470
ID ADA19099 standard; cDNA; 693 BP.
DE Human PRO polynucleotide #250.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 693;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;

RESULT 1471
ID ADA61722 standard; cDNA; 693 BP.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 693;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1472
ID ADB19507 standard; cDNA; 693 BP.
DE Novel human secreted and transmembrane protein PRO1286 cDNA.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 693;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1473
ID ADB28048 standard; cDNA; 693 BP.
DE cDNA encoding human PRO polypeptide #250.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 693;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1474
ID ADA86527 standard; cDNA; 693 BP.
DE Novel human secreted and transmembrane protein PRO1286 cDNA.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 693;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1475
ID ADB16091 standard; cDNA; 693 BP.
DE Human PRO polynucleotide #250.
PN US2003073215-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 693;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1476
ID ADA47877 standard; cDNA; 693 BP.
DE Human PRO polynucleotide #250.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 693;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1477
ID ACD68338 standard; cDNA; 693 BP.
DE Novel human secreted and transmembrane protein PRO1286 cDNA.
PN US2003073330-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 693;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1478
ID ADA67672 standard; cDNA; 693 BP.
DE Human PRO polynucleotide #250.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 693;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1479
ID ADB30679 standard; cDNA; 693 BP.
DE cDNA encoding human PRO polypeptide #250.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 693;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1480
ID ADB30679 standard; cDNA; 693 BP.
DE cDNA encoding human PRO polypeptide #250.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 58; DB 9; Length 693;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;

ID ADA95975 standard; cDNA; 693 BP.
DE Novel human secreted and transmembrane protein PRO1286 cDNA.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 693;
Query Match Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1481
ID ADA97187 standard; cDNA; 693 BP.
DE Human PRO polynucleotide #250.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 693;
Query Match Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1482
ID ADA79491 standard; cDNA; 693 BP.
DE Human PRO polynucleotide #250.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 693;
Query Match Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1483
ID ADA7630 standard; cDNA; 693 BP.
DE Novel human secreted and transmembrane protein PRO1286 cDNA.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 693;
Query Match Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1484
ID ADB16832 standard; cDNA; 693 BP.
DE Human PRO polynucleotide #250.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 693;
Query Match Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1485
ID ADA91924 standard; cDNA; 693 BP.
DE Novel human secreted and transmembrane protein PRO1286 cDNA.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 693;
Query Match Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1486
ID ADB14987 standard; cDNA; 693 BP.
DE Human PRO polynucleotide #250.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 693;
Query Match Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1487
ID ADB16948 standard; cDNA; 693 BP.
DE Novel human secreted and transmembrane protein PRO1286 cDNA.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 693;
Query Match Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1488
ID ADA94163 standard; cDNA; 693 BP.
DE Human PRO polynucleotide #250.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 693;
Query Match Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1489
ID ADB20059 standard; cDNA; 693 BP.

DE Novel human secreted and transmembrane protein PRO1286 cDNA.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 693;
Query Match Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1490
ID ADB13371 standard; cDNA; 693 BP.
DE Human PRO polynucleotide #250.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 693;
Query Match Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1491
ID ACD98673 standard; cDNA; 693 BP.
DE Novel human secreted and transmembrane protein PRO1286 cDNA.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 693;
Query Match Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1492
ID ADA74625 standard; cDNA; 693 BP.
DE Human PRO polynucleotide #250.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 693;
Query Match Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1493
ID ADB24858 standard; cDNA; 693 BP.
DE Human PRO polynucleotide SEQ ID NO 499.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 693;
Query Match Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1494
ID ADA82382 standard; cDNA; 693 BP.
DE Human PRO polynucleotide #250.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 693;
Query Match Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1495
ID ADA75345 standard; cDNA; 693 BP.
DE Human PRO polynucleotide #250.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 693;
Query Match Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1496
ID ADA85423 standard; cDNA; 693 BP.
DE Novel human secreted and transmembrane protein PRO1286 cDNA.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 693;
Query Match Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1497
ID ADA84871 standard; cDNA; 693 BP.
DE Novel human secreted and transmembrane protein PRO1286 cDNA.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 693;
Query Match Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1498
ID ADB30127 standard; cDNA; 693 BP.
DE cDNA encoding human PRO polypeptide #250.

PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 693;
Query Match
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1499
ID ADA80655 standard; cDNA; 693 BP.
DE Human PRO polynucleotide #250.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 693;
Query Match
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 1500
ID ADA75897 standard; cDNA; 693 BP.
DE Human PRO polynucleotide #250.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 58; DB 9; Length 693;
Query Match
Best Local Similarity 100.0%; Pred. No. 2.8e-10;

THIRTY EIGHT BLANK (USPTO)

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 1, 2005, 15:43:38 ; Search time 6337 Seconds
(without alignments)
12892.201 Million cell updates/sec

Title: US-10-036-342-56

Perfect score: 2242

Sequence: 1 gaatgaataacctcgagacc.....aaaaaaaaaaaaaaaaaaaaa 2242

Scoring table: OLIGO NUC

Gapop_60.0 , Gapext 60.0

Searched: 32822875 seqs, 18219865908 residues

Word size : 6

Total number of hits satisfying chosen parameters: 65638880

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1500 summaries

Database :

EST:*

1: gb_est1.*

2: gb_est2.*

3: gb_hcc.*

4: gb_est3.*

5: gb_est4.*

6: gb_est5.*

7: gb_est6.*

8: gb_gss1.*

9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1901	84.8	2105	3	CR610360 full-length
2	1425	63.6	1528	3	BC004271 Homo sapi
3	688	30.7	913	5	EX453730 BX453730
4	687	30.6	928	5	EX432016 BX432016
5	679	30.3	799	4	BI754224 BI754224
6	670	29.9	1006	5	EX422768 BX422768
7	625	27.9	730	4	BI667149 BI667149
8	592	26.4	674	4	BI598229 BI598229
9	577	25.7	602	4	BM691429 BM691429
10	577	25.7	772	4	BI489508 BI489508
11	576	25.7	742	1	AI933620 AI933620
12	570	25.4	630	4	BM669584 BI669584
13	567	25.3	567	5	BI110726 BI110726
14	563	25.1	887	4	BI600248 BI600248
15	553	24.7	748	4	BI597871 BI597871
16	548	24.4	666	4	BI604126 BI604126
17	548	24.4	675	4	BI201754 BI201754
18	542	24.2	684	4	BI202368 BI202368
19	535	23.9	710	2	BI386438 BI386438
20	529	23.6	807	4	BI708811 BI708811
21	523	23.3	632	2	AW300620 AW300620
22	517	23.1	600	1	AI589129 AI589129
23	501	22.3	882	4	BI489822 BI489822
24	485	21.6	668	1	AI480056 AI480056

25	480	21.4	593	5	EX094414
26	475	21.2	770	1	BI549771
27	468	20.9	519	1	AI911546
28	454	20.2	454	1	AI361251
29	454	20.2	580	2	AW961851
30	448	20.0	684	4	BI821574
31	439	19.6	763	4	BI600841
32	435	19.4	630	2	BE386547
33	430	19.2	581	2	BF920454
34	428	19.1	428	1	AV725146
35	428	19.1	633	2	AW300615
36	424	18.9	804	4	BI545916
37	413	18.4	550	4	BM662490
38	398	17.8	884	4	EG715910
39	397	17.7	720	4	BI604230
40	390	17.4	959	4	BI550988
41	382	17.0	1107	5	EX422767
42	381	17.0	1054	4	BM920701
43	377	16.8	420	5	EX508591
44	368	16.4	967	4	BI597577
45	367	16.4	450	1	AI498527
46	366	16.3	438	4	BM698797
47	361	16.1	590	5	EX642327
48	351	15.7	932	4	BI600150
49	327	14.6	842	4	BI667377
50	324	14.5	426	2	AW901919
51	299	13.3	806	4	EG705917
52	286	12.8	350	4	BI040121
53	274	12.2	755	2	BE967591
54	270	12.0	908	1	AV726263
55	265	11.8	806	4	EG705311
56	262	11.7	435	7	H41544
57	256	11.4	775	4	BI598812
58	239	10.7	543	4	BI186833
59	233	10.4	233	1	AI422476
60	201	9.0	753	4	BI490686
61	198	8.8	658	4	BI667905
62	197	8.8	424	8	AQ172837
63	183	8.2	491	4	BI667376
64	180	8.0	231	1	AA348503
65	169	7.5	220	1	AA912288
66	151	6.7	884	5	EQ434981
67	136	6.1	144	5	BQ338465
68	128	5.7	846	4	EG705992
69	116	5.2	527	7	CR556283
70	116	5.2	568	4	BI489676
71	110	4.9	112	5	EQ338471
72	106	4.7	648	7	CO048865
73	106	4.7	968	7	CN802889
74	98	4.4	98	1	AI423129
75	95	4.2	153	8	BM608638
76	89	4.0	89	8	BM608637
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80	70	3.1	349	1	AA326679
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92	61	2.7	180	6	CB011938
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99	61	2.7	222	7	CO180267	CO180267	EC01329.5	C 172	61	2.7	816	5	BUS564811	BUS564811	AGENCYCOURT
100	61	2.7	223	4	BM561325	BM561325	AGENCYCOURT	C 173	61	2.7	818	2	BE964743	BE964743	AGENCYCOURT
101	61	2.7	225	1	AA597154	AA597154	VO35903.f	C 174	61	2.7	824	7	CNI57645	CNI57645	946385 MA
C 102	61	2.7	244	6	CB972639	CB972639	CAB30001	C 175	61	2.7	843	7	CK194951	CK194951	FGAS00338
C 103	61	2.7	250	6	CD671248	CD671248	FG02F02.x	C 176	61	2.7	865	7	CK396515	CK396515	AGENCYCOURT
104	61	2.7	255	7	CO194180	CO194180	EC37566.5	C 177	61	2.7	876	5	BUS534311	BUS534311	AGENCYCOURT
105	61	2.7	274	5	BP432150	BP432150	BP432150	C 178	61	2.7	893	4	BI523117	BI523117	603175824
C 106	61	2.7	293	4	BI491319	BI491319	df07B02.w	C 179	61	2.7	909	3	CR707691	CR707691	Tetradon
C 107	61	2.7	294	6	CB345423	CB345423	CA48EN000	C 180	61	2.7	909	7	CK195964	CK195964	FGAS00441
108	61	2.7	295	4	BG508371	BG508371	SAC95905.	C 181	61	2.7	946	7	CF580919	CF580919	AGENCYCOURT
C 109	61	2.7	298	2	AW60594	AW60594	EST372665	C 182	61	2.7	977	5	BQ926818	BQ926818	AGENCYCOURT
C 110	61	2.7	307	4	BM496458	BM496458	IPCGBR2.1	C 183	61	2.7	1041	6	CD051043	CD051043	AGENCYCOURT
C 111	61	2.7	307	6	CD809585	CD809585	250 LingU	C 184	61	2.7	1378	4	BI490467	BI490467	603032288
C 112	61	2.7	313	2	AW190242	AW190242	X160G08.x	C 185	61	2.7	4319	3	BC069040	BC069040	MUS muscu
C 113	61	2.7	317	2	AW021588	AW021588	df25F03.y	C 186	60	2.7	78	6	CF327666	CF327666	NACL--02-
C 114	61	2.7	319	2	AW170731	AW170731	X197G11.x	C 187	60	2.7	80	1	AA785747	AA785747	h1h02a1.f
C 115	61	2.7	322	1	AI613523	AI613523	tw22907.x	C 188	60	2.7	85	1	AI539707	AI539707	tp77B02.x
C 116	61	2.7	323	1	AI395113	AI395113	MA002449.	C 189	60	2.7	87	1	AI539781	AI539781	tp77f12.x
C 117	61	2.7	328	6	CF298861	CF298861	7LEAF--02	C 190	60	2.7	89	2	AW081383	AW081383	xc41F06.x
C 118	61	2.7	328	7	F36859	F36859	HSPD34763 H	C 191	60	2.7	98	6	CF315597	CF315597	HD--04-J0
C 119	61	2.7	335	1	AI285431	AI285431	QC83b11.x	C 192	60	2.7	101	1	AJ500653	AJ500653	AD500653
C 120	61	2.7	342	1	AV689723	AV689723	AV689723	C 193	60	2.7	101	7	CK119050	CK119050	214119.pl
C 121	61	2.7	350	7	CO256376	CO256376	WS0082.B2	C 194	60	2.7	102	4	BI496873	BI496873	df128h09.
C 122	61	2.7	355	7	CF804954	CF804954	1ad59b03.	C 195	60	2.7	105	2	BF572734	BF572734	602079377
C 123	61	2.7	356	2	AW105455	AW105455	xc53a01.x	C 196	60	2.7	106	6	CB075468	CB075468	hz46007.b
C 124	61	2.7	359	7	CO184089	CO184089	EC27086.5	C 197	60	2.7	107	1	AI589428	AI589428	tr75h03.x
C 125	61	2.7	361	5	BQ385855	BQ385855	NISC_mml4	C 198	60	2.7	109	6	CF215082	CF215082	CAST0001
C 126	61	2.7	363	4	BM554614	BM554614	AGENCYCOURT	C 199	60	2.7	111	7	CK191988	CK191988	213m18.pl
C 127	61	2.7	368	6	CA722301	CA722301	WGS1C.pk0	C 200	60	2.7	112	6	CD400416	CD400416	Gm ck2227
C 128	61	2.7	376	1	AI558302	AI558302	fb7d10.x	C 201	60	2.7	112	6	CF328795	CF328795	NACL--03-
C 129	61	2.7	376	1	AI647063	AI647063	ub74c11.x	C 202	60	2.7	114	2	AW191844	AW191844	x176b03.x
C 130	61	2.7	376	6	CB079487	CB079487	hp72a03.b	C 203	60	2.7	114	4	BI491270	BI491270	df06a01.w
C 131	61	2.7	378	1	AV681682	AV681682	AGENCYCOURT	C 204	60	2.7	114	6	CF214394	CF214394	CGF100081
C 132	61	2.7	383	7	CF520808	CF520808	AGENCYCOURT	C 205	60	2.7	115	6	CF311750	CF311750	ABF--07-C
C 133	61	2.7	387	1	AI697177	AI697177	tg06f04.x	C 206	60	2.7	116	4	BI491375	BI491375	df08a04.w
C 134	61	2.7	388	6	CF123150	CF123150	UI-HF-CHO	C 207	60	2.7	121	2	BE325423	BE325423	NF088G11S
C 135	61	2.7	391	1	AI887211	AI887211	wm37d11.x	C 208	60	2.7	127	7	CR558711	CR558711	DKF2p468D
C 136	61	2.7	394	1	AJ788571	AJ788571	AJ788571	C 209	60	2.7	129	1	AI345677	AI345677	tb78h05.x
C 137	61	2.7	403	2	BF191104	BF191104	237824 MA	C 210	60	2.7	134	4	BI015375	BI015375	MR4-ET024
C 138	61	2.7	405	6	CA852848	CA852848	E12F12.K1	C 211	60	2.7	137	7	CF667178	CF667178	RTCNTL.28
C 139	61	2.7	410	7	CF405497	CF405497	CSEC05054E	C 212	60	2.7	137	7	CNI56325	CNI56325	EST 18277
C 140	61	2.7	411	1	AT001678	AT001678	AT001678	C 213	60	2.7	138	1	AL836657	AL836657	AL836657
C 141	61	2.7	413	6	CB073120	CB073120	taa28e10.	C 214	60	2.7	139	1	AA123279	AA123279	mm23c05.r
C 142	61	2.7	415	1	AI361586	AI361586	gy48f10.x	C 215	60	2.7	139	2	BE907440	BE907440	601500177
C 143	61	2.7	426	6	CA722842	CA722842	WGS1C.pk0	C 216	60	2.7	139	6	CB973884	CB973884	CAB30003
C 144	61	2.7	431	7	CO191531	CO191531	EC31328.5	C 217	60	2.7	142	1	AI249877	AI249877	QX03604.x
C 145	61	2.7	432	7	CO191324	CO191324	EC30708.5	C 218	60	2.7	142	7	CK616330	CK616330	ou16e12.y
C 146	61	2.7	436	6	CD996103	CD996103	QBB9403.p	C 219	60	2.7	143	7	CNI56305	CNI56305	EST 18257
C 147	61	2.7	456	6	CB045766	CB045766	NISC_gc12	C 220	60	2.7	144	6	CF318389	CF318389	HD--08-H2
C 148	61	2.7	462	5	BQ524998	BQ524998	NISC_1n008	C 221	60	2.7	144	7	CK360784	CK360784	AGENCYCOURT
C 149	61	2.7	488	5	BQ395463	BQ395463	NISC_1g15	C 222	60	2.7	144	7	CNI272400	CNI272400	170006000
C 150	61	2.7	498	7	CO182279	CO182279	EC2369.5	C 223	60	2.7	147	6	CB977208	CB977208	CAB40003
C 151	61	2.7	502	9	CC853416	CC853416	NDL.21E21	C 224	60	2.7	147	7	CNI527893	CNI527893	UI-M-HQ0-
C 152	61	2.7	510	6	CB052268	CB052268	NISC_g106	C 225	60	2.7	148	5	BQ384842	BQ384842	NISC mm09
C 153	61	2.7	528	6	CB348563	CB348563	CAB28G000	C 226	60	2.7	148	4	BQ384842	BQ384842	NISC mm09
C 154	61	2.7	534	1	AA615853	AA615853	vo94f04.r	C 227	60	2.7	149	1	AJ499525	AJ499525	601658238
C 155	61	2.7	548	1	AI571049	AI571049	tu26b06.x	C 228	60	2.7	150	2	BE964700	BE964700	601658238
C 156	61	2.7	552	6	CB247053	CB247053	UI-M-F10-	C 229	60	2.7	150	6	CF336864	CF336864	JMT--07-B
C 157	61	2.7	574	5	BU688209	BU688209	UI-CF-EC1	C 230	60	2.7	151	1	AI537643	AI537643	7120h01.x
C 158	61	2.7	590	6	CA347558	CA347558	678700 NC	C 231	60	2.7	152	6	CB455595	CB455595	712748 MA
C 159	61	2.7	594	5	BQ400399	BQ400399	NISC_1n008	C 232	60	2.7	152	7	CK384839	CK384839	lah55a12.
C 160	61	2.7	594	6	CD416515	CD416515	Gm ck5891	C 233	60	2.7	152	7	CK617056	CK617056	ou32g06.y
C 161	61	2.7	601	7	CNI786814	CNI786814	4120863 B	C 234	60	2.7	154	6	CF313028	CF313028	HD--01-A0
C 162	61	2.7	625	3	CNI984035	CNI984035	52752.126	C 235	60	2.7	154	7	CF510746	CF510746	wx9b02.x
C 163	61	2.7	680	3	CR702672	CR702672	Tetradon	C 236	60	2.7	155	1	AI953765	AI953765	AGENCYCOURT
C 164	61	2.7	699	7	CNI842027	CNI842027	AGENCYCOURT	C 237	60	2.7	156	7	CR547142	CR547142	DKF2p468A
C 165	61	2.7	703	3	CR689517	CR689517	Tetradon	C 238	60	2.7	158	7	CR630352	CR630352	DKF2p469J
C 166	61	2.7	716	6	CA342493	CA342493	CA32EN000	C 239	60	2.7	160	4	BM496442	BM496442	1pCGBr2.1
C 167	61	2.7	728	4	BG572322	BG572322	602594547	C 240	60	2.7	160	6	CA570655	CA570655	w1su1.pf0
C 168	61	2.7	734	9	CG848156	CG848156	ZMWBB031	C 241	60	2.7	160	6	CB977957	CB977957	CAB40005
C 169	61	2.7	763	3	CNI802656	CNI802656	ILLUMIGEN	C 242	60	2.7	161	7	CK817434	CK817434	hag8009xc
C 170	61	2.7	767	5	BX490481	BX490481	DKF2p686K	C 243	60	2.7	161	6	CF330162	CF330162	NACL--05-

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247 60 2.7 165 2 BE543089 601069026
C 248 60 2.7 168 6 CF322022 HD--13-H1
C 249 60 2.7 170 2 AN081255
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253 60 2.7 175 5 BX953641 DKP2p781M
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C 258 60 2.7 180 1 A1501575
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C 263 60 2.7 182 6 CB303454 w8a0001.I
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C 298 60 2.7 205 6 CB084459 hq15f07.b
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1 A1889953 wms5e11.x
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1 AL041331 DKF2p434P
1 AL509380 AL509380
1 CF213920 CGF100081
1 A1358213 qv96h06.x
1 AW414897 48898.MAR
1 BU764177 sae53f02.
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1 AW190042 xl11b07.x
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1 CB044549 NISC_gc05
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1 AW632844 bl01a04.x
1 BY529448 BY529448
1 CF333987 JMT--03-B
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1 CD681829 rj31g03.Y
1 AW169827 xj33d05.x
1 BU745342 BJ745342
1 CN435699 BE030012A
1 CD771114 AGENCOURT
1 AL039508 DKF2p434A
1 AW169234 xj30g09.x
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1 A1439801 ti56b06.x
1 A1566724 to21h06.x
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1 CD572085 PBL_13_H1
1 CK430840 oj54e10.Y
1 A1500146 tn70h12.x
1 B1346956 376332.MA
1 BX557267 BX557267
1 BX645506 DKF2p781D
1 CA669423 wlsu1.pk0
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C 390	60	2.7	265	1	AI269469	AI269469	QW93h08.x	C 463	60	2.7	313	2	AW074638	AW074638	xa89d09.x
C 391	60	2.7	266	1	AI609181	AI609181	tw21a06.x	C 464	60	2.7	314	1	AI537076	AI537076	to82h01.x
C 392	60	2.7	267	2	AW619318	AW619318	690 MARC	C 465	60	2.7	315	6	CF291737	CF291737	14ROOT--0
C 393	60	2.7	267	6	CD405142	CD405142	Gm_CK2840	C 466	60	2.7	316	1	AI453315	AI453315	tj21e12.x
C 394	60	2.7	268	1	AI1299650	AI1299650	gm12b02.x	C 467	60	2.7	316	1	CF281935	CF281935	14ETU--09
C 395	60	2.7	268	1	AI610756	AI610756	tp38a03.x	C 468	60	2.7	317	7	CN537157	CN537157	UI-M-HSO-
C 396	60	2.7	269	1	AI827226	AI827226	w109d08.x	C 469	60	2.7	318	1	AI378080	AI378080	tc97h05.x
C 397	60	2.7	269	1	AI094118	AI094118	AI094118	C 470	60	2.7	318	1	AI690410	AI690410	tx87d03.x
C 398	60	2.7	269	5	BM949627	BM949627	UI-M-EGOp	C 471	60	2.7	318	5	AW193288	AW193288	x173a07.x
C 399	60	2.7	271	1	AI3774857	AI3774857	ta62d07.x	C 472	60	2.7	318	5	BQ389767	BQ389767	NISC mq09
C 400	60	2.7	271	4	BI787205	BI787205	seg7d03.x	C 473	60	2.7	319	6	CD676507	CD676507	ho01h04.y
C 401	60	2.7	272	1	AI445571	AI445571	tj30h04.x	C 474	60	2.7	320	1	AI932988	AI932988	wo56g10.x
C 402	60	2.7	272	6	CF329919	CF329919	NACL--05-	C 475	60	2.7	321	1	AI282376	AI282376	qv03g10.x
C 403	60	2.7	274	5	BU537121	BU537121	AGENCOURT	C 476	60	2.7	321	1	AI451579	AI451579	mu49f05.x
C 404	60	2.7	275	1	AI273791	AI273791	AI08C06.x	C 477	60	2.7	321	4	BG359256	BG359256	BOVMS1-00
C 405	60	2.7	275	1	AU172778	AU172778	QAU0807.x	C 478	60	2.7	321	6	CB075969	CB075969	gz21a05.g
C 406	60	2.7	276	1	AI801766	AI801766	tc095b12.x	C 479	60	2.7	321	6	CB519742	CB519742	UI-M-GH0
C 407	60	2.7	276	1	AU031474	AU031474	AU031474	C 480	60	2.7	321	5	BQ524248	BQ524248	NISC mq03
C 408	60	2.7	276	2	AW170663	AW170663	xl79h09.x	C 481	60	2.7	324	6	CB045043	CB045043	CB045043
C 409	60	2.7	276	2	CB083629	CB083629	hq01e10.b	C 482	60	2.7	324	6	CB083331	CB083331	hp96b07.b
C 410	60	2.7	277	2	AW085681	AW085681	xd42e02.x	C 483	60	2.7	325	6	CB079414	CB079414	hp71a02.b
C 411	60	2.7	278	1	AI289629	AI289629	qw29c06.x	C 484	60	2.7	327	1	AI536738	AI536738	to80b10.x
C 412	60	2.7	278	2	BE058442	BE058442	sn16b05.y	C 485	60	2.7	327	1	AI619581	AI619581	ty50d07.x
C 413	60	2.7	279	6	CB083421	CB083421	hp97d05.b	C 486	60	2.7	327	1	AI682743	AI682743	wc65f05.x
C 414	60	2.7	280	1	AI689637	AI689637	tx95d09.x	C 487	60	2.7	327	1	AI812003	AI812003	tw32h12.x
C 415	60	2.7	280	8	CC157656	CC157656	ik51g12.b	C 488	60	2.7	327	1	AJ006250	AJ006250	hql3f11.b
C 416	60	2.7	281	1	AI627866	AI627866	ty20a07.x	C 489	60	2.7	327	6	CB084332	CB084332	hq13f11.b
C 417	60	2.7	282	1	AI700146	AI700146	q21a10.x	C 490	60	2.7	328	1	AI872724	AI872724	wm9a01.x
C 418	60	2.7	283	1	AI471898	AI471898	ti51h02.x	C 491	60	2.7	328	6	CA935877	CA935877	sa02g10.
C 419	60	2.7	283	1	AI537735	AI537735	tp34f09.x	C 492	60	2.7	329	2	AW632940	AW632940	bl02a05.x
C 420	60	2.7	286	1	AI283914	AI283914	qt66b04.x	C 493	60	2.7	329	6	CF291913	CF291913	14ROOT--0
C 421	60	2.7	286	1	AI679095	AI679095	tu61b08.x	C 494	60	2.7	332	6	CB046259	CB046259	NISC gf03
C 422	60	2.7	286	1	AI963058	AI963058	wf26f11.x	C 495	60	2.7	334	1	AI283143	AI283143	gm57c03.x
C 423	60	2.7	286	6	CF302765	CF302765	7LEAF--08	C 496	60	2.7	336	1	AI933012	AI933012	wo57h08.x
C 424	60	2.7	287	6	CA738065	CA738065	wp12g.pk0	C 497	60	2.7	337	1	AI161278	AI161278	qb54a05.x
C 425	60	2.7	288	1	AI449557	AI449557	mq02h12.x	C 498	60	2.7	337	1	AI679504	AI679504	tu74g07.x
C 426	60	2.7	288	6	CF315774	CF315774	HD--04-N0	C 499	60	2.7	337	6	CF314435	CF314435	HD--02-P0
C 427	60	2.7	289	2	AW458015	AW458015	sh7b08.y	C 500	60	2.7	339	1	AI972109	AI972109	wf62f01.x
C 428	60	2.7	290	1	AI678778	AI678778	tu59a03.x	C 501	60	2.7	339	7	CK999804	CK999804	to90c06.b
C 429	60	2.7	291	1	AI537011	AI537011	to82d12.x	C 502	60	2.7	340	4	BG120656	BG120656	602346794
C 430	60	2.7	291	1	AI684021	AI684021	tw95b05.x	C 503	60	2.7	341	1	AI679891	AI679891	tu67b02.x
C 431	60	2.7	292	1	AI476147	AI476147	tn62e10.x	C 504	60	2.7	341	2	AW786632	AW786632	119974 MA
C 432	60	2.7	292	2	AW237857	AW237857	xm83d08.x	C 505	60	2.7	342	1	AI656412	AI656412	tt50g12.x
C 433	60	2.7	297	1	AI560011	AI560011	tc38b11.x	C 506	60	2.7	342	5	BQ264881	BQ264881	NISC f102
C 434	60	2.7	297	1	AI885982	AI885982	wm73h11.x	C 507	60	2.7	343	2	AW149079	AW149079	xf09g02.x
C 435	60	2.7	299	6	CB094437	CB094437	hz70a05.b	C 508	60	2.7	344	2	AW149079	AW149079	ty49c07.x
C 436	60	2.7	301	1	AI540821	AI540821	tp68a03.x	C 509	60	2.7	345	1	AI619513	AI619513	ty49c07.x
C 437	60	2.7	302	1	AI700358	AI700358	w06g11.x	C 510	60	2.7	345	6	AI813913	AI813913	wk61g10.x
C 438	60	2.7	302	1	AI761468	AI761468	wh98e07.x	C 511	60	2.7	346	6	BY742850	BY742850	BY742850
C 439	60	2.7	303	1	AI287391	AI287391	qv07h03.x	C 512	60	2.7	346	6	CD409674	CD409674	hq08b02.b
C 440	60	2.7	303	2	AW082088	AW082088	xb60c08.x	C 513	60	2.7	346	6	CD409674	CD409674	Gm ck3681
C 441	60	2.7	303	2	AW459300	AW459300	sh23c02.y	C 514	60	2.7	347	1	AI449589	AI449589	mq05g11.x
C 442	60	2.7	304	2	AW745571	AW745571	WS1_35_G1	C 515	60	2.7	348	1	AI092027	AI092027	o297c03.x
C 443	60	2.7	304	2	AW780507	AW780507	sl71g12.y	C 516	60	2.7	348	2	AW195943	AW195943	x185b12.x
C 444	60	2.7	304	6	CD395639	CD395639	Gm ck1568	C 517	60	2.7	349	2	AW195943	AW195943	x185b12.x
C 445	60	2.7	305	1	AI505057	AI505057	vk23f03.x	C 518	60	2.7	350	2	AW172878	AW172878	xj05a12.x
C 446	60	2.7	305	2	AW12461	AW12461	x184a09.x	C 519	60	2.7	351	5	EX559630	EX559630	EX559630
C 447	60	2.7	306	2	AW429331	AW429331	67211 WAR	C 520	60	2.7	352	7	CF621961	CF621961	lae6h07.
C 448	60	2.7	306	4	BM495074	BM495074	IPCGBR1_4	C 521	60	2.7	352	7	AW168402	AW168402	x182e10.x
C 449	60	2.7	307	1	AI883958	AI883958	f66b11.x	C 522	60	2.7	353	2	AI434281	AI434281	tl38g11.x
C 450	60	2.7	307	7	CK403599	CK403599	AUF IFHdk	C 523	60	2.7	354	6	CF331790	CF331790	NACL--08-
C 451	60	2.7	308	2	BE035838	BE035838	MO11a02 M	C 524	60	2.7	354	1	AI443393	AI443393	8a31e09.x
C 452	60	2.7	308	7	CF925736	CF925736	lq6b0b01.	C 525	60	2.7	355	1	AI811529	AI811529	tw43h07.x
C 453	60	2.7	309	1	AI579991	AI579991	tc45b03.x	C 526	60	2.7	355	5	BQ168352	BQ168352	WHE2102.D
C 454	60	2.7	309	5	EX485063	EX485063	DKP2p86K	C 527	60	2.7	356	1	AI679672	AI679672	tu65c01.x
C 455	60	2.7	309	6	CF327140	CF327140	NACL--01-	C 528	60	2.7	356	2	AW087814	AW087814	x538c02.x
C 456	60	2.7	309	7	CK378466	CK378466	lah96f04.	C 529	60	2.7	357	1	AI687482	AI687482	tp96g02.x
C 457	60	2.7	310	6	CF338084	CF338084	JMT--08-M	C 530	60	2.7	357	6	CF318866	CF318866	HD--09-C1
C 458	60	2.7	311	1	AI933780	AI933780	wn2b06.x	C 531	60	2.7	358	1	AI952145	AI952145	wx48f08.x
C 459	60	2.7	311	6	CB053164	CB053164	NTSC_g112	C 532	60	2.7	359	6	CF290836	CF290836	14ROOT--0
C 460	60	2.7	312	1	AI955943	AI955943	wt32b10.x	C 533	60	2.7	360	1	AI952145	AI952145	wx48f08.x
C 461	60	2.7	312	6	CF308273	CF308273	ABF--02-A	C 534	60	2.7	361	6	CB083492	CB083492	hp98d06.b
C 462	60	2.7	313	1	AU029574	AU029574	AU029574	C 535	60	2.7	363	6	CF312014	CF312014	ABF--07-I

C 536	60	2.7	364	6	CF309103	ABF--03-C	C 609	60	2.7	409	1	AI679098	tu61c01.x
537	60	2.7	365	4	BM720122	UI-E-E00-	C 610	60	2.7	409	5	BQ524504	NISC nc05
538	60	2.7	367	6	CB079522	CB079522	C 611	60	2.7	409	6	CB410006	NISC nc08
C 539	60	2.7	367	6	CF316124	HD--05-E1	C 612	60	2.7	410	2	BF475206	ES7a0b1E5
C 540	60	2.7	367	6	CF327665	NACL--02-	C 613	60	2.7	410	6	BY668300	BY668300
C 541	60	2.7	368	1	AA713511	nv67d09.s	C 614	60	2.7	412	1	AI886016	wm75c09.x
C 542	60	2.7	368	6	CF299899	7LEAF--04	C 615	60	2.7	412	5	BY391751	BY391751
C 543	60	2.7	369	1	AI499391	to11b12.x	C 616	60	2.7	412	6	CB075778	h251b09.b
C 544	60	2.7	369	1	AI624693	ts43g02.x	C 617	60	2.7	413	1	AI619777	tz53a06.x
C 545	60	2.7	370	6	CD722174	oj06d10.y	C 618	60	2.7	413	1	AI921232	wo22b08.x
C 546	60	2.7	371	7	CF922700	hags017xp	C 619	60	2.7	414	6	CF318478	HD--08-J2
C 547	60	2.7	372	1	AI865441	AI865441	C 620	60	2.7	416	2	AW166975	xg69c08.x
C 548	60	2.7	372	2	BE331303	so97d01.y	C 621	60	2.7	417	1	AI584416	fb93d03.x
C 549	60	2.7	373	1	AI609360	tw30f04.x	C 622	60	2.7	417	1	AI666394	mz66e03.x
C 550	60	2.7	373	4	BM567099	kj10b06.y	C 623	60	2.7	417	1	AI680420	tw81d09.x
C 551	60	2.7	373	6	CF311301	ABF--06-H	C 624	60	2.7	418	5	BQ524298	NISC nc04
C 552	60	2.7	374	6	CF311202	ABF--07-I	C 625	60	2.7	418	6	CF317293	HD--06-P0
C 553	60	2.7	375	1	AI438663	fb34d11.x	C 626	60	2.7	419	6	CD404328	Gm_ck2715
C 554	60	2.7	375	1	AI921420	wo34f04.x	C 627	60	2.7	420	1	AI357283	qx15f07.x
C 555	60	2.7	375	7	CK999090	ip39e04.b	C 628	60	2.7	422	1	AI282967	qt88a01.x
C 556	60	2.7	377	1	AI738852	tr29g09.x	C 629	60	2.7	422	1	AI588381	fc01b04.x
C 557	60	2.7	377	5	BA482584	DKF2p686J	C 630	60	2.7	423	2	BF724797	bx08g10.x
C 558	60	2.7	377	6	CB045096	CB045096	C 631	60	2.7	424	2	AW262042	qx30g10.x
C 559	60	2.7	377	7	CK429883	CK429883	C 632	60	2.7	425	5	BY391155	BY391155
C 560	60	2.7	378	1	AI333638	qp91d10.x	C 633	60	2.7	425	6	CD477196	eca01-30m
C 561	60	2.7	379	1	AI357075	AI357075	C 634	60	2.7	426	6	CF316656	HD--06-A1
C 562	60	2.7	379	6	CB258515	02-E01084	C 635	60	2.7	426	6	CF331475	NACL--07-
563	60	2.7	380	2	BE664656	152264 MA	C 636	60	2.7	426	1	AI634682	wa07h08.x
564	60	2.7	380	5	BY392811	BY392811	C 637	60	2.7	426	4	BI775361	467793 MA
C 565	60	2.7	380	6	CB094401	h259e08.b	C 638	60	2.7	428	1	AI889493	w05b12.x
C 566	60	2.7	381	6	CA392520	cb25f07.y	C 639	60	2.7	428	6	CF319081	HD--09-H1
C 567	60	2.7	383	6	CB083388	hp96g07.b	C 640	60	2.7	428	6	CF328724	NACL--03-
C 568	60	2.7	386	1	AI860817	w116c06.x	C 641	60	2.7	430	2	AW084000	xc47a05.x
C 569	60	2.7	386	6	CF314047	HD--02-G2	C 642	60	2.7	430	2	AW104641	xs55b09.x
C 570	60	2.7	387	6	CF333125	JMT--01-O	C 643	60	2.7	430	5	BQ521633	NISC nl12
C 571	60	2.7	388	4	BM544883	BM544883	C 644	60	2.7	430	6	CB046984	CB046984
C 572	60	2.7	388	6	CF276248	14ETL--01	C 645	60	2.7	430	6	CB075623	h249c09.b
C 573	60	2.7	389	1	AI588360	fb99g09.x	C 646	60	2.7	430	6	CF318681	HD--08-O1
C 574	60	2.7	389	1	AI677646	wc79f01.x	C 647	60	2.7	431	1	AI498067	tm65h03.x
C 575	60	2.7	389	6	CB044164	NISC gc02	C 648	60	2.7	432	6	CB535872	770118 MA
C 576	60	2.7	390	4	BM570340	BM570340	C 649	60	2.7	433	5	BQ526726	NISC no18
C 577	60	2.7	390	5	BQ388787	BQ388787	C 650	60	2.7	434	5	BQ520653	NISC nl06
C 578	60	2.7	390	5	BQ526631	NISC no17	C 651	60	2.7	435	5	BQ391273	NISC mq17
C 579	60	2.7	391	1	AI863466	tz41a08.x	C 652	60	2.7	435	5	BA473046	DKF2p686P
C 580	60	2.7	391	5	BQ520767	NISC nl07	C 653	60	2.7	436	1	AI554444	tg11f01.x
581	60	2.7	391	7	CB995453	CB995453	C 654	60	2.7	436	5	BQ527780	NISC no24
C 582	60	2.7	392	5	BQ396364	NISC ng20	C 655	60	2.7	438	1	AI798385	tr34c12.x
C 583	60	2.7	392	5	BQ523600	NISC nl23	C 656	60	2.7	438	6	CF321419	HD--12-K1
C 584	60	2.7	393	1	AI830026	wj95h05.x	C 657	60	2.7	438	6	CF331979	NACL--08-
C 585	60	2.7	393	6	CF332711	JMT--01-F	C 658	60	2.7	440	6	CF329601	NACL--04-
C 586	60	2.7	394	1	AI921469	wo25d11.x	C 659	60	2.7	442	6	CF314063	HD--02-H0
C 587	60	2.7	394	2	AW090238	AW090238	C 660	60	2.7	443	5	BY446387	BY446387
588	60	2.7	394	6	CB820496	CB820496	C 661	60	2.7	443	6	CF333652	JMT--02-K
589	60	2.7	395	6	BY668062	BY668062	C 662	60	2.7	443	5	BQ524972	NISC no08
C 590	60	2.7	395	6	CB080326	CB080326	C 663	60	2.7	445	7	CK371847	la119g12.
C 591	60	2.7	398	1	AI953767	wx69b05.x	C 664	60	2.7	447	2	BF724651	bx07c08.x
C 592	60	2.7	400	2	BF739747	BF739747	C 665	60	2.7	447	6	CF336964	JMT--07-D
C 593	60	2.7	400	6	CF336419	CF336419	C 666	60	2.7	448	4	BQ972564	602841150
C 594	60	2.7	401	1	AI819202	AI819202	C 667	60	2.7	448	4	BI495231	df116b01.
C 595	60	2.7	401	2	AW261842	AW261842	C 668	60	2.7	449	1	AI446704	198b04.x
C 596	60	2.7	401	6	CF336774	JMT--06-P	C 669	60	2.7	450	1	AI802554	tp03h12.x
597	60	2.7	403	5	BU585045	BU585045	C 670	60	2.7	450	5	BA492871	DKF2p7810
C 598	60	2.7	403	6	CB083374	CB083374	C 671	60	2.7	451	4	BI495232	df116b01.
C 599	60	2.7	403	6	CF300744	CF300744	C 672	60	2.7	452	6	CF328587	NACL--03-
C 600	60	2.7	403	6	CF320561	HD--11-I0	C 673	60	2.7	452	6	CF332439	NACL--08-
C 601	60	2.7	404	1	AI872091	wm55a11.x	C 674	60	2.7	453	2	AW632845	bl01a05.x
C 602	60	2.7	404	5	BQ394634	BQ394634	C 675	60	2.7	453	6	CF309506	ABF--03-L
C 603	60	2.7	404	6	CF313612	HD--01-M2	C 676	60	2.7	454	6	CB410508	NISC nc12
C 604	60	2.7	404	6	CF331254	NACL--07-	C 677	60	2.7	454	7	CK360740	AGENCOURT
C 605	60	2.7	405	1	AI655841	tt40e10.x	C 678	60	2.7	455	6	CB043920	NISC gc01
C 606	60	2.7	405	6	CF316565	HD--05-O0	C 679	60	2.7	456	2	BE329508	so86c05.y
C 607	60	2.7	406	6	CD416928	Gm_ck7403	C 680	60	2.7	456	6	CB044515	NISC gc05
608	60	2.7	408	7	CF545537	lae80g06.	C 681	60	2.7	457	1	AL719889	AL719889

682	60	2.7	459	6	CB084385	hql4d10.b	CB084385	hql4d10.b	60	2.7	534	1	AJ658317	AJ658317
683	60	2.7	460	1	AU056605	AU056605	AU056605	AU056605	60	2.7	537	6	CA816820	CA816820
684	60	2.7	460	5	BQ387565	NISC mn24	BQ387565	NISC mn24	60	2.7	540	6	CF299588	CF299588
685	60	2.7	461	6	CB456671	713949 MA	CB456671	713949 MA	60	2.7	542	1	A1813579	WJ8h03.x
686	60	2.7	462	2	AW008090	wv4f08.x	AW008090	wv4f08.x	60	2.7	542	6	CD316912	CD316912
687	60	2.7	462	2	AW083770	xc51609.x	AW083770	xc51609.x	60	2.7	543	6	CF299770	7LEAF--03
688	60	2.7	462	6	CA670216	wlsup.pko	CA670216	wlsup.pko	60	2.7	545	4	BM065131	BM065131
689	60	2.7	462	6	CB736011	AMGNNUC:C	CB736011	AMGNNUC:C	60	2.7	545	6	CB055082	NISC gm07
690	60	2.7	463	6	CF291654	14ROOT--0	CF291654	14ROOT--0	60	2.7	545	6	CD405224	Gm ck2848
691	60	2.7	463	6	CF291730	14ROOT--0	CF291730	14ROOT--0	60	2.7	545	6	CD405224	Gm ck2848
692	60	2.7	466	1	AI624956	t84807.x	AI624956	t84807.x	60	2.7	548	1	AA898637	AA898637
693	60	2.7	466	6	CB053424	NISC gl14	CB053424	NISC gl14	60	2.7	548	6	CA729868	wplc.pko
694	60	2.7	469	2	AW193457	xl75d10.x	AW193457	xl75d10.x	60	2.7	551	6	CD433205	CD433205
695	60	2.7	470	6	CB104542	ADP SQ021	CB104542	ADP SQ021	60	2.7	553	6	CB724184	CB724184
696	60	2.7	471	6	CB079481	hp71h06.b	CB079481	hp71h06.b	60	2.7	553	6	BQ399202	BQ399202
697	60	2.7	473	1	AI624971	t848f07.x	AI624971	t848f07.x	60	2.7	554	5	BQ394230	BQ394230
698	60	2.7	473	2	AW024564	wu7e02.x	AW024564	wu7e02.x	60	2.7	554	5	BQ520719	NISC nl06
699	60	2.7	475	1	AI144116	db52409.x	AI144116	db52409.x	60	2.7	554	6	CF314767	HD--03-G1
700	60	2.7	476	6	CF334909	UJT--04-G	CF334909	UJT--04-G	60	2.7	555	7	CSN90409	TTE000101
701	60	2.7	477	6	CF290856	14ROOT--0	CF290856	14ROOT--0	60	2.7	555	7	BQ525827	NISC no12
702	60	2.7	480	5	BQ394907	NISC ng11	BQ394907	NISC ng11	60	2.7	556	5	BQ525827	NISC no12
703	60	2.7	480	6	CB075789	hz51G12.b	CB075789	hz51G12.b	60	2.7	556	7	CSN90415	TTE000107
704	60	2.7	481	1	AI634719	t209601.x	AI634719	t209601.x	60	2.7	558	1	AA901807	NCM4G9T7
705	60	2.7	482	4	BG180270	602329890	BG180270	602329890	60	2.7	558	5	BQ521234	NISC nl09
706	60	2.7	482	6	CB053355	NISC gl13	CB053355	NISC gl13	60	2.7	565	1	AA901504	NCC4F9T7
707	60	2.7	483	5	BQ395230	NISC ng13	BQ395230	NISC ng13	60	2.7	565	6	CB340736	CB340736
708	60	2.7	485	6	CF276510	14ETL--01	CF276510	14ETL--01	60	2.7	566	6	CF319654	CF319654
709	60	2.7	486	6	CF326810	NACL--01-	CF326810	NACL--01-	60	2.7	568	6	CB463751	CB463751
710	60	2.7	486	7	CSN90220	TTE000115	CSN90220	TTE000115	60	2.7	572	5	BQ388905	BQ388905
711	60	2.7	488	6	CF310530	ABF--05-D	CF310530	ABF--05-D	60	2.7	572	7	CSN90449	CSN90449
712	60	2.7	488	6	CS561353	CS561353	CS561353	CS561353	60	2.7	574	7	CSN90458	TTE000088
713	60	2.7	489	6	CF313165	HD--01-D0	CF313165	HD--01-D0	60	2.7	577	4	BI495519	df118g07.
714	60	2.7	491	1	AI538686	tp66e10.x	AI538686	tp66e10.x	60	2.7	578	1	AI584402	AI584402
715	60	2.7	491	5	BQ526901	NISC no19	BQ526901	NISC no19	60	2.7	581	6	CD316817	CD316817
716	60	2.7	491	6	CF321910	HD--13-F0	CF321910	HD--13-F0	60	2.7	582	5	BQ390079	BQ390079
717	60	2.7	493	1	AI861982	ty30G05.x	AI861982	ty30G05.x	60	2.7	582	6	C25616	C25616
718	60	2.7	493	1	AV755793	AV755793	AV755793	AV755793	60	2.7	584	3	BC039986	BC039986
719	60	2.7	493	6	CF130283	UT-HF-ES0	CF130283	UT-HF-ES0	60	2.7	589	5	BQ525006	NISC no08
720	60	2.7	494	1	AA898430	NCC1B2T7	AA898430	NCC1B2T7	60	2.7	590	7	CO106895	GR_Eb003
721	60	2.7	495	7	CF403974	CSECS017H	CF403974	CSECS017H	60	2.7	591	6	CB052703	NISC gl09
722	60	2.7	495	7	CO752765	Mdf13025b	CO752765	Mdf13025b	60	2.7	591	7	CF933351	TrEST-B28
723	60	2.7	496	6	CF314114	HD--02-I0	CF314114	HD--02-I0	60	2.7	594	7	CK144544	CK144544
724	60	2.7	496	7	CO809799	AGENCOURT	CO809799	AGENCOURT	60	2.7	596	6	CD76506	ho01h04.x
725	60	2.7	497	6	CF314398	HD--02-O1	CF314398	HD--02-O1	60	2.7	598	6	CF136966	UI-HF-BNO
726	60	2.7	499	1	AI434274	t338904.x	AI434274	t338904.x	60	2.7	603	4	BM367348	BM367348
727	60	2.7	499	1	AI619813	ty53f04.x	AI619813	ty53f04.x	60	2.7	604	5	BQ388710	BQ388710
728	60	2.7	499	3	CR707228	Tetraodon	CR707228	Tetraodon	60	2.7	607	1	AI961278	w16a12.x
729	60	2.7	503	6	CB045532	NISC gc11	CB045532	NISC gc11	60	2.7	611	6	CD395213	Gm ck1520
730	60	2.7	505	1	AJ656374	AJ656374	AJ656374	AJ656374	60	2.7	613	4	CB346794	CAB25G000
731	60	2.7	506	2	BF030168	601556810	BF030168	601556810	60	2.7	613	8	CC167613	CC167613
732	60	2.7	506	6	CF299138	7LEAF--03	CF299138	7LEAF--03	60	2.7	622	1	AI560673	AI560673
733	60	2.7	506	6	CF321816	HD--13-D0	CF321816	HD--13-D0	60	2.7	623	7	CSN90537	CSN90537
734	60	2.7	506	6	CF406029	CSECS062H	CF406029	CSECS062H	60	2.7	626	7	CSN90544	CSN90544
735	60	2.7	507	6	CB419895	592793 MA	CB419895	592793 MA	60	2.7	632	6	BM563245	BM563245
736	60	2.7	507	6	CD391612	Gm ck1053	CD391612	Gm ck1053	60	2.7	632	6	CSN964024	UI-M-EQO-
737	60	2.7	507	6	CF316166	HD--05-F1	CF316166	HD--05-F1	60	2.7	635	5	BM964024	UI-M-EQO-
738	60	2.7	508	4	BM512647	kk77910.y	BM512647	kk77910.y	60	2.7	635	6	CA759955	CA759955
739	60	2.7	508	6	CB044051	NISC gc02	CB044051	NISC gc02	60	2.7	635	6	CA759955	CA759955
740	60	2.7	509	5	BQ391709	NISC mq20	BQ391709	NISC mq20	60	2.7	635	6	CA759955	CA759955
741	60	2.7	510	5	BQ397270	NISC mq26	BQ397270	NISC mq26	60	2.7	638	1	AU058340	AU058340
742	60	2.7	510	6	CF279054	14ETL--05	CF279054	14ETL--05	60	2.7	638	5	AX489642	AX489642
743	60	2.7	510	6	CF329780	NACL--05-	CF329780	NACL--05-	60	2.7	644	4	BQ390432	Gm ck0860
744	60	2.7	510	6	CB054101	NISC gm02	CB054101	NISC gm02	60	2.7	647	6	CD460368	CD460368
745	60	2.7	512	6	CD722461	oj10a08.y	CD722461	oj10a08.y	60	2.7	648	6	CD390432	Gm ck2479
746	60	2.7	520	6	CF058280	QC07d08.y	CF058280	QC07d08.y	60	2.7	649	7	CD402185	CD402185
747	60	2.7	521	6	CD678155	hp01h12.x	CD678155	hp01h12.x	60	2.7	656	2	BB632395	BB632395
748	60	2.7	525	5	BQ526176	NISC no14	BQ526176	NISC no14	60	2.7	657	2	BB632395	BB632395
749	60	2.7	526	5	BM562569	BM562569	BM562569	BM562569	60	2.7	658	7	CD360748	CD360748
750	60	2.7	527	4	BM475916	AGENCOURT	BM475916	AGENCOURT	60	2.7	664	2	AW081812	AW081812
751	60	2.7	529	5	BQ521108	NISC nl09	BQ521108	NISC nl09	60	2.7	666	7	CD446924	CD446924
752	60	2.7	532	1	AI686749	tx09f02.x	AI686749	tx09f02.x	60	2.7	679	6	CD446924	CD446924
753	60	2.7	533	1	AA898829	NCP3H8T7	AA898829	NCP3H8T7	60	2.7	695	1	AI366922	AI366922
754	60	2.7	534	1	AA898098	NCC1A10T7	AA898098	NCC1A10T7	60	2.7	697	7	CO647917	ILLUMIGEN

C 828	60	2.7	705	7	CNI159690	948783	MA	C 901	60	2.7	915	7	CF580246	CF580246	AGENCYCOURT
C 829	60	2.7	721	2	BE890783	601431223		C 902	60	2.7	915	7	CF883973	CF883973	trf036x1
C 830	60	2.7	721	4	BI860482	603386742		C 903	60	2.7	915	7	CK160067	CK160067	FGAS04160
C 831	60	2.7	721	6	C9232702	TcAmap106		C 904	60	2.7	932	2	BE965171	BE965171	601658967
C 832	60	2.7	728	6	CB348687	CAB2SG000		C 905	60	2.7	932	7	CK164886	CK164886	FGAS04881
C 833	60	2.7	735	2	BE228957	98A533222		C 906	60	2.7	933	7	CF581052	CF581052	AGENCYCOURT
C 834	60	2.7	745	4	BE290459	602388317		C 907	60	2.7	940	5	BU555079	BU555079	AGENCYCOURT
C 835	60	2.7	761	7	CK367542	AGENCYCOURT		C 908	60	2.7	942	5	BU192613	BU192613	AGENCYCOURT
C 836	60	2.7	763	1	AI096613	qb57a05.x		C 909	60	2.7	943	5	BU911084	BU911084	AGENCYCOURT
C 837	60	2.7	764	6	CK572033	AGENCYCOURT		C 910	60	2.7	944	5	CK403255	CK403255	AUF IfHdk
C 838	60	2.7	769	4	BI416959	hasp002xd		C 911	60	2.7	948	4	BG034554	BG034554	602302678
C 839	60	2.7	770	1	AI037054	AI037054		C 912	60	2.7	964	4	EM416130	EM416130	OP21217 M
C 840	60	2.7	772	1	AI009266	EST203717		C 913	60	2.7	973	6	CA971670	CA971670	AGENCYCOURT
C 841	60	2.7	774	7	CK032603	AGENCYCOURT		C 914	60	2.7	977	6	CD511450	CD511450	AGENCYCOURT
C 842	60	2.7	775	7	CK038690	AGENCYCOURT		C 915	60	2.7	980	5	BQ918578	BQ918578	AGENCYCOURT
C 843	60	2.7	778	1	AA748343	AA748343		C 916	60	2.7	994	2	BF526889	BF526889	602070455
C 844	60	2.7	784	5	BU554900	AGENCYCOURT		C 917	60	2.7	1010	4	EM416351	EM416351	OP21442 M
C 845	60	2.7	785	6	CF271335	AGENCYCOURT		C 918	60	2.7	1012	6	CB756570	CB756570	AGENCYCOURT
C 846	60	2.7	789	5	BU554596	AGENCYCOURT		C 919	60	2.7	1012	7	CF582470	CF582470	AGENCYCOURT
C 847	60	2.7	792	4	BG255770	602368248		C 920	60	2.7	1025	5	BU185581	BU185581	AGENCYCOURT
C 848	60	2.7	795	5	BQ137245	BQ137245		C 921	60	2.7	1039	2	BE900527	BE900527	601673795
C 849	60	2.7	797	4	BG574560	602596538		C 922	60	2.7	1042	7	CO772410	CO772410	608618 ES
C 850	60	2.7	801	7	CK130051	AGENCYCOURT		C 923	60	2.7	1045	8	BH157021	BH157021	ENTQY85TF
C 851	60	2.7	801	7	CK197514	AGENCYCOURT		C 924	60	2.7	1056	4	BM907536	BM907536	AGENCYCOURT
C 852	60	2.7	814	7	CK200124	FGAS00863		C 925	60	2.7	1074	8	BH154154	BH154154	ENTQY50TF
C 853	60	2.7	814	7	CK200261	AGENCYCOURT		C 926	60	2.7	1108	7	CK165877	CK165877	FGAS04989
C 854	60	2.7	814	7	CK200263	AGENCYCOURT		C 927	60	2.7	1128	7	CK165682	CK165682	FGAS04966
C 855	60	2.7	817	7	CK398945	AGENCYCOURT		C 928	60	2.7	1129	7	CK166699	CK166699	FGAS05088
C 856	60	2.7	817	7	CK195733	AGENCYCOURT		C 929	60	2.7	1131	7	CK168016	CK168016	FGAS05249
C 857	60	2.7	821	7	CK200359	AGENCYCOURT		C 930	60	2.7	1154	4	BM907445	BM907445	AGENCYCOURT
C 858	60	2.7	823	5	BU537474	AGENCYCOURT		C 931	60	2.7	1154	4	BM907445	BM907445	AGENCYCOURT
C 859	60	2.7	823	7	CO799940	AGENCYCOURT		C 932	60	2.7	1221	3	BC029836	BC029836	Homo sapi
C 860	60	2.7	830	7	CF782886	AGENCYCOURT		C 933	60	2.7	1221	3	CK167723	CK167723	FGAS05214
C 861	60	2.7	832	7	CO385354	AGENCYCOURT		C 934	60	2.7	1242	4	BM563461	BM563461	AGENCYCOURT
C 862	60	2.7	835	5	BU537583	AGENCYCOURT		C 935	60	2.7	1243	7	CK167591	CK167591	FGAS05199
C 863	60	2.7	842	7	CK201001	FGAS00951		C 936	60	2.7	1249	3	AI107817	AI107817	Zea mays
C 864	60	2.7	844	7	CK197616	AGENCYCOURT		C 937	60	2.7	1329	2	BF342709	BF342709	602013662
C 865	60	2.7	845	6	CA453861	AGENCYCOURT		C 938	60	2.7	1333	5	BU509014	BU509014	AGENCYCOURT
C 866	60	2.7	846	5	BU555935	AGENCYCOURT		C 939	60	2.7	1345	3	CO382807	CO382807	AGENCYCOURT
C 867	60	2.7	849	7	CK198254	AGENCYCOURT		C 940	60	2.7	1392	3	AI108971	AI108971	Zea mays
C 868	60	2.7	850	7	CK196881	AGENCYCOURT		C 941	60	2.7	1556	4	BI489022	BI489022	603020993
C 869	60	2.7	851	7	CK196840	AGENCYCOURT		C 942	60	2.7	1575	4	BG028429	BG028429	602294335
C 870	60	2.7	852	7	CK200159	AGENCYCOURT		C 943	60	2.7	1576	3	BC033108	BC033108	Homo sapi
C 871	60	2.7	855	7	CK196558	AGENCYCOURT		C 944	60	2.7	1663	3	BC050648	BC050648	Homo sapi
C 872	60	2.7	857	2	AW084797	xc63b10.x		C 945	60	2.7	1857	3	AP119909	AP119909	Homo sapi
C 873	60	2.7	858	7	CK195618	AGENCYCOURT		C 946	60	2.7	2030	3	BC010091	BC010091	Homo sapi
C 874	60	2.7	859	5	BU534700	AGENCYCOURT		C 947	59	2.6	2030	3	BC010091	BC010091	Homo sapi
C 875	60	2.7	861	4	BI258815	602969616		C 948	59	2.6	61	6	CB258402	CB258402	29-E01409
C 876	60	2.7	867	4	BG262014	602373845		C 949	59	2.6	62	6	CF311486	CF311486	ABF--06-L
C 877	60	2.7	868	7	CK157510	FGAS03863		C 950	59	2.6	62	6	CF327983	CF327983	NACL--02-
C 878	60	2.7	868	7	CK198316	AGENCYCOURT		C 951	59	2.6	63	4	BG939764	BG939764	cr61g10.x
C 879	60	2.7	869	2	BE279800	601157111		C 952	59	2.6	64	6	CF338194	CF338194	JMT--08-P
C 880	60	2.7	869	7	CF583927	AGENCYCOURT		C 953	59	2.6	66	1	AI698265	AI698265	tx11a04.x
C 881	60	2.7	869	7	CK164434	AGENCYCOURT		C 954	59	2.6	66	7	N46357	N46357	YY74f11.s1
C 882	60	2.7	871	7	CK196891	AGENCYCOURT		C 955	59	2.6	70	1	AI225248	AI225248	qx12d07.x
C 883	60	2.7	881	7	CK198209	AGENCYCOURT		C 956	59	2.6	73	1	AI211208	AI211208	o0g11a1.f
C 884	60	2.7	882	5	BU173715	AGENCYCOURT		C 957	59	2.6	74	7	N22999	N22999	YX74f10.s1
C 885	60	2.7	882	7	CK158449	AGENCYCOURT		C 958	59	2.6	75	2	N34355	N34355	YY12d04.s1
C 886	60	2.7	883	7	CF783962	AGENCYCOURT		C 959	59	2.6	76	2	BF225301	BF225301	uz45d05.Y
C 887	60	2.7	884	7	CG575939	602598369		C 960	59	2.6	77	4	BI490993	BI490993	fd02c02.w
C 888	60	2.7	885	7	CK156391	FGAS03735		C 961	59	2.6	77	5	BQ265165	BQ265165	NISC ff03
C 889	60	2.7	885	7	CK159367	AGENCYCOURT		C 962	59	2.6	80	6	CF337525	CF337525	JMT--07-P
C 890	60	2.7	885	6	CD243551	AGENCYCOURT		C 963	59	2.6	81	1	AI689614	AI689614	tx95b04.x
C 891	60	2.7	887	5	BU532733	AGENCYCOURT		C 964	59	2.6	81	5	BQ285370	BQ285370	NISC ff05
C 892	60	2.7	894	7	CK799015	AGENCYCOURT		C 965	59	2.6	82	2	AW189933	AW189933	xx110C09.x
C 893	60	2.7	896	7	CK156192	AGENCYCOURT		C 966	59	2.6	82	6	CF302120	CF302120	7LEAF--07
C 894	60	2.7	896	7	CK164670	AGENCYCOURT		C 967	59	2.6	84	1	AI270039	AI270039	qt91b11.x
C 895	60	2.7	897	7	CK156041	AGENCYCOURT		C 968	59	2.6	84	4	BM445850	BM445850	11L16F12
C 896	60	2.7	903	7	CK156206	AGENCYCOURT		C 969	59	2.6	84	7	N46347	N46347	YY74c09.s1
C 897	60	2.7	909	7	CF580345	AGENCYCOURT		C 970	59	2.6	85	6	CD404453	CD404453	Gm ck2728
C 898	60	2.7	913	7	CK165175	AGENCYCOURT		C 971	59	2.6	85	6	CF314799	CF314799	HD--03-H1
C 899	60	2.7	914	2	BE964415	601658121		C 972	59	2.6	87	4	BM445810	BM445810	11L16B12
C 900	60	2.7	914	5	BQ222594	AGENCYCOURT		C 973	59	2.6	88	4	BI495871	BI495871	df121d03.
											88	5	BQ265163	BQ265163	NISC ff03

C 974	59	2.6	88	6	CD399147	CD399147 Gm_ck2060	C1047	59	2.6	112	1	AI249946	AI249946 Qx47b01.x
C 975	59	2.6	88	7	N74355	N74355 za52b01.s1	C1048	59	2.6	112	6	CB410038	CB410038 NISC inc09
C 976	59	2.6	88	1	AI28574	AI28574 w142d08.x	C1049	59	2.6	112	6	CF334957	CF334957 JMT--04-H
C 977	59	2.6	90	2	BF458032	BF458032 UI-M-BZ1	C1050	59	2.6	112	6	CF337940	CF337940 JMT--08-J
C 978	59	2.6	90	6	CF291813	CF291813 14ROOT--0	C1051	59	2.6	113	4	BM495149	BM495149 IPCGBx1.6
C 979	59	2.6	90	6	CF298069	CF298069 7LEAF--01	C1052	59	2.6	114	7	CK616588	CK616588 ou22c01.y
C 980	59	2.6	91	2	BF633562	BF633562 NF058E07D	C1053	59	2.6	115	2	BE613727	BE613727 601504529
C 981	59	2.6	92	1	AI242736	AI242736 qt86d12.x	C1054	59	2.6	115	4	BG980787	BG980787 MR3-CN014
C 982	59	2.6	92	1	AA124213	AA124213 m46c01.f	C1055	59	2.6	115	6	CB052012	CB052012 NISC_g105
C 983	59	2.6	92	1	BF643410	BF643410 NF003B05E	C1056	59	2.6	115	7	CO534692	CO534692 3530_1.22
C 984	59	2.6	92	7	CK616738	CK616738 ou25d01.y	C1057	59	2.6	116	1	AI583578	AI583578 t515h09.x
C 985	59	2.6	93	6	CF3021130	CF3021130 7LEAF--07	C1058	59	2.6	116	5	BQ586431	BQ586431 S013307-0
C 986	59	2.6	93	6	CF333228	CF333228 JMT--02-A	C1059	59	2.6	116	6	CB817178	CB817178 q3b08pz.f
C 987	59	2.6	93	6	CF336292	CF336292 JMT--06-E	C1060	59	2.6	116	6	CF316173	CF316173 HD--05-F2
C 988	59	2.6	93	7	CK616543	CK616543 ou21d05.y	C1061	59	2.6	117	6	CF292121	CF292121 14ROOT--0
C 989	59	2.6	94	1	AI866786	AI866786 t253b05.x	C1062	59	2.6	118	2	AW347176	AW347176 30517 MAR
C 990	59	2.6	94	4	BG496656	BG496656 602545044	C1063	59	2.6	118	6	CB089318	CB089318 q807902.b
C 991	59	2.6	94	6	CF281066	CF281066 14ETL--07	C1064	59	2.6	118	6	CB606769	CB606769 AMGNNUC.S
C 992	59	2.6	94	7	CK615940	CK615940 ou07h07.y	C1065	59	2.6	118	6	CB972851	CB972851 UBSW_H34F
C 993	59	2.6	96	2	AW332994	AW332994 S15H10 AG	C1066	59	2.6	119	4	BG972885	BG972885 HTSW_H18B
C 994	59	2.6	96	6	CF316463	CF316463 HD--05-M0	C1067	59	2.6	119	4	BG817171	BG817171 UTSW_H18B
C 995	59	2.6	97	6	CB053740	CB053740 NISC_g116	C1068	59	2.6	119	4	BI014412	BI014412 MR3-ET025
C 996	59	2.6	98	6	CB054081	CB054081 NISC_gm02	C1069	59	2.6	119	4	BI015377	BI015377 MR4-ET024
C 997	59	2.6	99	1	AI452857	AI452857 t126803.x	C1070	59	2.6	119	6	CF326816	CF326816 NACL--01-
C 998	59	2.6	99	7	CN546690	CN546690 EST_18461	C1071	59	2.6	120	1	AI550318	AI550318 vx03h11.x
C 999	59	2.6	100	1	AI446124	AI446124 t107b06.x	C1072	59	2.6	120	2	AW858254	AW858254 GM1-CF033
C 1000	59	2.6	100	1	AI623736	AI623736 t838f07.x	C1073	59	2.6	120	4	BG991132	BG991132 MR2-HT118
C 1001	59	2.6	100	6	CF307943	CF307943 ABF--01-J	C1074	59	2.6	121	1	AA514684	AA514684 nf58f05.s
C 1002	59	2.6	100	7	CK617039	CK617039 ou32d08.y	C1075	59	2.6	122	1	AI677797	AI677797 wg80e03.x
C 1003	59	2.6	101	1	AI619370	AI619370 486093D07	C1076	59	2.6	122	5	AW082600	AW082600 xc20b10.x
C 1004	59	2.6	101	6	CB079792	CB079792 hp76f07.b	C1077	59	2.6	122	5	BQ524894	BQ524894 NISC_no07
C 1005	59	2.6	101	7	CK616032	CK616032 ou09g07.y	C1078	59	2.6	122	6	CF321272	CF321272 HD--12-H1
C 1006	59	2.6	102	1	AI045630	AI045630 DXFP2434P	C1079	59	2.6	122	6	CF328903	CF328903 NACL--04-
C 1007	59	2.6	102	5	BQ385719	BQ385719 NISC_mn13	C1080	59	2.6	123	1	AI472536	AI472536 t177907.x
C 1008	59	2.6	102	6	CF977914	CF977914 CAB4004	C1081	59	2.6	123	6	CF337275	CF337275 JMT--07-K
C 1009	59	2.6	102	6	CD538640	CD538640 B0205C04-	C1082	59	2.6	124	1	AL045324	AL045324 DXFZ8434A
C 1010	59	2.6	103	5	BU068740	BU068740 2567_B08	C1083	59	2.6	124	1	BF817746	BF817746 MR2-C1012
C 1011	59	2.6	103	6	CA336726	CA336726 NISC_lv04	C1084	59	2.6	125	2	FA778959	FA778959 MPL384_11
C 1012	59	2.6	103	6	CD330858	CD330858 Gm_ck0255	C1085	59	2.6	125	6	CF327201	CF327201 NACL--01-
C 1013	59	2.6	103	6	CF202825	CF202825 RR890915N	C1086	59	2.6	125	6	CK894586	CK894586 SGP160194
C 1014	59	2.6	103	7	CN640199	CN640199 264F07.55	C1087	59	2.6	125	7	CK894586	CK894586 SGP160194
C 1015	59	2.6	104	2	BE172499	BE172499 MR0-HT055	C1088	59	2.6	126	6	CB088871	CB088871 if06h08.b
C 1016	59	2.6	104	6	CD403321	CD403321 Gm_ck2604	C1089	59	2.6	126	7	CK615858	CK615858 ou05h09.y
C 1017	59	2.6	104	6	CD405413	CD405413 Gm_ck2879	C1090	59	2.6	126	7	CK615858	CK615858 ou05h09.y
C 1018	59	2.6	104	7	CF519095	CF519095 CAP0006_I	C1091	59	2.6	127	2	AW265004	AW265004 XRS9d11.x
C 1019	59	2.6	105	6	CB346432	CB346432 CAB2SG000	C1092	59	2.6	127	2	AW999906	AW999906 MR0-BN007
C 1020	59	2.6	105	6	CB975252	CB975252 CAB30006	C1093	59	2.6	127	2	BE393551	BE393551 601310247
C 1021	59	2.6	105	6	CF313736	CF313736 HD--01-PI	C1094	59	2.6	127	4	BI496442	BI496442 df125d01
C 1022	59	2.6	105	6	CF344459	CF344459 HD--02-PI	C1095	59	2.6	127	4	BM030766	BM030766 435270 MA
C 1023	59	2.6	105	6	CF330299	CF330299 NACL--05-	C1096	59	2.6	127	6	BM030766	BM030766 hq26802.b
C 1024	59	2.6	106	1	AI434242	AI434242 t133c05.x	C1097	59	2.6	127	6	CB977737	CB977737 CAB40004
C 1025	59	2.6	106	1	AI805769	AI805769 tx89h05.x	C1098	59	2.6	128	1	AI250627	AI250627 Qx46b05.x
C 1026	59	2.6	106	2	BE238676	BE238676 946006F11	C1099	59	2.6	128	1	BF814449	BF814449 MR2-C1018
C 1027	59	2.6	106	2	BE238676	BE238676 946006F11	C1100	59	2.6	128	2	BE538466	BE538466 601068105
C 1028	59	2.6	106	5	BQ393762	BQ393762 NISC_g105	C1101	59	2.6	128	2	BE538466	BE538466 601068105
C 1029	59	2.6	106	6	CB051709	CB051709 NISC_g102	C1102	59	2.6	129	2	AW085786	AW085786 xc55g11.x
C 1030	59	2.6	106	6	CB094428	CB094428 h269h08.b	C1103	59	2.6	129	4	CB286160	CB286160 QV1-CF075
C 1031	59	2.6	106	6	CF299320	CF299320 7LEAF--03	C1104	59	2.6	129	6	CB286160	CB286160 CMD31_F12
C 1032	59	2.6	106	7	CK616265	CK616265 ou15c03.y	C1105	59	2.6	130	1	AI661490	AI661490 v339h01.x
C 1033	59	2.6	107	1	AI553669	AI553669 t46f09.x	C1106	59	2.6	130	5	BQ525571	BQ525571 NISC_no11
C 1034	59	2.6	107	4	BG942081	BG942081 ax20h05.x	C1107	59	2.6	130	6	CF309778	CF309778 ABF--04-B
C 1035	59	2.6	107	4	BG995919	BG995919 MR4-HT119	C1108	59	2.6	130	7	CF511928	CF511928 CABud0004
C 1036	59	2.6	107	6	CF291299	CF291299 14ROOT--0	C1109	59	2.6	131	4	BG941911	BG941911 ax18g09.x
C 1037	59	2.6	107	6	CF308130	CF308130 ABF--01-N	C1110	59	2.6	131	4	BI019663	BI019663 MR3-WT032
C 1038	59	2.6	108	2	AW161098	AW161098 au78h03.y	C1111	59	2.6	131	4	BI024247	BI024247 CM3-MT035
C 1039	59	2.6	108	4	BI024831	BI024831 MR3-WT033	C1112	59	2.6	131	6	CB971631	CB971631 CAB10005
C 1040	59	2.6	109	2	AW331462	AW331462 707013G08	C1113	59	2.6	131	6	CF202166	CF202166 RR890915N
C 1041	59	2.6	110	4	BI002877	BI002877 MR3-HN015	C1114	59	2.6	132	2	BE964497	BE964497 601658609
C 1042	59	2.6	110	6	CF315453	CF315453 HD--04-G0	C1115	59	2.6	132	4	BI001166	BI001166 MR3-HN012
C 1043	59	2.6	110	6	CF320328	CF320328 HD--11-C2	C1116	59	2.6	133	1	AI365256	AI365256 Qx65a08.x
C 1044	59	2.6	111	6	CD018392	CD018392 NXIV_022	C1117	59	2.6	133	1	AL718314	AL718314 AL718314
C 1045	59	2.6	111	6	CF208461	CF208461 CAB2003-	C1118	59	2.6	133	2	AW079334	AW079334 x553d05.x
C 1046	59	2.6	112	1	AI244380	AI244380 q176d12.x	C1119	59	2.6	133	4	BI019339	BI019339 MR3-WT032

c1120	59	2.6	133	6	CB346420	CB346420	CAB2SG000	c1193	59	2.6	149	6	CF327124	CF327124	NACL--01-
c1121	59	2.6	133	6	CD541170	CD541170	B0229C10-	c1194	59	2.6	150	1	AI866608	AI866608	tz51h07.x
c1122	59	2.6	133	6	CF214608	CF214608	CGF100081	c1195	59	2.6	150	4	BG991108	BG991108	MR2-HT118
c1123	59	2.6	134	1	AI589993	AI589993	tx74e08.x	c1196	59	2.6	150	5	BP869360	BP869360	12-87-P18
c1124	59	2.6	134	2	AW059713	AW059713	ARUTH.bes	c1197	59	2.6	150	5	BU924529	BU924529	7032-95-M
c1125	59	2.6	134	2	AW149876	AW149876	xg30e01.x	c1198	59	2.6	150	6	CB047590	CB047590	NISC_gg03
c1126	59	2.6	134	2	CB0806612	CB0806612	ILLUMIGEN	c1199	59	2.6	150	7	CN000048	CN000048	io93c01.b
c1127	59	2.6	135	1	AA848053	AA848053	cd41h05.s	c1200	59	2.6	151	1	AI560679	AI560679	tg55a06.x
c1128	59	2.6	135	4	BI001670	BI001670	MR3-HN015	c1201	59	2.6	151	1	AI873638	AI873638	wm27g11.x
c1129	59	2.6	135	4	BI519352	BI519352	603062145	c1202	59	2.6	151	1	AL585970	AL585970	AL585970
c1130	59	2.6	135	6	CA814292	CA814292	CA48LN091	c1203	59	2.6	151	1	AL598374	AL598374	DKF2p313B
c1131	59	2.6	135	6	CB410429	CB410429	NISC_nc11	c1204	59	2.6	151	2	AW632918	AW632918	b101906.x
c1132	59	2.6	136	1	AI330333	AI330333	fa91a07.x	c1205	59	2.6	151	4	BM307176	BM307176	sak37fi12.
c1133	59	2.6	136	2	AW334729	AW334729	S37C11 AG	c1206	59	2.6	152	1	AI573026	AI573026	tn65d11.x
c1134	59	2.6	136	4	BM469626	BM469626	IPCGR3.2	c1207	59	2.6	152	2	AW500379	AW500379	UI-HF-BNO
c1135	59	2.6	136	5	BQ590040	BQ590040	E012844-0	c1208	59	2.6	152	4	BI015395	BI015395	MR4-ET024
c1136	59	2.6	136	6	CA521807	CA521807	KS11034D0	c1209	59	2.6	152	4	BI492305	BI492305	df22d10.w
c1137	59	2.6	136	6	CB054043	CB054043	NISC_gm01	c1210	59	2.6	152	4	BM612283	BM612283	170006871
c1138	59	2.6	137	1	CK615664	CK615664	ou01a08.y	c1211	59	2.6	152	5	BU068781	BU068781	2567_H04
c1139	59	2.6	137	1	AI357599	AI357599	qu20e06.x	c1212	59	2.6	152	5	CR630205	CR630205	DKF2p469G
c1140	59	2.6	137	1	AI696626	AI696626	tx68f07.x	c1213	59	2.6	153	1	AL046463	AL046463	DKF2p434A
c1141	59	2.6	137	2	BF816031	BF816031	MR2-CI018	c1214	59	2.6	153	6	CA673454	CA673454	w1e02.pk0
c1142	59	2.6	137	6	CB410347	CB410347	NISC_nc11	c1215	59	2.6	153	6	CA735721	CA735721	wp1i8.pk0
c1143	59	2.6	137	7	CF790710	CF790710	875874_MA	c1216	59	2.6	153	6	CB052185	CB052185	NISC_g106
c1144	59	2.6	137	7	CK616743	CK616743	ou35d09.y	c1217	59	2.6	153	6	CB052782	CB052782	NISC_g110
c1145	59	2.6	138	1	AI888621	AI888621	wn3h10.x	c1218	59	2.6	153	6	CB089286	CB089286	gs07c10.b
c1146	59	2.6	138	1	AI951222	AI951222	wx65a07.x	c1219	59	2.6	153	6	CF305051	CF305051	ABF1--06-
c1147	59	2.6	138	2	AW900453	AW900453	CM0-NN100	c1220	59	2.6	153	6	CF329786	CF329786	NACL--05-
c1148	59	2.6	138	6	CF337786	CF337786	JMT--08-G	c1221	59	2.6	154	1	AI539771	AI539771	tp77e11.x
c1149	59	2.6	139	1	AA830821	AA830821	oc56f09.s	c1222	59	2.6	154	1	AI620093	AI620093	tu9ze01.x
c1150	59	2.6	139	4	BI015376	BI015376	MR4-ET024	c1223	59	2.6	154	1	AI929108	AI929108	au65b12.y
c1151	59	2.6	139	5	BQ796051	BQ796051	EST_4989	c1224	59	2.6	154	1	AV669940	AV669940	AV669940
c1152	59	2.6	139	6	CB975895	CB975895	CAB40001	c1225	59	2.6	154	4	BG939829	BG939829	crf63-c03.x
c1153	59	2.6	140	2	AW083804	AW083804	xc35d07.x	c1226	59	2.6	154	4	BG977627	BG977627	CR2-CI018
c1154	59	2.6	140	4	BI015380	BI015380	MR4-ET024	c1227	59	2.6	154	4	BI053610	BI053610	MR3-GN046
c1155	59	2.6	140	6	CB0805381	CB0805381	UI-M-GW0-	c1228	59	2.6	154	6	CA672344	CA672344	w1e02.pk0
c1156	59	2.6	140	7	CK635663	CK635663	UI-M-H00-	c1229	59	2.6	156	6	CB978449	CB978449	CAB40005
c1157	59	2.6	140	7	CR545113	CR545113	DKF2p4700	c1230	59	2.6	157	1	AI570966	AI570966	to24f08.x
c1158	59	2.6	141	2	BS990379	BS990379	UI-M-B21-	c1231	59	2.6	157	2	BE964767	BE964767	601658419
c1159	59	2.6	141	4	BG995984	BG995984	MR4-HT127	c1232	59	2.6	155	4	BG981972	BG981972	MR3-MT033
c1160	59	2.6	141	7	CO176589	CO176589	NDL1_62_H	c1233	59	2.6	155	4	BI041310	BI041310	MR3-CN014
c1161	59	2.6	142	1	AA437448	AA437448	fb33910.x	c1234	59	2.6	156	6	CA673486	CA673486	w1e02.pk0
c1162	59	2.6	142	2	BF913615	BF913615	MR3-UT012	c1235	59	2.6	156	6	CB978449	CB978449	CAB40005
c1163	59	2.6	142	6	CB054093	CB054093	NISC_gm02	c1236	59	2.6	157	1	AI570966	AI570966	to24f08.x
c1164	59	2.6	142	6	CF314594	CF314594	HD--03-C2	c1237	59	2.6	157	2	BE964767	BE964767	601658419
c1165	59	2.6	143	4	BI019338	BI019338	MR3-MT032	c1238	59	2.6	157	4	BI001155	BI001155	MR3-HN012
c1166	59	2.6	143	6	CF309146	CF309146	ABF--03-D	c1239	59	2.6	157	4	BI015378	BI015378	MR4-ET024
c1167	59	2.6	143	6	CF327284	CF327284	NACL--01-	c1240	59	2.6	157	4	BI0684383	BI0684383	BJ684383
c1168	59	2.6	143	7	CF651657	CF651657	04-L02058	c1241	59	2.6	157	6	CA674135	CA674135	w1e02.pk0
c1169	59	2.6	144	1	AI611743	AI611743	tu77h07.x	c1242	59	2.6	157	6	CB970689	CB970689	CAB10004
c1170	59	2.6	144	2	BF816041	BF816041	MR2-CI018	c1243	59	2.6	157	6	CF314238	CF314238	HD--02-K2
c1171	59	2.6	144	4	BI053613	BI053613	MR3-GN046	c1244	59	2.6	158	1	AI419440	AI419440	tf38f05.x
c1172	59	2.6	144	6	CB051843	CB051843	NISC_g103	c1245	59	2.6	158	4	BG287559	BG287559	603384586
c1173	59	2.6	144	6	CB950442	CB950442	AGENCOURT	c1246	59	2.6	158	4	BI002556	BI002556	MR3-HN014
c1174	59	2.6	144	6	CB353178	CB353178	UI-M-GLO-	c1247	59	2.6	158	6	CA598443	CA598443	wy1c.pk0
c1175	59	2.6	145	1	AI805688	AI805688	tx15903.x	c1248	59	2.6	158	6	CF215202	CF215202	CAS70001
c1176	59	2.6	145	1	AW057087	AW057087	MR2-CI018	c1249	59	2.6	158	7	CK615927	CK615927	ou07f07.y
c1177	59	2.6	145	4	BG977644	BG977644	MR2-CI018	c1250	59	2.6	158	7	CN472181	CN472181	hh.Ab.Bra
c1178	59	2.6	145	4	BG980524	BG980524	MR3-CN014	c1251	59	2.6	159	1	AI470293	AI470293	cj41g11.x
c1179	59	2.6	145	4	BG992475	BG992475	MR3-HT099	c1252	59	2.6	159	1	AI539153	AI539153	tp73c08.x
c1180	59	2.6	145	6	CF300622	CF300622	7LEAF--05	c1253	59	2.6	159	4	BG996109	BG996109	MR4-HT119
c1181	59	2.6	146	2	AW633023	AW633023	b102h11.x	c1254	59	2.6	159	6	CA672755	CA672755	w1e02.pk0
c1182	59	2.6	146	4	BM585447	BM585447	170006872	c1255	59	2.6	159	6	CF330943	CF330943	NACL--06-
c1183	59	2.6	146	6	CB304008	CB304008	wsa0030.I	c1256	59	2.6	159	7	CN546646	CN546646	EST_18417
c1184	59	2.6	146	7	CN546431	CN546431	EST_18384	c1257	59	2.6	160	1	AI636719	AI636719	ts57f04.x
c1185	59	2.6	147	6	CB075436	CB075436	hz46a06.b	c1258	59	2.6	160	1	AI866082	AI866082	w125e05.x
c1186	59	2.6	147	6	CF318469	CF318469	HD--08-J1	c1259	59	2.6	160	4	BG991077	BG991077	MR2-HT118
c1187	59	2.6	147	6	CF319925	CF319925	HD--10-J2	c1260	59	2.6	160	4	BI042317	BI042317	MR4-NT014
c1188	59	2.6	147	7	CK616694	CK616694	ou24c12.y	c1261	59	2.6	160	5	BK645532	BK645532	DKF2p781J
c1189	59	2.6	148	5	BM947466	BM947466	UI-M-EG0P	c1262	59	2.6	160	6	CB976068	CB976068	w1e02.pk0
c1190	59	2.6	148	6	CF336873	CF336873	JMT--07-B	c1263	59	2.6	160	6	CB975909	CB975909	CAB40001
c1191	59	2.6	149	2	AW073898	AW073898	xb04f10.x	c1264	59	2.6	161	1	AI366549	AI366549	ao83f03.x
c1192	59	2.6	149	6	CF315389	CF315389	HD--04-E1	c1265	59	2.6	161	1	AI669639	AI669639	tw34907.x

1266	59	2.6	161	4	EG991140	CG1339	59	2.6	173	6	CB973491	CB973491
1267	59	2.6	161	5	BX955084	1340	59	2.6	173	7	AA603709	CR559321
1268	59	2.6	161	6	CA671998	1341	59	2.6	174	1	AX503608	DXF2P468G
1269	59	2.6	161	6	CA672056	1342	59	2.6	174	5	BX503608	DXF2P468G
1270	59	2.6	161	6	CF334139	1343	59	2.6	174	5	CA667523	wlsu1.pk0
1271	59	2.6	162	1	AI545030	1344	59	2.6	174	6	CF291867	14ROOT--0
1272	59	2.6	162	1	AI805638	1345	59	2.6	175	1	AI698401	tx64e10.x
1273	59	2.6	162	4	EG991087	1346	59	2.6	175	1	AI802240	tj36e02.x
1274	59	2.6	162	4	BI015391	1347	59	2.6	175	1	AI922577	wn89102.x
1275	59	2.6	162	4	BM537512	1348	59	2.6	175	2	AW129230	xf21h03.x
1276	59	2.6	162	6	CA337690	1349	59	2.6	175	2	AW130863	x66606.x
1277	59	2.6	162	6	CB082953	1350	59	2.6	175	4	EG993627	MR3-HT127
1278	59	2.6	163	2	AW156320	1351	59	2.6	175	4	EG996281	MR4-HT119
1279	59	2.6	163	2	BE027512	1352	59	2.6	175	4	BI002835	MR3-HN016
1280	59	2.6	163	2	BE072233	1353	59	2.6	175	4	BM532325	fY06608.Y
1281	59	2.6	164	1	AI643690	1354	59	2.6	175	6	CF302180	7LEAF--07
1282	59	2.6	164	1	AW088899	1355	59	2.6	176	1	AL719759	AL719759
1283	59	2.6	164	2	AW409775	1356	59	2.6	176	2	BF337479	602035215
1284	59	2.6	164	2	BE963918	1357	59	2.6	176	2	BI002842	MR3-HN016
1285	59	2.6	164	6	CB083541	1358	59	2.6	176	6	CD679051	hQ03h07.Y
1286	59	2.6	164	6	CF209989	1359	59	2.6	177	1	AI364788	qu18f06.x
1287	59	2.6	164	6	CF211607	1360	59	2.6	177	1	AI919345	tu57607.x
1288	59	2.6	164	7	CN269469	1361	59	2.6	177	2	AW088903	xd31h03.x
1289	59	2.6	165	2	AW088944	1362	59	2.6	177	2	AW151714	xf68c08.x
1290	59	2.6	165	2	AW089006	1363	59	2.6	177	4	EG027628	602296211
1291	59	2.6	165	5	BU778029	1364	59	2.6	177	5	BQ894953	AGENCOURT
1292	59	2.6	165	6	CA669317	1365	59	2.6	177	6	CA668992	wlsu1.pk0
1293	59	2.6	165	6	CB258462	1366	59	2.6	177	6	CB978729	CAB40006
1294	59	2.6	166	2	BE666175	1367	59	2.6	177	6	CF313976	HD--02-F0
1295	59	2.6	166	5	BU770824	1368	59	2.6	178	1	AI537617	tp05d10.x
1296	59	2.6	166	6	CA598254	1369	59	2.6	178	1	AI680498	tw63f03.x
1297	59	2.6	166	6	CD394052	1370	59	2.6	178	6	CF215957	CAST00002
1298	59	2.6	166	6	CA672154	1371	59	2.6	179	1	AI004911	ou59f04.x
1299	59	2.6	167	1	AI679550	1372	59	2.6	179	2	AW193203	x171907.x
1300	59	2.6	167	6	CB970037	1373	59	2.6	179	4	BX956705	DXF2P781M
1301	59	2.6	168	1	AI642413	1374	59	2.6	179	5	BX956705	DXF2P781M
1302	59	2.6	168	1	AL589450	1375	59	2.6	179	7	CO732676	SILL01b03
1303	59	2.6	168	2	AW681728	1376	59	2.6	180	1	AI499974	tn69a11.x
1304	59	2.6	168	6	CA672154	1377	59	2.6	180	1	AI698427	tx65b10.x
1305	59	2.6	168	6	CA672564	1378	59	2.6	180	1	AI699011	wc62f07.x
1306	59	2.6	168	6	CB977323	1379	59	2.6	180	1	AJ465885	AJ465885
1307	59	2.6	168	6	CD453325	1380	59	2.6	180	1	AJ484750	AJ484750
1308	59	2.6	168	6	CF319725	1381	59	2.6	180	4	BI019323	MR3-WT032
1309	59	2.6	168	6	CF320327	1382	59	2.6	180	4	BI870913	603394458
1310	59	2.6	168	7	CK996023	1383	59	2.6	180	4	BJ365372	BU365372
1311	59	2.6	169	2	AW834355	1384	59	2.6	180	6	CF291836	14ROOT--0
1312	59	2.6	169	4	BI019332	1385	59	2.6	180	7	CF511415	CABud0002
1313	59	2.6	169	4	BI054915	1386	59	2.6	180	7	CN281024	170004182
1314	59	2.6	169	6	CB083355	1387	59	2.6	181	1	AI567637	tp62d02.x
1315	59	2.6	170	1	AI471361	1388	59	2.6	181	1	AI569328	tx79908.x
1316	59	2.6	170	4	BG956250	1389	59	2.6	181	1	AL715700	AL715700
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ALIGNMENTS

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RESULT 1
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LOCUS full-length cDNA clone CSODN001YK12 of Adult brain of Homo sapiens
DEFINITION CR610360
ACCESSION CR610360.1 GI:50491167
VERSION HRC; CNSLT_cDNA.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 2105)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 2105)
REFERENCE Genoscope.
AUTHORS Direct Submission
TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES Location/Qualifiers
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Best Local Similarity 99.8%; Pred. No. 0;
Matches 2101; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Db 1 AATAGCTCCACTATACAGGCTCGTCTCTTCCTCCGGGGGACACAGTGGGTGAGGCGACAG 60

Oy 100 AGAGATATTTAATGTCACCTCTTGGGGCTTCATGGAGCTCCCTCTGCCACATTTTGTG 159
Db 61 AGAGATATTTAATGTCACCTCTTGGGGCTTCATGGAGCTCCCTCTGCCACATTTTGTG 120

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QY	160	GAGGTTGGGAAAGCTTGCTAGAGCTTTCAGAACTCCAGCGCTAATGATCCCAAACTCGGGA	219
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QY	220	GAATGGCTGGCTCCCTGCTGGCTGTGCTGCTGCTGCTGAGCGCGGCAATGTTTCCT	279
DB	181	GAATGGCTGGCTCCCTGCTGGCTGTGCTGCTGCTGCTGAGCGCGCATGTTTCCT	240
QY	280	CACCTTCCCGCCCCCGGCGCTGTAGAGAAAGTCTTCAGTACATTCAGCTCCCATCAGG	339
DB	241	CACCTTCCCGCCCCCGGCGCTGTAGAGAAAGTCTTCAGTACATTCAGCTCCCATCAGG	300
QY	340	ATGAATTTGTGCAGACGCTGAAGAGTGGGTGGCCATCGAGAGCACTCTGTCCAGCCTG	399
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QY	400	TGCCTCGCTTCAGACAAGAGCTCTTCAGAAATGATGGCCGTGCTGCGGACACGCTGACG	459
DB	361	TGCCTCGCTTCAGACAAGAGCTCTTCAGAAATGATGGCCGTGCTGCGGACACGCTGACG	420
QY	460	GCCTGGGGGCGCGTGTGGCTTCGGTGACATGGGTCTTCAGCAGCTGCCGATGTCAGA	519
DB	421	GCCTGGGGGCGCGTGTGGCTTCGGTGACATGGGTCTTCAGCAGCTGCCGATGTCAGA	480
QY	520	GTCTTCCAAATACCTCCCGTCACTCTGCCGAACTGGGAGCGATCCCAAGAAAGCACCG	579
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QY	640	ACCCCTATGCTCAACGAGGTAGACGGGAACTTTATGGACGAGCAGCAGCGACAACA	699
DB	601	ACCCCTATGCTCAACGAGGTAGACGGGAACTTTATGGACGAGCAGCAGCGACAACA	660
QY	700	AAGGCCCTGTCTGGCTTGGATCAATGCTGTGAGCGCTTCAGAGCCCTGGAGCAAGATC	759
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QY	940	GCTACTTTCATGGTGGAGTGAAATGCGAGACCAAGATTTTCACTCAGGAACCTTTGGTG	999
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QY	1000	GCATCTTTCATGAACCAATGCTGATCTGGTGTCTTCTCGGTAGCTCGGTAGACTCGT	1059
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Db	1561	TAATTCCGCTGGGAGCTGTGATGTGGAGAACATTCGACAGATGAGAAAATCAAACAGT	1620
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Qy	1840	CCTTCCATTTAAATGTCTGGGATATCTGGATCAGTAAATAAAATATTTCAAAGGCACAG	1899
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Qy	1900	ATGTTGGAAATGGTTTAAAGGTCCCCACTGCACACCTTCTCAAGTCATAGTGTCTGCA	1959
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Qy	1960	GCAACTTGAATTTCCCAAGTCTGTGCAATAGCCCAAGATTCGGATTCCTTCCAAACCTTTT	2019
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Qy	2080	CTCAAGTGCTGTCGACACATAATCATTTCCATCCAAATGATCGCCTTGTCTTTACCACTCTT	2139
Db	2041	CTCAAGTGCTGTCGACACATAATCATTTCCATCCAAATGATCGCCTTGTCTTTACCACTCTT	2100
Qy	2140	TCCTTT 2144	
Db	2101	TCCTT 2105	

RESULT 2	
BC004271	BC004271
LOCUS	1528 bp mRNA linear HTC 26-APR-2004
DEFINITION	Homo sapiens carnosine dipeptidase 1 (metalloproteinase M20 family), mRNA (CDNA clone IMAGE13614507), with apparent retained intron.
ACCESSION	BC004271
VERSION	BC004271.1 GI:13279082
KEYWORDS	HTC.
SOURCE	Homo sapiens (human)

QY	1896	ACAGATGTTGGAAATGGTTTAAGTCCCCACCTGCACACCTTCCTCAAGTCATAGTGCT	1955
Db	1220	ACAGATGTTGGAAATGGTTTAAGTCCCCACCTGCACACCTTCCTCAAGTCATAGTGCT	1279
QY	1956	TGACGAACTTGAATTTCCCAAGTCTGTGCAATAGCCCAAGATTTGGATTCTTCCCAAC	2015
Db	1280	TGACGAACTTGAATTTCCCAAGTCTGTGCAATAGCCCAAGATTTGGATTCTTCCCAAC	1339
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Db	1400	GGTCCTCAAGTGTGTGACACATAATCAATCCATCAATGATCGCTTGTCTTACCAAC	1459
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Db	1460	TCCTTCTCTTTATCTTAATTAATAAATGTTGTCTCCACCCTG	1504
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BX453730/c			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
Contact: Genoscope			
Genoscope - Centre National de Sequencage			
BP 191 91006 EVRY cedex - France			
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr			
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime			
end enriched, double-strand cDNA was digested with Not I and cloned			
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library			
was not normalized. Library was constructed by Life Technologies, a			
division of Invitrogen.			
This sequence belongs to sequence cluster 9111.f			
For more information about this cluster, see			
http://www.genoscope.cns.fr/cdna?s=CS0BA1053ZD09_CS05060_1&c=9111.f			
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vector. Library was not normalized."			
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Best Local Similarity			
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30.7%; Score 688; DB 5; Length 913;			
99.9%; Pred. No. 0;			
Mismatches 1; Indels 0; Gaps 0;			
QY	511	ATGGTCAGAGTCTTCAATACCTCCGTCATCTTGGCGAAGTGGGAGCGATCCACGA	570

into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Invitrogen.
This sequence belongs to sequence cluster 9111.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna/s=CS0BAG089ZALL_CS06609_1kc=9111.f

FEATURES
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ORIGIN
Query Match 30.6%; Score 687; DB 5; Length 928;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 76 GGAACCCGGGGAACAGCTACTTTCATGCTGAGGTGAATCAGACGACGAGTTCAC 135
Qy 984 TCAGAACTTTGGTGGCATCTTTCATGAACCAATGGCTGATCTGTTGCTTCTCGGT 1043
Db 136 TCAGAACTTTGGTGGCATCTTTCATGAACCAATGGCTGATCTGTTGCTTCTCGGT 195
Qy 1044 AGCTGTGATGACTGCTGTGTCATATCTGCTGCTTCCCTGGAATCTATGATGAAGTGTCT 1103
Db 196 AGCTGTGATGACTGCTGTGTCATATCTGCTGCTTCCCTGGAATCTATGATGAAGTGTCT 255
Qy 1104 CTTACAGAGAGGAATAAATACATACAAAGCCATCCATCTAGACCTAGAGATACCGG 1163
Db 256 CTTACAGAGAGGAATAAATACATACAAAGCCATCCATCTAGACCTAGAGATACCGG 315
Qy 1164 AATAGCAGCCGGTGTGAGAAATTTCTGTCGATCTAAGGAGGAGATCTTAATGACCTC 1223
Db 316 AATAGCAGCCGGTGTGAGAAATTTCTGTCGATCTAAGGAGGAGATCTTAATGACCTC 375
Qy 1224 TGGAGGTACCATCTCTTTCTATTTCATGGGATCGAGGGCGGTTTGTATGAGCCTGGAACT 1283
Db 376 TGGAGGTACCATCTCTTTCTATTTCATGGGATCGAGGGCGGTTTGTATGAGCCTGGAACT 435
Qy 1284 AAACAGTTCATCTGCGGAGTTATAGGAAATTTTCAATCCCTAGTCCCTCAGATG 1343
Db 436 AAACAGTTCATCTGCGGAGTTATAGGAAATTTTCAATCCCTAGTCCCTCAGATG 495
Qy 1344 AATGTGTCTGCGGTGGAAGAAACAGGTGACAGCATCTTGAAGATGTGTTCTCAAGAA 1403
Db 496 AATGTGTCTGCGGTGGAAGAAACAGGTGACAGCATCTTGAAGATGTGTTCTCAAGAA 555
Qy 1404 AATAGTTCACAGAGTGTGTTTCCATGACTTAGAGCTACACCCGTGGATTCAGAA 1463
Db 556 AATAGTTCACAGAGTGTGTTTCCATGACTTAGAGCTACACCCGTGGATTCAGAA 615
Qy 1464 ATTGATGACCCAGTATCTCGAGCAAAAGAGGATCAGAACAGTGTGGAACAGAA 1523
Db 616 ATTGATGACCCAGTATCTCGAGCAAAAGAGGATCAGAACAGTGTGGAACAGAA 675
Qy 1524 CCAGATATGATCCGGGATGGATCCACCAATTCGCAAAATGTTCCAGGAGATCGTC 1583
Db 676 CCAGATATGATCCGGGATGGATCCACCAATTCGCAAAATGTTCCAGGAGATCGTC 735
Qy 1584 CACAAGAGCGGTGCTTAATTCGCTG 1610
|||||

Db 736 CACAAGAGCGGTGCTTAATTCGCTG 762
RESULT 5
BI754224
LOCUS
DEFINITION 603025522F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5196053 5', mRNA sequence.
ACCESSION BI754224
VERSION BI754224.1 GI:15745802
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 799)
AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@rs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LJM11490 row: 1 column: 06
High quality sequence stop: 797.
Location/Qualifiers
1. 799
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/clone="IMAGE:5196053"
/lab_host="DH10B"
/clone_lib="NIH_MGC_114"
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruher (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH_MGC Library."

ORIGIN
Query Match 30.3%; Score 679; DB 4; Length 799;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 244 TGCTGTGCTGCTGCTGAGCGGCGCATGTTCTCTCACCTCCCGCCCGCGCTGT 303
Db 94 TGCTGTGCTGCTGCTGAGCGGCGCATGTTCTCTCACCTCCCGCCCGCGCTGT 153
Qy 304 TAGAGAAAGTCTTCCAGTACATTCACCTCCATCAGGATGAATTTGTGCAGACGCTGAAG 363
Db 154 TAGAGAAAGTCTTCCAGTACATTCACCTCCATCAGGATGAATTTGTGCAGACGCTGAAG 213
Qy 364 AGTGGGTGGCCATCGAGAGCGACTCTCTCCAGCTGTGCTCGCTTCAGACAGAGCTCT 423
Db 214 AGTGGGTGGCCATCGAGAGCGACTCTCTCCAGCTGTGCTCGCTTCAGACAGAGCTCT 273
Qy 424 TCAGAAATGATGGCGGTGGCTGCGGACACGCTGCAGCGCTGGGGGCCCGTGTGGCCCTCGG 483
Db 274 TCAGAAATGATGGCGGTGGCTGCGGACACGCTGCAGCGCTGGGGGCCCGTGTGGCCCTCGG 333
Qy 484 TGGACATGGTCTCAGCAGCTGCCCGATGGTCAGAGTCTTCCATACCTCCCGCTCATCC 543
Db 334 TGGACATGGTCTCAGCAGCTGCCCGATGGTCAGAGTCTTCCATACCTCCCGCTCATCC 393
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QY	544	TGCGCGAACTGGGAGCGATCCACAGAAAGGCACCGTGTGCTTCTACGGCCACTTGGAGG	603
Db	394	TGCGCGAACTGGGAGCGATCCACAGAAAGGCACCGTGTGCTTCTACGGCCACTTGGAGG	453
QY	604	TGCAGGCTCTGACCGGGGCGATGGGTGCTCACGGACCCCTATGTGTGTGACGGAGGTAG	663
Db	454	TGCAGGCTCTGACCGGGGCGATGGGTGCTCACGGACCCCTATGTGTGTGACGGAGGTAG	513
QY	664	ACGGGAAACTTTATGACGAGGAGCGACCGACAAAGAGCCCTGTCTGGCTTGGATCA	723
Db	514	ACGGGAAACTTTATGACGAGGAGCGACCGACAAAGAGCCCTGTCTGGCTTGGATCA	573
QY	724	ATGCTGTGAGCGCTTTCAGAGCCCTCGAGCAAGATCTTCTGTGATATCAAAATTCATCA	783
Db	574	ATGCTGTGAGCGCTTTCAGAGCCCTCGAGCAAGATCTTCTGTGATATCAAAATTCATCA	633
QY	784	TTGAGGGGATGGAAGAGGCTGGCTCTGTTGCCCTGGAGGAACCTTGTGAAAAAGAAAGG	843
Db	634	TTGAGGGGATGGAAGAGGCTGGCTCTGTTGCCCTGGAGGAACCTTGTGAAAAAGAAAGG	693
QY	844	ACCGATTTCTCTGTGTGGATACATATGTAATTTTCAGATAACCTGTGGATCAGCCAAA	903
Db	694	ACCGATTTCTCTGTGTGGATACATATGTAATTTTCAGATAACCTGTGGATCAGCCAAA	753
QY	904	GGAGCCAGCAATCACTTA 922	
Db	754	GGAGCCAGCAATCACTTA 772	

RESULT 6
BX422768
LOCUS
DEFINITION BX422768 Homo sapiens ADULT BRAIN Homo sapiens cDNA clone
CS0DN001YK12 5-PRIME, mRNA sequence.
BX422768
VERSION BX422768.2 GI:46934365
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 13, 2003 this sequence version replaced gi:30655387.

Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 9111.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0DN001BF06QPl&c=9111.f.

FEATURES
Location/Qualifiers
1..1006
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/db_xref="taxon:9606"
/clone="CS0DN001YK12"
/tissue_type="ADULT BRAIN"
/dev_stage="adult"
/clone_lib="Homo sapiens ADULT BRAIN"
/note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."

ORIGIN

Query Match		29.9%; Score 670; DB 5; Length 1006;
Best Local Similarity		100.0%; Pred. No. 0;
Matches		670; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	244	TGCTGTCTGTCTGTGGAGCGGGCATGTTCTCTCACCTCCCGCCCGCGCGCTGT 303
Db	208	TGCTGTCTGTCTGTGGAGCGGGCATGTTCTCTCACCTCCCGCCCGCGCGCTGT 267
QY	304	TAGAGAAAGTCTTCCAGTACATTGACCTCCATCAGGATGAATTTGTGCAGACGCTGAAGG 363
Db	268	TAGAGAAAGTCTTCCAGTACATTGACCTCCATCAGGATGAATTTGTGCAGACGCTGAAGG 327
QY	364	AGTGGGTGGCCATCGAGAGCGACTCTGTTCAGCCTGTGCTCGCTTCAGACAGAGCTCT 423
Db	328	AGTGGGTGGCCATCGAGAGCGACTCTGTTCAGCCTGTGCTCGCTTCAGACAGAGCTCT 387
QY	424	TCAGAAATGATGGCCGTGTGCGGACACGCTGCAGCGCTGGGGCCCGTGTGGCCTCGG 483
Db	388	TCAGAAATGATGGCCGTGTGCGGACACGCTGCAGCGCTGGGGCCCGTGTGGCCTCGG 447
QY	484	TGGACATGGGTCTCTCAGCAGCTGCCCGATGGTTCAGAGTCTTCCAAATACCTCCCGTCATCC 543
Db	448	TGGACATGGGTCTCTCAGCAGCTGCCCGATGGTTCAGAGTCTTCCAAATACCTCCCGTCATCC 507
QY	544	TGGCCGAACTGGGAGCGATCCACGAAAGGCACCGTGTGCTTCTACGGCCACTTGGACG 603
Db	508	TGGCCGAACTGGGAGCGATCCACGAAAGGCACCGTGTGCTTCTACGGCCACTTGGACG 567
QY	604	TGCAGCTGTCTGACCGGGCGATGGTGTGCTCACGGACCCCTATGTGTGACGGAGGTAG 663
Db	568	TGCAGCTGTCTGACCGGGCGATGGTGTGCTCACGGACCCCTATGTGTGACGGAGGTAG 627
QY	664	ACGGGAAACTTTATGAGAGGAGCGACCGACAAAGAGCCCTGTCTGGCTTGGATCA 723
Db	628	ACGGGAAACTTTATGAGAGGAGCGACCGACAAAGAGCCCTGTCTGGCTTGGATCA 687
QY	724	ATGCTGTGAGCGCCTTTCAGAGCCCTGGAGCAAGATCTTCTGTGAAATCAAAATTCATCA 783
Db	688	ATGCTGTGAGCGCCTTTCAGAGCCCTGGAGCAAGATCTTCTGTGAAATCAAAATTCATCA 747
QY	784	TTGAGGGGATGGAAGAGGCTGGCTCTGTTGCCCTGGAGGAACCTTGTGAAAAAGAAAGG 843
Db	748	TTGAGGGGATGGAAGAGGCTGGCTCTGTTGCCCTGGAGGAACCTTGTGAAAAAGAAAGG 807
QY	844	ACCGATTTCTCTGTGTGGACTACATTTGTAATTTTCAGATAACCTGTGGATCAGCCAAA 903
Db	808	ACCGATTTCTCTGTGTGGACTACATTTGTAATTTTCAGATAACCTGTGGATCAGCCAAA 867
QY	904	GGAGCCAGC 913
Db	868	GGAGCCAGC 877
RESULT 7		
Bi6671149		
LOCUS		
DEFINITION		
730 bp mRNA linear EST 12-SEP-2001		
603291543F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5310730 5',		
mRNA sequence.		
Bi6671149		
Bi6671149.1 GI:15581382		
EST.		
Homo sapiens (human)		
Homo sapiens		
Homo sapiens		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
1 (bases 1 to 730)		
NIH-MGC http://mgs.nci.nih.gov/		
National Institutes of Health, Mammalian Gene Collection (MGC)		
Unpublished (1999)		
Contact: Robert Strausberg, Ph.D.		
Email: cgabb-r@mail.nih.gov		
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.		
REFERENCE		
AUTHORS		
TITLE		
JOURNAL		
COMMENT		

RESULT 7
BX422768
LOCUS
DEFINITION 603291543F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5310730 5',
mRNA sequence.
BX422768
VERSION BX422768.1 GI:15581382
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 730)
NIH-MGC http://mgs.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

Qy	633	CTCAGGACCCCTATGTGCTGACGGAGGTAGACGGGAACCTTTATGGACGAGGAGCGACC	692
Db	606	CTCAGGACCCCTATGTGCTGACGGAGGTAGACGGGAACCTTTATGGACGAGGAGCGACC	665
Qy	693	GACAAACAAGGCCCTG	708
Db	666	GACAAACAAGGCCCTG	681

RESIT.T 8

RESULT 8	
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LOCUS	674 bp mRNA linear EST 07-SEP-2001
DEFINITION	603245407F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:528787 5', mRNA sequence.
ACCESSION	BI598229
VERSION	BI598229.1
KEYWORDS	GI:15491168
SOURCE	EST.
ORGANISM	Homo sapiens (human)
	Homo sapiens
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 674)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraiki Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLAM11727 row: n column: 02
High quality sequence stop: 674.

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Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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High quality sequence stop: 674.
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/lab_host="DH10B"
/clone_lib="NIH MGC 96"
/notes="Organ: brain; Vector: pBluescriptR (modified
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI
(ctcgag); Oligo-dT primed using primer
5'-TTTTTTTTTTTTTTTTVN-3', size-selected for average
insert size 2.3 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIMH/NHGRI, National Institutes of Health). Note: this is
a NIH_MGC Library."

ORIGIN

Query Match 26.4%; Score 592; DB 4; Length 674;
Best Local Similarity 99.8%; Pred. No. 4.6e-278;
Matches 642; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAATGAATACCTCCGAAGCGCGTTGTTCTCCAGATGTGAATAGCTCCATACAGCC 60
Db |||
32 GAATGAATACCTCCGAAGCGCGTTGTTCTCCAGATGTGAATAGCTCCATACAGCC 91
Qy |||
61 TCGTCTTCTCCGGGGGACACGTGGGTGAGGCACAGAGATATTTAATGTACACCT 120
Db |||
92 TCGTCTTCTCCGGGGGACACGTGGGTGAGGCACAGAGATATTTAATGTACACCT 151
Qy |||
121 CTTGGGCGCTTCATGGGACTCCCTCTCGCCACATTTTTTTCGAGGTTGGGAAAGTTGCTAGA 180

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ORIGIN
a NIN_MGC LIBRARY.

Query Match	26.4%	Score 592;	DB 4;	Length 674;
Best Local Similarity	99.8%	Pred. No. 4.6e-278;		
Matches 642;	Conservative	0;	Mismatches 1;	Indels 0;
				Gaps 0;

Qy	1	GAATGAATACCTCCGAAGCGCGTTTGTTCAGATGTGAATAGTCTCCATATACAGCC	60
Db	32	GAATGAATACCTCCGAAGCGCGTTTGTTCAGATGTGAATAGTCTCCATATACAGCC	91
Qy	61	TGCTTTCTTCCTCCGGGGACACGTCGGTTCAGGGCACAGAGATATTTAAATGTCAACCT	120
Db	92	TGCTTTCTTCCTCCGGGGACACGTCGGTTCAGGGCACAGAGATATTTAAATGTCAACCT	151
Qy	121	CTTTGGGCGCTTTCATGGGACTCCCTCTGCCACACATTTTTCGAGGTTCGGAAAGTTGCTAGA	180

ORIGIN


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Qy 2085 GTGCTCGTGACATAATCATTCATCAATGATCGCTTTGCTTTTACCACCTCTTTTCCTT 2144
Db 107 GTGCTCGTGACATAATCATTCATCAATGATCGCTTTGCTTTTACCACCTCTTTTCCTT 48
Qy 2145 TTATCTTATTATAAAAAATGTTGCTCTCCA 2174
Db 47 TTATCTTATTATAAAAAATGTTGCTCTCCA 18

RESULT 13
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LOCUS
DEFINITION BX110726 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:5288268 1910
IMAGE:2015275, mRNA sequence.
ACCESSION BX110726
VERSION BX110726
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE (bases 1 to 567)
JOURNAL Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M.,
COMMENT Radelof, U., Schneider, D. and Korn, B.
Human Unigeneset - RZPD3
Unpublished (2003)
Contact: Ina Rofls
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGp998204957.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
http://www.rzpd.de/CloneCards/cgi-bin/showlib.pl.cgi?response?libNo=972 Contact: Ina Rofls
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (Clone@rzpd.de) for further information. Seq primer:
M13r, Primer sequence: TTTCCACAGGAACACGCTATGAC.
LOCATION/Qualifiers
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/clone_lib="NCI_CGAP_Brn23"
/notes="Organ: brain; Vector: p773D-Pac (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGCATATCTTTTCTTTTCTTTTCTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified p773 vector.
Library is normalized, and was constructed by Bento
Soares and M.Patima Bonaldo."

ORIGIN
Query Match 25.3%; Score 567; DB 5; Length 567;
Best Local Similarity 100.0%; Pred. No. 8e-266;
Matches 567; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1611 GGAGCTGTTGATGAGAACATTCGAGAAATGAGAAATCAACAGGTGAACTACATA 1670
Db 1 GGAGCTGTTGATGAGAACATTCGAGAAATGAGAAATCAACAGGTGAACTACATA 60
Qy 1671 GAGGAACCAAAATATTGCTGCTTTTCTTAGAGATGGCCAGCTCCATTAATCAAA 1730

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Db 61 GAGGAACCAAAATATTGCTGCTTTTCTTAGAGATGGCCAGCTCCATTAATCAAA 120
Qy 1731 GAACCTTTAGTCTGATCTGATCCACAGTACAGATTTACCTCCCCACATCCCTAGACAGG 1790
Db 121 GAACCTTTAGTCTGATCTGATCCACAGTACAGATTTACCTCCCCACATCCCTAGACAGG 180
Qy 1791 GATGGAATGTAATATCCAGAGAAATTTGGGTCTAGTATAGTACATTTTCCCTTCCATTTA 1850
Db 181 GATGGAATGTAATATCCAGAGAAATTTGGGTCTAGTATAGTACATTTTCCCTTCCATTTA 240
Qy 1851 AAATGCTTTGGGATATCTGATCAGTAATAAATAATTTTCAAGGCACAGATGTTGGAAAT 1910
Db 241 AAATGCTTTGGGATATCTGATCAGTAATAAATAATTTTCAAGGCACAGATGTTGGAAAT 300
Qy 1911 GGTTTAAGGTCCCCCACTGCACACCTTCCCTCAAGTCATAGCTGCTGCAGCAACTTGATT 1970
Db 301 GGTTTAAGGTCCCCCACTGCACACCTTCCCTCAAGTCATAGCTGCTGCAGCAACTTGATT 360
Qy 1971 TCCCCAAGTCCTGTGCAATAGCCCCAGGATTTGGATTCCTTCCAACTTTTAGCATATCTC 2030
Db 361 TCCCCAAGTCCTGTGCAATAGCCCCAGGATTTGGATTCCTTCCAACTTTTAGCATATCTC 420
Qy 2031 CAACCTTTGCAATTTGATTGGCAATAATCACCCTCCGCTTTGCTTTCTAGTCTCAAGTGCTC 2090
Db 421 CAACCTTTGCAATTTGATTGGCAATAATCACCCTCCGCTTTGCTTTCTAGTCTCAAGTGCTC 480
Qy 2091 GTGACACATAATCATTCATCCATCCATGATCGCTTTGCTTTTACCACTCTTTTCTTTTATCT 2150
Db 481 GTGACACATAATCATTCATCCATCCATGATCGCTTTGCTTTTACCACTCTTTTCTTTTATCT 540
Qy 2151 TATTATAAAAAATGTTGGTCTCCACCA 2177
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RESULT 14
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DEFINITION BI600248 603245955F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5288268 5',
mRNA sequence.
ACCESSION BI600248
VERSION BI600248.1 GI:15493187
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 887)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@emall.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11728 row: n column: 13
High quality sequence stop: 819.
LOCATION/Qualifiers
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Qy      576 ACCGTGTGCTTCTACGGCCACTTTGGACGTGACCGTGTGACCCGGGGCGATGGGTGGCTC 635
Db      549 ACCGTGTGCTTCTACGGCCACTTTGGACGTGACCGTGTGACCCGGGGCGATGGGTGGCTC 608
Qy      636 ACGGACCCCTATGTGCTGACCGGAGGTAGACGGGAACTTTATGGACGAGGAGCGA 690
Db      609 ACGGACCCCTATGTGCTGACCGGAGGTAGACGGGAACTTTATGGACGAGGAGCGA 663
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Search completed: February 1, 2005, 18:51:45
Job time : 6496 secs

THIT SHIT
EAGLE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 1, 2005, 16:50:12 ; Search time 210 Seconds
(without alignments)
7588:517 Million cell updates/sec

Title: US-10-036-342-56

Perfect score: 2242

Sequence: 1 gaatgaataacctccgaagcc.....aaaaaaaaaaaaaaaaaaaa 2242

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 824507 seqs, 355394441 residues

Word size : 6

Total number of hits satisfying chosen parameters: 1614795

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1500 summaries

Database : Issued_Patents_NA.*

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- 5: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	314	14.0	672	4	US-09-621-976-97
2	180	8.0	300	4	US-09-513-999C-13950
3	61	2.7	1733	3	US-09-073-569-1
4	60	2.7	146	4	US-09-621-976-8550
5	60	2.7	147	4	US-09-621-976-8551
6	60	2.7	1904	4	US-10-140-002-99
7	60	2.7	4086	4	US-09-702-705-1801
8	60	2.7	4086	4	US-09-736-457-1801
9	60	2.7	4086	4	US-09-671-325-1801
10	59	2.6	157	4	US-09-621-976-10271
11	59	2.6	190	4	US-09-621-976-16784
12	59	2.6	342	4	US-09-270-767-13044
13	59	2.6	639	4	US-09-482-273-49
14	59	2.6	1651	4	US-09-800-729-41
15	59	2.6	1868	4	US-09-739-455-1
16	59	2.6	1878	4	US-09-732-025-1
17	59	2.6	2083	4	US-09-716-129-41
18	59	2.6	2989	6	5378464-1
19	58	2.6	80	1	US-07-920-281C-25
20	58	2.6	80	3	US-08-466-277-25
21	58	2.6	80	4	US-09-688-842-25
22	58	2.6	196	4	US-09-644-460-40
23	58	2.6	253	4	US-09-621-976-12799
24	58	2.6	263	4	US-09-031-097-26
25	58	2.6	441	4	US-09-601-537-10
26	58	2.6	470	3	US-09-020-956-102
27	58	2.6	470	3	US-09-030-607-102

101	58	2.6	3350	2	US-08-288-065A-1	Sequence 1, Appl1	174	57	2.5	1307	2	US-08-960-022-17	Sequence 17, Appl1
102	58	2.6	3350	2	US-08-362-240A-1	Sequence 1, Appl1	175	57	2.5	1319	2	US-08-504-459-7	Sequence 7, Appl1
103	58	2.6	3350	5	PCT-US95-10245-1	Sequence 1, Appl1	176	57	2.5	1332	2	US-09-057-762-1	Sequence 1, Appl1
104	58	2.6	4121	4	US-09-601-537-9	Sequence 9, Appl1	177	57	2.5	1332	3	US-08-326-119A-1	Sequence 1, Appl1
105	58	2.6	8100	4	US-09-554-337-4	Sequence 4, Appl1	178	57	2.5	1359	3	US-09-387-574-11	Sequence 11, Appl1
106	58	2.6	11517	1	US-07-920-281C-1	Sequence 1, Appl1	179	57	2.5	1359	3	US-09-668-096-11	Sequence 11, Appl1
107	58	2.6	11517	3	US-08-466-277-1	Sequence 1, Appl1	180	57	2.5	1441	3	US-08-821-994-63	Sequence 63, Appl1
108	58	2.6	11517	4	US-09-688-842-1	Sequence 1, Appl1	181	57	2.5	1445	3	US-08-814-951A-1	Sequence 1, Appl1
109	58	2.6	15538	4	US-09-554-337-1	Sequence 1, Appl1	182	57	2.5	1459	4	US-09-537-654-3	Sequence 3, Appl1
110	57	2.5	92	4	US-09-621-976-13620	Sequence 13620, A	183	57	2.5	1538	4	US-09-205-258-193	Sequence 193, Appl1
111	57	2.5	97	4	US-09-621-976-9086	Sequence 9086, Ap	184	57	2.5	1540	4	US-09-560-761-3	Sequence 3, Appl1
112	57	2.5	109	4	US-09-621-976-14592	Sequence 14592, A	185	57	2.5	1545	4	US-09-559-023-1	Sequence 1, Appl1
113	57	2.5	127	4	US-09-621-976-13933	Sequence 13933, A	186	57	2.5	1559	4	US-09-489-847-42	Sequence 42, Appl1
114	57	2.5	134	4	US-09-621-976-18433	Sequence 18433, A	187	57	2.5	1602	1	US-08-530-950-3	Sequence 3, Appl1
115	57	2.5	137	4	US-09-621-976-18434	Sequence 18434, A	188	57	2.5	1602	3	US-08-888-429A-3	Sequence 3, Appl1
116	57	2.5	142	4	US-09-621-976-10801	Sequence 10801, A	189	57	2.5	1602	3	US-09-149-879-3	Sequence 3, Appl1
117	57	2.5	147	4	US-09-621-976-10254	Sequence 10254, A	190	57	2.5	1602	4	US-09-057-003-3	Sequence 3, Appl1
118	57	2.5	150	4	US-09-621-976-8656	Sequence 8656, Ap	191	57	2.5	1602	4	US-09-593-653-3	Sequence 3, Appl1
119	57	2.5	160	4	US-09-621-976-10335	Sequence 10335, A	192	57	2.5	1639	2	US-08-737-524B-1	Sequence 1, Appl1
120	57	2.5	163	4	US-09-621-976-9608	Sequence 9608, Ap	193	57	2.5	1813	3	US-09-071-224-3	Sequence 3, Appl1
121	57	2.5	165	4	US-09-621-976-8127	Sequence 8127, Ap	194	57	2.5	1827	4	US-09-720-318A-9	Sequence 9, Appl1
122	57	2.5	169	4	US-09-621-976-8127	Sequence 8127, Ap	195	57	2.5	1827	4	US-09-370-253-1	Sequence 1, Appl1
123	57	2.5	176	4	US-09-621-976-11249	Sequence 11249, A	196	57	2.5	1882	4	US-09-419-673-3	Sequence 3, Appl1
124	57	2.5	177	4	US-09-621-976-13903	Sequence 13903, A	197	57	2.5	1883	4	US-10-140-002-501	Sequence 501, Appl1
125	57	2.5	179	4	US-09-621-976-9575	Sequence 9575, Ap	198	57	2.5	1895	4	US-09-444-336-7	Sequence 7, Appl1
126	57	2.5	194	4	US-09-621-976-801	Sequence 801, Appl	199	57	2.5	2082	2	US-08-785-310A-2	Sequence 2, Appl1
127	57	2.5	249	4	US-09-621-976-19144	Sequence 19144, A	200	57	2.5	2158	1	US-07-602-608-1	Sequence 1, Appl1
128	57	2.5	271	4	US-09-621-976-10380	Sequence 10380, A	201	57	2.5	2158	1	US-08-261-578-1	Sequence 1, Appl1
129	57	2.5	272	4	US-09-270-767-11902	Sequence 11902, A	202	57	2.5	2186	4	US-09-360-545-66	Sequence 66, Appl1
130	57	2.5	304	4	US-09-621-976-16099	Sequence 16099, A	203	57	2.5	2276	4	US-10-140-003-9	Sequence 9, Appl1
131	57	2.5	316	4	US-09-513-999C-838	Sequence 838, Appl	204	57	2.5	2381	1	US-08-021-608D-9	Sequence 9, Appl1
132	57	2.5	331	4	US-09-621-976-16100	Sequence 16100, A	205	57	2.5	2381	1	US-08-726-160-9	Sequence 9, Appl1
133	57	2.5	324	4	US-09-621-976-16434	Sequence 16434, A	206	57	2.5	2381	5	PCT-US94-01782-9	Sequence 9, Appl1
134	57	2.5	350	4	US-09-621-976-16342	Sequence 16342, A	207	57	2.5	2384	1	US-08-021-608D-1	Sequence 1, Appl1
135	57	2.5	491	4	US-09-311-021-1591	Sequence 1591, Appl	208	57	2.5	2384	1	US-08-726-160-1	Sequence 1, Appl1
136	57	2.5	558	4	US-09-043-861-3	Sequence 3, Appl1	209	57	2.5	2384	5	PCT-US94-01782-1	Sequence 1, Appl1
137	57	2.5	578	4	US-09-602-877A-95	Sequence 95, Appl1	210	57	2.5	2442	4	US-09-575-081B-3	Sequence 3, Appl1
138	57	2.5	593	4	US-09-904-615-59	Sequence 59, Appl1	211	57	2.5	2718	4	US-09-667-135-1	Sequence 1, Appl1
139	57	2.5	630	1	US-08-185-414B-1	Sequence 1, Appl1	212	57	2.5	2806	4	US-09-653-839-9	Sequence 9, Appl1
140	57	2.5	674	4	US-09-620-405B-465	Sequence 465, Appl	213	57	2.5	2806	4	US-10-202-619-9	Sequence 9, Appl1
141	57	2.5	674	4	US-09-433-826B-465	Sequence 465, Appl	214	57	2.5	2852	3	US-09-027-137-2	Sequence 2, Appl1
142	57	2.5	674	4	US-09-604-287A-465	Sequence 465, Appl	215	57	2.5	2852	3	US-09-344-441-2	Sequence 2, Appl1
143	57	2.5	674	4	US-09-834-759-465	Sequence 465, Appl	216	57	2.5	2933	4	US-10-140-003-345	Sequence 345, Appl
144	57	2.5	674	4	US-09-590-751A-465	Sequence 465, Appl	217	57	2.5	2964	4	US-09-578-063-25	Sequence 25, Appl1
145	57	2.5	703	3	US-09-313-300-6	Sequence 6, Appl1	218	57	2.5	3080	3	US-09-099-041A-25	Sequence 25, Appl1
146	57	2.5	708	4	US-09-270-767-13081	Sequence 13081, A	219	57	2.5	3080	4	US-09-245-281-25	Sequence 25, Appl1
147	57	2.5	732	4	US-09-149-476-66	Sequence 66, Appl1	220	57	2.5	3080	4	US-09-207-359B-25	Sequence 25, Appl1
148	57	2.5	756	4	US-09-614-912-93	Sequence 93, Appl1	221	57	2.5	3080	4	US-09-340-620A-25	Sequence 25, Appl1
149	57	2.5	857	1	US-08-308-883-1	Sequence 1, Appl1	222	57	2.5	3080	4	US-09-865-364-25	Sequence 25, Appl1
150	57	2.5	857	1	US-08-730-163-1	Sequence 1, Appl1	223	57	2.5	3116	4	US-09-311-021-187	Sequence 187, Appl
151	57	2.5	857	3	US-08-256-799-1	Sequence 1, Appl1	224	57	2.5	3275	4	US-09-370-838-151	Sequence 151, Appl
152	57	2.5	857	3	US-08-462-437-1	Sequence 1, Appl1	225	57	2.5	3275	4	US-09-854-133-151	Sequence 151, Appl
153	57	2.5	882	4	US-09-311-021-107	Sequence 107, Appl	226	57	2.5	3300	3	US-09-336-643A-82	Sequence 82, Appl1
154	57	2.5	931	4	US-09-482-273-31	Sequence 31, Appl1	227	57	2.5	3338	4	US-10-164-595-29	Sequence 29, Appl1
155	57	2.5	960	3	US-09-248-335-57	Sequence 57, Appl1	228	57	2.5	3819	4	US-10-140-002-405	Sequence 405, Appl
156	57	2.5	972	1	US-07-915-934-1	Sequence 1, Appl1	229	57	2.5	3848	3	US-09-112-096-28	Sequence 28, Appl1
157	57	2.5	972	1	US-08-325-743-1	Sequence 1, Appl1	230	57	2.5	4419	4	US-09-620-312D-187	Sequence 187, Appl
158	57	2.5	972	4	US-09-549-831-5	Sequence 5, Appl1	231	57	2.5	4874	4	US-09-187-330-2	Sequence 2, Appl1
159	57	2.5	985	4	US-09-322-409-25	Sequence 25, Appl1	232	57	2.5	4880	3	US-09-031-563-1	Sequence 1, Appl1
160	57	2.5	985	4	US-09-322-409-27	Sequence 27, Appl1	233	57	2.5	4880	4	US-09-392-277-1	Sequence 1, Appl1
161	57	2.5	985	4	US-09-451-527-25	Sequence 25, Appl1	234	57	2.5	4880	4	US-09-258-000-1	Sequence 1, Appl1
162	57	2.5	985	4	US-09-451-527-27	Sequence 27, Appl1	235	57	2.5	5125	3	US-09-031-563-4	Sequence 4, Appl1
163	57	2.5	1023	1	US-08-252-966B-16	Sequence 16, Appl1	236	57	2.5	5125	4	US-09-392-277-4	Sequence 4, Appl1
164	57	2.5	1023	4	US-09-429-947-38	Sequence 38, Appl1	237	57	2.5	5125	4	US-09-258-000-4	Sequence 4, Appl1
165	57	2.5	1046	1	US-08-361-467B-4	Sequence 4, Appl1	238	57	2.5	5152	4	US-10-204-708-47	Sequence 47, Appl1
166	57	2.5	1046	1	US-08-484-332C-4	Sequence 4, Appl1	239	57	2.5	5668	3	US-09-112-096-14	Sequence 14, Appl1
167	57	2.5	1066	1	US-08-157-101A-4	Sequence 4, Appl1	240	57	2.5	5668	4	US-09-636-215-777	Sequence 777, Appl
168	57	2.5	1098	3	US-09-248-335-35	Sequence 35, Appl1	241	57	2.5	5668	4	US-09-685-166A-777	Sequence 777, Appl
169	57	2.5	1196	4	US-09-065-040-2	Sequence 2, Appl1	242	57	2.5	5668	4	US-09-679-426-777	Sequence 777, Appl
170	57	2.5	1206	4	US-09-465-558-53	Sequence 53, Appl1	243	57	2.5	7386	3	US-09-331-581-3	Sequence 3, Appl1
171	57	2.5	1214	4	US-09-780-717-28	Sequence 28, Appl1	244	57	2.5	7386	3	US-09-331-581-14	Sequence 14, Appl1
172	57	2.5	1248	4	US-09-489-847-101	Sequence 101, Appl	245	57	2.5	10660	3	US-08-267-803B-8	Sequence 8, Appl1
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247	56	2.5	56	4	US-09-621-976-12139	Sequence 12139, A	c 320	56	2.5	91	4	US-09-338-933-201	Sequence 201, App
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250	56	2.5	57	4	US-09-621-976-13937	Sequence 13937, A	c 323	56	2.5	91	4	US-09-216-003A-201	Sequence 201, App
251	56	2.5	58	4	US-09-621-976-14827	Sequence 14827, A	c 324	56	2.5	91	4	US-09-667-857-201	Sequence 201, App
252	56	2.5	59	4	US-09-621-976-13084	Sequence 13084, A	c 325	56	2.5	92	4	US-09-621-976-14689	Sequence 14689, A
253	56	2.5	59	4	US-09-621-976-13752	Sequence 13752, A	c 326	56	2.5	94	4	US-09-404-879A-261	Sequence 261, App
254	56	2.5	60	3	US-09-457-959-8	Sequence 8, Appl	c 327	56	2.5	94	4	US-09-338-933-261	Sequence 261, App
255	56	2.5	60	4	US-09-621-976-12480	Sequence 12480, A	c 328	56	2.5	94	4	US-09-215-681-261	Sequence 261, App
256	56	2.5	60	4	US-09-621-976-13761	Sequence 13761, A	c 329	56	2.5	94	4	US-09-216-003A-261	Sequence 261, App
257	56	2.5	60	4	US-09-621-976-14742	Sequence 14742, A	c 330	56	2.5	94	4	US-09-667-857-261	Sequence 261, App
258	56	2.5	60	4	US-09-621-976-14884	Sequence 14884, A	c 331	56	2.5	97	4	US-09-621-976-12430	Sequence 12430, A
259	56	2.5	60	4	US-10-073-178-8	Sequence 8, Appl	c 332	56	2.5	98	1	US-08-088-658-42	Sequence 42, Appl
260	56	2.5	61	4	US-09-621-976-14680	Sequence 14680, A	c 333	56	2.5	98	2	US-08-471-907A-42	Sequence 42, Appl
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265	56	2.5	62	4	US-09-621-976-11091	Sequence 11091, A	c 338	56	2.5	101	4	US-09-404-879A-293	Sequence 293, App
266	56	2.5	62	4	US-09-621-976-14130	Sequence 14130, A	c 339	56	2.5	101	4	US-09-338-933-293	Sequence 293, App
267	56	2.5	62	4	US-09-621-976-14936	Sequence 14936, A	c 340	56	2.5	101	4	US-09-215-681-293	Sequence 293, App
268	56	2.5	63	4	US-09-621-976-13480	Sequence 13480, A	c 341	56	2.5	101	4	US-09-216-003A-293	Sequence 293, App
269	56	2.5	63	4	US-09-621-976-13842	Sequence 13842, A	c 342	56	2.5	101	4	US-09-667-857-293	Sequence 293, App
270	56	2.5	63	4	US-09-621-976-14756	Sequence 14756, A	c 343	56	2.5	102	4	US-09-621-976-11436	Sequence 11436, A
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272	56	2.5	65	4	US-09-621-976-14743	Sequence 14743, A	c 345	56	2.5	105	3	US-09-284-627-23	Sequence 23, Appl
273	56	2.5	65	4	US-09-621-976-14853	Sequence 14853, A	c 346	56	2.5	105	4	US-09-621-976-13820	Sequence 23, Appl
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275	56	2.5	66	4	US-09-621-976-14819	Sequence 14819, A	c 348	56	2.5	111	4	US-09-621-976-14677	Sequence 23, Appl
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277	56	2.5	67	4	US-09-621-976-13917	Sequence 13917, A	c 350	56	2.5	121	3	US-09-297-535-20	Sequence 20, Appl
278	56	2.5	67	4	US-09-621-976-14753	Sequence 14753, A	c 351	56	2.5	123	4	US-09-621-976-12330	Sequence 12330, A
279	56	2.5	68	4	US-09-621-976-11613	Sequence 11613, A	c 352	56	2.5	130	4	US-09-621-976-12892	Sequence 12892, A
280	56	2.5	68	4	US-09-621-976-11912	Sequence 11912, A	c 353	56	2.5	138	4	US-09-621-976-9595	Sequence 9595, Ap
281	56	2.5	68	4	US-09-621-976-12005	Sequence 12005, A	c 354	56	2.5	140	1	US-08-628-417-5	Sequence 5, Appl
282	56	2.5	69	1	US-08-702-344-7	Sequence 7, Appl	c 355	56	2.5	141	3	US-08-737-078A-1	Sequence 1, Appl
283	56	2.5	69	4	US-09-621-976-12006	Sequence 12006, A	c 356	56	2.5	141	5	PCT-US94-04706-1	Sequence 1, Appl
284	56	2.5	69	4	US-09-621-976-14105	Sequence 14105, A	c 357	56	2.5	144	1	US-08-702-344-26	Sequence 26, Appl
285	56	2.5	69	4	US-09-621-976-14869	Sequence 14869, A	c 358	56	2.5	145	4	US-09-621-976-16688	Sequence 16688, A
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289	56	2.5	72	4	US-09-621-976-9837	Sequence 9837, Ap	c 362	56	2.5	146	4	US-09-621-976-16695	Sequence 16695, A
290	56	2.5	72	4	US-09-621-976-10145	Sequence 10145, A	c 363	56	2.5	147	4	US-09-621-976-10393	Sequence 10393, A
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294	56	2.5	73	4	US-09-621-976-14729	Sequence 14729, A	c 367	56	2.5	156	4	US-09-621-976-9095	Sequence 9095, Ap
295	56	2.5	73	4	US-09-621-976-14963	Sequence 14963, A	c 368	56	2.5	159	4	US-09-621-976-17448	Sequence 17448, A
296	56	2.5	75	4	US-09-621-976-12516	Sequence 12516, A	c 369	56	2.5	160	4	US-09-621-976-18071	Sequence 18071, A
297	56	2.5	75	4	US-09-621-976-14892	Sequence 14892, A	c 370	56	2.5	162	4	US-09-621-976-18068	Sequence 18068, A
298	56	2.5	76	4	US-09-621-976-12446	Sequence 12446, A	c 371	56	2.5	166	4	US-09-621-976-18390	Sequence 18390, A
299	56	2.5	76	4	US-09-621-976-14831	Sequence 14831, A	c 372	56	2.5	179	4	US-09-621-976-18074	Sequence 18054, A
300	56	2.5	76	4	US-09-621-976-14915	Sequence 14915, A	c 373	56	2.5	185	4	US-09-621-976-16779	Sequence 16779, A
301	56	2.5	77	4	US-08-956-171E-2883	Sequence 2883, Ap	c 374	56	2.5	189	4	US-09-621-976-10364	Sequence 10364, A
302	56	2.5	77	4	US-09-621-976-14176	Sequence 14176, A	c 375	56	2.5	189	4	US-09-621-976-14761	Sequence 14761, A
303	56	2.5	77	4	US-08-781-986A-2883	Sequence 2883, Ap	c 376	56	2.5	193	4	US-09-621-976-10543	Sequence 10543, Ap
304	56	2.5	78	4	US-09-621-976-14824	Sequence 14824, A	c 377	56	2.5	194	4	US-09-621-976-9596	Sequence 9596, Ap
305	56	2.5	78	4	US-09-621-976-15092	Sequence 15092, A	c 378	56	2.5	194	4	US-09-621-976-15317	Sequence 15317, A
306	56	2.5	79	4	US-09-621-976-15090	Sequence 15090, A	c 379	56	2.5	195	4	US-09-621-976-15314	Sequence 15314, A
307	56	2.5	81	4	US-09-621-976-13152	Sequence 13152, A	c 380	56	2.5	196	4	US-09-442-054A-42	Sequence 42, Appl
308	56	2.5	81	4	US-09-513-999C-17324	Sequence 17324, A	c 381	56	2.5	196	4	US-09-442-054A-42	Sequence 42, Appl
309	56	2.5	83	4	US-09-621-976-14751	Sequence 14751, A	c 382	56	2.5	204	4	US-09-621-976-1323	Sequence 1323, Ap
310	56	2.5	83	4	US-09-621-976-14959	Sequence 14959, A	c 383	56	2.5	206	4	US-09-621-976-16536	Sequence 16536, A
311	56	2.5	84	1	US-08-664-586B-3	Sequence 3, Appl	c 384	56	2.5	213	4	US-09-621-976-9843	Sequence 9843, Ap
312	56	2.5	84	1	US-08-738-367-3	Sequence 3, Appl	c 385	56	2.5	215	4	US-09-621-976-15321	Sequence 15321, A
313	56	2.5	84	4	US-09-621-976-14571	Sequence 14571, A	c 386	56	2.5	227	3	US-08-520-678A-28	Sequence 28, Appl
314	56	2.5	84	4	US-09-621-976-14577	Sequence 14577, A	c 387	56	2.5	227	3	US-08-897-126-28	Sequence 28, Appl
315	56	2.5	85	4	US-09-621-976-13395	Sequence 13395, A	c 388	56	2.5	231	4	US-09-621-976-16317	Sequence 16317, A
316	56	2.5	85	4	US-09-621-976-14949	Sequence 14949, A	c 389	56	2.5	231	4	US-09-621-976-16456	Sequence 16456, A
317	56	2.5	89	4	US-09-621-976-14749	Sequence 14749, A	c 390	56	2.5	232	4	US-09-621-976-17701	Sequence 17701, A
318	56	2.5	89	4	US-09-621-976-14974	Sequence 14974, A	c 391	56	2.5	233	4	US-09-621-976-16559	Sequence 16559, A
319	56	2.5	91	4	US-09-404-879A-201	Sequence 201, App	c 392	56	2.5	234	4	US-09-621-976-16557	Sequence 16557, A

393	56	2.5	235	4	US-09-621-976-16550	Sequence 16550, A	466	56	2.5	496	4	US-10-140-002-533	Sequence 533, App
394	56	2.5	240	1	US-08-628-417-6	Sequence 6, Appli	467	56	2.5	530	4	US-09-461-325-28	Sequence 28, Appl
395	56	2.5	240	4	US-09-621-976-1324	Sequence 1324, Ap	468	56	2.5	530	4	US-10-012-542-28	Sequence 28, Appl
396	56	2.5	242	4	US-09-621-976-16320	Sequence 16320, A	469	56	2.5	530	4	US-10-115-123-28	Sequence 1, Appli
397	56	2.5	242	4	US-09-621-976-16324	Sequence 16324, A	470	56	2.5	536	2	US-08-341-568-1	Sequence 5, Appli
398	56	2.5	246	4	US-09-621-976-13617	Sequence 13617, A	471	56	2.5	536	2	US-08-911-020-1	Sequence 111, App
399	56	2.5	246	4	US-09-621-976-16288	Sequence 16288, A	472	56	2.5	550	4	US-09-010-1478-5	Sequence 111, App
400	56	2.5	246	4	US-09-621-976-1322	Sequence 1322, Ap	473	56	2.5	552	4	US-09-461-325-111	Sequence 111, App
401	56	2.5	249	4	US-09-621-976-16291	Sequence 16291, A	474	56	2.5	552	4	US-10-012-542-111	Sequence 111, App
402	56	2.5	249	4	US-09-621-976-16292	Sequence 16292, A	475	56	2.5	552	4	US-10-115-123-111	Sequence 14, Appl
403	56	2.5	250	4	US-09-621-976-16293	Sequence 16293, A	476	56	2.5	554	4	US-09-696-169A-14	Sequence 10, Appl
404	56	2.5	253	2	US-08-620-678A-25	Sequence 25, Appl	477	56	2.5	570	1	US-07-885-970A-10	Sequence 10, Appl
405	56	2.5	253	3	US-08-897-126-25	Sequence 25, Appl	478	56	2.5	570	1	US-08-298-687A-10	Sequence 10, Appl
406	56	2.5	255	4	US-09-621-976-9406	Sequence 9406, Ap	479	56	2.5	570	1	US-08-298-829-10	Sequence 5, Appli
407	56	2.5	258	4	US-09-621-976-15353	Sequence 15353, A	480	56	2.5	572	3	US-09-342-653-5	Sequence 9, Appli
408	56	2.5	259	4	US-09-621-976-16294	Sequence 16294, A	481	56	2.5	609	1	US-08-530-797-9	Sequence 9, Appli
409	56	2.5	260	2	US-08-520-678A-29	Sequence 29, Appl	482	56	2.5	609	2	US-08-787-335-9	Sequence 9, Appli
410	56	2.5	260	3	US-08-897-126-29	Sequence 29, Appl	483	56	2.5	612	4	US-09-270-767-11643	Sequence 11643, A
411	56	2.5	266	4	US-09-621-976-16813	Sequence 16813, A	484	56	2.5	664	4	US-09-904-615-66	Sequence 66, Appl
412	56	2.5	269	4	US-09-621-976-16936	Sequence 16936, A	485	56	2.5	675	4	US-09-621-976-2461	Sequence 2461, Ap
413	56	2.5	270	2	US-08-520-678A-30	Sequence 30, Appl	486	56	2.5	711	4	US-09-621-976-17854	Sequence 17854, A
414	56	2.5	270	3	US-08-897-126-30	Sequence 30, Appl	487	56	2.5	730	4	US-09-270-767-14600	Sequence 14600, A
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416	56	2.5	282	4	US-09-621-976-18648	Sequence 18648, A	489	56	2.5	748	1	US-08-361-467B-3	Sequence 3, Appli
417	56	2.5	283	4	US-09-621-976-16989	Sequence 16989, A	490	56	2.5	748	1	US-08-484-332C-3	Sequence 3, Appli
418	56	2.5	289	1	US-08-341-568-3	Sequence 3, Appli	491	56	2.5	755	4	US-10-140-002-153	Sequence 153, App
419	56	2.5	289	2	US-08-311-020-3	Sequence 3, Appli	492	56	2.5	763	4	US-09-743-207-3	Sequence 3, Appli
420	56	2.5	293	4	US-09-621-976-16965	Sequence 16965, A	493	56	2.5	773	4	US-09-149-476-20	Sequence 20, Appl
421	56	2.5	299	4	US-09-621-976-10211	Sequence 10211, A	494	56	2.5	783	4	US-10-140-002-321	Sequence 321, App
422	56	2.5	299	4	US-09-621-976-16226	Sequence 16226, A	495	56	2.5	789	3	US-09-020-956-32	Sequence 32, Appl
423	56	2.5	318	4	US-09-621-976-10247	Sequence 10247, A	496	56	2.5	789	3	US-09-030-607-32	Sequence 32, Appl
424	56	2.5	323	4	US-09-621-976-10374	Sequence 10374, A	497	56	2.5	789	3	US-09-439-313-32	Sequence 32, Appl
425	56	2.5	329	4	US-09-621-976-16012	Sequence 16012, A	498	56	2.5	789	3	US-09-352-616A-32	Sequence 32, Appl
426	56	2.5	332	4	US-09-621-976-16031	Sequence 16031, A	499	56	2.5	789	4	US-09-232-149A-32	Sequence 32, Appl
427	56	2.5	332	4	US-09-621-976-16050	Sequence 16050, A	500	56	2.5	789	4	US-09-159-812-32	Sequence 32, Appl
428	56	2.5	332	4	US-09-621-976-16053	Sequence 16053, A	501	56	2.5	789	4	US-09-636-215-32	Sequence 32, Appl
429	56	2.5	333	4	US-09-621-976-16032	Sequence 16032, A	502	56	2.5	789	4	US-09-685-166A-32	Sequence 32, Appl
430	56	2.5	334	4	US-09-621-976-16045	Sequence 16045, A	503	56	2.5	789	4	US-09-115-453-32	Sequence 32, Appl
431	56	2.5	334	4	US-09-621-976-16044	Sequence 16044, A	504	56	2.5	789	4	US-09-688-489-32	Sequence 32, Appl
432	56	2.5	335	4	US-09-621-976-16061	Sequence 16061, A	505	56	2.5	789	4	US-09-679-426-32	Sequence 32, Appl
433	56	2.5	336	4	US-09-621-976-16013	Sequence 16013, A	506	56	2.5	795	4	US-09-270-767-14068	Sequence 14068, A
434	56	2.5	338	4	US-09-621-976-16041	Sequence 16041, A	507	56	2.5	796	1	US-08-104-073-2	Sequence 2, Appli
435	56	2.5	341	4	US-09-621-976-16135	Sequence 16135, A	508	56	2.5	812	4	US-09-091-097-7	Sequence 7, Appli
436	56	2.5	347	4	US-09-621-976-16026	Sequence 16026, A	509	56	2.5	844	4	US-09-690-942-3	Sequence 3, Appli
437	56	2.5	351	4	US-08-621-976-15134	Sequence 15134, A	510	56	2.5	903	5	PCU-US95-06406A-21	Sequence 21, Appl
438	56	2.5	357	4	US-09-621-976-16058	Sequence 16058, A	511	56	2.5	941	4	US-09-205-258-186	Sequence 186, App
439	56	2.5	358	4	US-09-621-976-927	Sequence 927, App	512	56	2.5	958	2	US-08-757-048A-5	Sequence 5, Appli
440	56	2.5	359	4	US-09-621-976-16008	Sequence 16008, A	513	56	2.5	958	3	US-09-447-208-5	Sequence 5, Appli
441	56	2.5	359	4	US-09-621-976-16019	Sequence 16019, A	514	56	2.5	958	3	US-09-135-988-5	Sequence 5, Appli
442	56	2.5	362	4	US-09-621-976-16010	Sequence 16010, A	515	56	2.5	958	3	US-09-277-716-5	Sequence 5, Appli
443	56	2.5	365	4	US-09-621-976-16042	Sequence 16042, A	516	56	2.5	958	3	US-08-597-274A-5	Sequence 5, Appli
444	56	2.5	366	4	US-09-640-173-10	Sequence 10, Appl	517	56	2.5	958	4	US-08-908-909-5	Sequence 5, Appli
445	56	2.5	366	4	US-09-640-173-16	Sequence 16, Appl	518	56	2.5	958	4	US-09-609-161B-5	Sequence 5, Appli
446	56	2.5	366	4	US-09-640-173-33	Sequence 33, Appl	519	56	2.5	958	4	US-08-990-103-5	Sequence 5, Appli
447	56	2.5	366	4	US-09-640-173-42	Sequence 42, Appl	520	56	2.5	958	4	US-09-746-485A-5	Sequence 5, Appli
448	56	2.5	366	4	US-09-640-173-53	Sequence 53, Appl	521	56	2.5	958	4	US-10-126-139-5	Sequence 5, Appli
449	56	2.5	366	4	US-09-713-550-10	Sequence 10, Appl	522	56	2.5	958	4	US-10-126-798-5	Sequence 5, Appli
450	56	2.5	366	4	US-09-713-550-16	Sequence 16, Appl	523	56	2.5	958	4	US-10-126-777-5	Sequence 5, Appli
451	56	2.5	366	4	US-09-713-550-33	Sequence 33, Appl	524	56	2.5	966	1	US-08-514-014-7	Sequence 7, Appli
452	56	2.5	366	4	US-09-713-550-42	Sequence 42, Appl	525	56	2.5	966	2	US-08-833-823-3	Sequence 7, Appli
453	56	2.5	366	4	US-09-713-550-53	Sequence 53, Appl	526	56	2.5	976	2	US-08-504-459-9	Sequence 9, Appli
454	56	2.5	366	4	US-09-825-294-10	Sequence 10, Appl	527	56	2.5	981	4	US-09-780-717-4	Sequence 4, Appli
455	56	2.5	366	4	US-09-825-294-16	Sequence 16, Appl	528	56	2.5	990	4	US-09-800-729-79	Sequence 79, Appl
456	56	2.5	366	4	US-09-825-294-33	Sequence 33, Appl	529	56	2.5	991	3	US-08-924-747-25	Sequence 25, Appl
457	56	2.5	366	4	US-09-825-294-42	Sequence 42, Appl	530	56	2.5	991	3	US-09-247-373B-25	Sequence 25, Appl
458	56	2.5	366	4	US-09-825-294-53	Sequence 53, Appl	531	56	2.5	991	3	US-09-296-715-25	Sequence 25, Appl
459	56	2.5	366	4	US-09-970-966-10	Sequence 10, Appl	532	56	2.5	997	4	US-09-907-794A-376	Sequence 376, App
460	56	2.5	366	4	US-09-970-966-16	Sequence 16, Appl	533	56	2.5	997	4	US-09-905-125A-376	Sequence 376, App
461	56	2.5	366	4	US-09-970-966-33	Sequence 33, Appl	534	56	2.5	997	4	US-09-902-775A-376	Sequence 376, App
462	56	2.5	366	4	US-09-970-966-42	Sequence 42, Appl	535	56	2.5	997	4	US-09-906-700-376	Sequence 376, App
463	56	2.5	366	4	US-09-970-966-53	Sequence 53, Appl	536	56	2.5	997	4	US-09-903-603A-376	Sequence 376, App
464	56	2.5	467	2	US-08-841-349-18	Sequence 18, Appl	537	56	2.5	1020	4	US-09-328-475C-43	Sequence 43, Appl
465	56	2.5	467	4	US-09-431-184A-18	Sequence 18, Appl	538	56	2.5	1024	4	US-09-328-475C-50	Sequence 50, Appl

539	56	2.5	1034	4	US-09-311-021-105	Sequence 105, App	612	56	2.5	1503	4	US-09-906-700-220	Sequence 220, App
540	56	2.5	1037	4	US-09-489-847-112	Sequence 112, App	613	56	2.5	1503	4	US-10-140-002-363	Sequence 363, App
541	56	2.5	1039	4	US-09-464-535-23	Sequence 23, Appl	614	56	2.5	1503	4	US-09-903-603A-220	Sequence 220, App
542	56	2.5	1048	4	US-09-489-847-38	Sequence 38, Appl	615	56	2.5	1505	2	US-08-909-965C-13	Sequence 13, Appl
543	56	2.5	1051	3	US-09-245-041-10	Sequence 10, Appl	616	56	2.5	1507	4	US-09-453-323-1	Sequence 1, Appl
544	56	2.5	1051	4	US-09-358-055B-10	Sequence 10, Appl	617	56	2.5	1508	3	US-09-039-046-1	Sequence 1, Appl
545	56	2.5	1051	4	US-09-893-238-10	Sequence 20, Appl	618	56	2.5	1509	4	US-09-149-476-179	Sequence 179, App
546	56	2.5	1052	4	US-09-489-847-23	Sequence 23, Appl	619	56	2.5	1510	4	US-10-140-002-399	Sequence 399, App
547	56	2.5	1057	4	US-09-716-129-16	Sequence 16, Appl	620	56	2.5	1522	3	US-09-413-574-1	Sequence 1, Appl
548	56	2.5	1069	3	US-09-372-422A-7	Sequence 7, Appl	621	56	2.5	1534	1	US-08-300-903A-6	Sequence 6, Appl
549	56	2.5	1074	3	US-09-248-335-67	Sequence 67, Appl	622	56	2.5	1534	4	US-08-988-197-6	Sequence 6, Appl
550	56	2.5	1075	3	US-08-400-006B-6	Sequence 6, Appl	623	56	2.5	1534	4	US-10-385-072-6	Sequence 6, Appl
551	56	2.5	1091	4	US-09-328-965-1	Sequence 1, Appl	624	56	2.5	1540	3	US-08-977-001-2	Sequence 2, Appl
552	56	2.5	1100	3	US-07-861-458C-4	Sequence 4, Appl	625	56	2.5	1544	4	US-09-187-999-14	Sequence 14, Appl
553	56	2.5	1114	4	US-09-152-060-41	Sequence 41, Appl	626	56	2.5	1546	4	US-09-901-151-1	Sequence 1, Appl
554	56	2.5	1117	3	US-09-247-373B-33	Sequence 33, Appl	627	56	2.5	1578	3	US-09-416-050A-1	Sequence 1, Appl
555	56	2.5	1123	4	US-09-152-060-15	Sequence 15, Appl	628	56	2.5	1578	3	US-09-664-800-1	Sequence 1, Appl
556	56	2.5	1129	3	US-09-227-357-40	Sequence 40, Appl	629	56	2.5	1578	3	US-09-665-309-1	Sequence 1, Appl
557	56	2.5	1133	4	US-09-916-204-1	Sequence 1, Appl	630	56	2.5	1578	3	US-09-661-569-1	Sequence 1, Appl
558	56	2.5	1133	4	US-10-282-048-1	Sequence 1, Appl	631	56	2.5	1582	3	US-08-545-196B-10	Sequence 10, Appl
559	56	2.5	1138	4	US-09-800-729-44	Sequence 44, Appl	632	56	2.5	1582	3	US-08-545-196B-12	Sequence 12, Appl
560	56	2.5	1141	4	US-09-800-729-78	Sequence 78, Appl	633	56	2.5	1604	1	US-08-665-966-9	Sequence 9, Appl
561	56	2.5	1147	1	US-08-665-716-1	Sequence 1, Appl	634	56	2.5	1604	3	US-09-041-780-9	Sequence 9, Appl
562	56	2.5	1153	4	US-09-149-476-41	Sequence 41, Appl	635	56	2.5	1606	4	US-09-820-004-1	Sequence 1, Appl
563	56	2.5	1154	3	US-08-651-136C-7	Sequence 7, Appl	636	56	2.5	1618	4	US-09-800-729-29	Sequence 29, Appl
564	56	2.5	1154	3	US-09-229-911A-7	Sequence 7, Appl	637	56	2.5	1633	4	US-10-140-002-217	Sequence 217, App
565	56	2.5	1166	5	PCT-US96-12129B-1	Sequence 1, Appl	638	56	2.5	1641	1	US-08-300-903A-8	Sequence 8, Appl
566	56	2.5	1172	1	US-07-945-288-9	Sequence 9, Appl	639	56	2.5	1641	4	US-08-988-197-8	Sequence 8, Appl
567	56	2.5	1172	1	US-08-462-831-9	Sequence 9, Appl	640	56	2.5	1641	4	US-10-385-072-8	Sequence 8, Appl
568	56	2.5	1172	1	US-08-461-809-9	Sequence 9, Appl	641	56	2.5	1660	4	US-09-722-971-9	Sequence 9, Appl
569	56	2.5	1172	1	US-08-461-441-9	Sequence 9, Appl	642	56	2.5	1662	4	US-09-668-097A-13	Sequence 13, Appl
570	56	2.5	1172	5	PCT-US93-08518-9	Sequence 9, Appl	643	56	2.5	1696	4	US-09-835-811-1	Sequence 1, Appl
571	56	2.5	1174	2	US-08-872-437-1	Sequence 1, Appl	644	56	2.5	1700	2	US-08-897-340-4	Sequence 4, Appl
572	56	2.5	1174	3	US-08-651-136C-11	Sequence 11, Appl	645	56	2.5	1700	3	US-09-252-329-4	Sequence 4, Appl
573	56	2.5	1174	3	US-09-229-911A-11	Sequence 11, Appl	646	56	2.5	1736	3	US-09-182-816-22	Sequence 22, Appl
574	56	2.5	1190	4	US-09-390-207-1	Sequence 1, Appl	647	56	2.5	1736	3	US-09-182-816-24	Sequence 24, Appl
575	56	2.5	1193	3	US-09-372-422A-23	Sequence 23, Appl	648	56	2.5	1736	3	US-09-471-528-22	Sequence 22, Appl
576	56	2.5	1198	3	US-09-248-335-27	Sequence 27, Appl	649	56	2.5	1736	3	US-09-471-528-24	Sequence 24, Appl
577	56	2.5	1201	4	US-09-461-325-36	Sequence 36, Appl	650	56	2.5	1736	3	US-09-634-530-22	Sequence 22, Appl
578	56	2.5	1201	4	US-10-012-542-36	Sequence 36, Appl	651	56	2.5	1736	3	US-09-634-530-24	Sequence 24, Appl
579	56	2.5	1201	4	US-10-115-123-36	Sequence 36, Appl	652	56	2.5	1738	2	US-08-379-482A-2	Sequence 2, Appl
580	56	2.5	1210	4	US-09-443-041A-29	Sequence 29, Appl	653	56	2.5	1738	4	US-09-918-909A-27	Sequence 27, Appl
581	56	2.5	1273	3	US-09-270-767-14731	Sequence 14731, A	654	56	2.5	1740	4	US-09-709-103-45	Sequence 45, Appl
582	56	2.5	1279	3	US-09-248-335-25	Sequence 25, Appl	655	56	2.5	1740	4	US-09-439-410A-45	Sequence 45, Appl
583	56	2.5	1296	4	US-09-461-325-29	Sequence 29, Appl	656	56	2.5	1746	4	US-09-485-529-57	Sequence 57, Appl
584	56	2.5	1296	4	US-10-012-542-29	Sequence 29, Appl	657	56	2.5	1768	4	US-09-485-529-13	Sequence 13, Appl
585	56	2.5	1296	4	US-10-115-123-29	Sequence 29, Appl	658	56	2.5	1771	4	US-09-907-794A-158	Sequence 158, App
586	56	2.5	1315	3	US-09-164-193-1	Sequence 1, Appl	659	56	2.5	1771	4	US-09-866-028-36	Sequence 36, Appl
587	56	2.5	1315	4	US-09-221-448A-1	Sequence 1, Appl	660	56	2.5	1771	4	US-09-905-125A-158	Sequence 158, App
588	56	2.5	1325	1	US-08-306-691B-51	Sequence 51, Appl	661	56	2.5	1771	4	US-09-902-775A-158	Sequence 158, App
589	56	2.5	1325	2	US-08-464-517-1	Sequence 1, Appl	662	56	2.5	1771	4	US-09-906-700-158	Sequence 158, App
590	56	2.5	1325	3	US-08-246-361A-1	Sequence 1, Appl	663	56	2.5	1771	4	US-09-944-457-36	Sequence 36, Appl
591	56	2.5	1325	3	US-08-463-772-1	Sequence 1, Appl	664	56	2.5	1771	4	US-09-903-603A-158	Sequence 158, App
592	56	2.5	1325	5	PCT-US93-05000-1	Sequence 1, Appl	665	56	2.5	1780	3	US-09-202-548B-5	Sequence 5, Appl
593	56	2.5	1361	4	US-09-489-847-64	Sequence 64, Appl	666	56	2.5	1780	4	US-09-942-858-5	Sequence 5, Appl
594	56	2.5	1378	4	US-09-149-476-208	Sequence 208, App	667	56	2.5	1781	4	US-09-818-512-1	Sequence 1, Appl
595	56	2.5	1383	4	US-09-735-846-1	Sequence 1, Appl	668	56	2.5	1798	3	US-09-797-906-1	Sequence 1, Appl
596	56	2.5	1406	4	US-10-000-489-81	Sequence 81, Appl	669	56	2.5	1801	4	US-09-709-103-3	Sequence 3, Appl
597	56	2.5	1411	3	US-08-984-127-5	Sequence 5, Appl	670	56	2.5	1801	4	US-09-439-410A-3	Sequence 3, Appl
598	56	2.5	1411	3	US-09-496-692-5	Sequence 5, Appl	671	56	2.5	1804	2	US-08-504-459-5	Sequence 5, Appl
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602	56	2.5	1454	3	US-09-372-422A-19	Sequence 19, Appl	675	56	2.5	1835	3	US-09-485-549-1	Sequence 1, Appl
603	56	2.5	1454	4	US-09-614-912-63	Sequence 63, Appl	676	56	2.5	1842	4	US-09-482-273-90	Sequence 90, Appl
604	56	2.5	1461	3	US-08-722-126A-4	Sequence 4, Appl	677	56	2.5	1844	4	US-10-003-392-7	Sequence 7, Appl
605	56	2.5	1461	5	PCT-US95-04258-4	Sequence 4, Appl	678	56	2.5	1864	4	US-09-149-476-130	Sequence 130, App
606	56	2.5	1474	3	US-08-821-994-64	Sequence 64, Appl	679	56	2.5	1872	3	US-09-801-052-1	Sequence 1, Appl
607	56	2.5	1485	3	US-09-372-422A-39	Sequence 39, Appl	680	56	2.5	1872	4	US-10-020-121-1	Sequence 1, Appl
608	56	2.5	1492	3	US-09-369-247-23	Sequence 23, Appl	681	56	2.5	1878	4	US-09-465-558-39	Sequence 39, Appl
609	56	2.5	1503	4	US-09-907-794A-220	Sequence 220, App	682	56	2.5	1898	1	US-08-342-411A-1	Sequence 1, Appl
610	56	2.5	1503	4	US-09-905-125A-220	Sequence 220, App	683	56	2.5	1925	4	US-09-148-545-128	Sequence 128, App
611	56	2.5	1503	4	US-09-902-775A-220	Sequence 220, App	684	56	2.5	1927	4	US-09-336-536-66	Sequence 66, Appl

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686	56	2.5	1963	4	US-09-482-273-91	Sequence 91, Appl	759	56	2.5	2481	3	US-09-235-839-1	Sequence 1, Appli
687	56	2.5	1963	4	US-09-482-273-27	Sequence 27, Appl	760	56	2.5	2481	3	US-09-327-035-1	Sequence 1, Appli
688	56	2.5	1981	4	US-09-720-317A-3	Sequence 3, Appli	761	56	2.5	2483	4	US-09-205-258-68	Sequence 68, Appl
689	56	2.5	1985	4	US-10-140-002-143	Sequence 143, App	762	56	2.5	2485	4	US-09-889-463A-9	Sequence 9, Appli
690	56	2.5	2010	1	US-07-864-475A-4	Sequence 4, Appli	763	56	2.5	2527	4	US-09-244-805-29	Sequence 29, Appli
691	56	2.5	2010	2	US-08-468-249A-4	Sequence 4, Appli	764	56	2.5	2550	6	5258287-23	Patent No. 5258287
692	56	2.5	2026	2	US-08-993-228-3	Sequence 3, Appli	765	56	2.5	2550	6	US-08-569-749-1	Sequence 1, Appli
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695	56	2.5	2096	3	US-09-008-481A-10	Sequence 10, Appl	768	56	2.5	2604	2	US-08-838-399-3	Sequence 3, Appli
696	56	2.5	2096	3	US-09-195-666A-16	Sequence 16, Appl	769	56	2.5	2604	2	US-09-235-839-3	Sequence 3, Appli
697	56	2.5	2096	3	US-09-309-592-10	Sequence 10, Appl	770	56	2.5	2604	3	US-09-327-035-3	Sequence 3, Appli
698	56	2.5	2096	3	US-09-635-705-16	Sequence 16, Appl	771	56	2.5	2608	4	US-09-904-615-16	Sequence 16, Appl
699	56	2.5	2096	4	US-09-634-858A-16	Sequence 16, Appl	772	56	2.5	2625	4	US-09-270-767-10080	Sequence 10080, A
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701	56	2.5	2146	4	US-10-003-392-3	Sequence 3, Appli	774	56	2.5	2668	4	US-10-140-002-511	Sequence 511, App
702	56	2.5	2184	3	US-08-955-918C-1	Sequence 1, Appli	775	56	2.5	2671	6	5168051-9	Patent No. 5168051
703	56	2.5	2184	3	US-08-697-766A-1	Sequence 1, Appli	776	56	2.5	2674	3	US-09-817-180-1	Sequence 1, Appli
704	56	2.5	2187	3	US-09-127-219B-2	Sequence 2, Appli	777	56	2.5	2674	4	US-09-232-200-44	Sequence 44, Appl
705	56	2.5	2202	4	US-09-465-558-59	Sequence 59, Appl	778	56	2.5	2710	3	US-09-232-200-70	Sequence 70, Appl
706	56	2.5	2203	4	US-09-801-861-1	Sequence 1, Appli	779	56	2.5	2710	3	US-09-232-197-44	Sequence 44, Appl
707	56	2.5	2203	4	US-10-224-562-1	Sequence 1, Appli	780	56	2.5	2710	3	US-09-232-197-70	Sequence 70, Appl
708	56	2.5	2205	3	US-08-888-077A-41	Sequence 41, Appl	781	56	2.5	2710	3	US-09-232-201-44	Sequence 44, Appl
709	56	2.5	2218	4	US-09-016-434-1157	Sequence 1157, Ap	782	56	2.5	2710	3	US-09-232-201-70	Sequence 70, Appl
710	56	2.5	2218	4	US-09-205-258-103	Sequence 103, App	783	56	2.5	2710	4	US-09-232-195-44	Sequence 44, Appl
711	56	2.5	2218	4	US-10-329-668-7	Sequence 7, Appli	784	56	2.5	2710	4	US-09-232-195-70	Sequence 70, Appl
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713	56	2.5	2233	1	US-08-496-631-1	Sequence 1, Appli	786	56	2.5	2744	3	US-09-369-618-1	Sequence 1, Appli
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716	56	2.5	2262	4	US-09-311-021-171	Sequence 171, App	789	56	2.5	2790	3	US-09-917-254-27	Sequence 27, Appl
717	56	2.5	2269	3	US-09-394-645-1	Sequence 1, Appli	790	56	2.5	2808	4	US-10-140-002-207	Sequence 207, App
718	56	2.5	2269	3	US-09-243-560B-1	Sequence 1, Appli	791	56	2.5	2808	4	US-09-904-615-35	Sequence 35, Appl
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724	56	2.5	2285	3	US-09-124-698-136	Sequence 136, App	797	56	2.5	3214	1	US-08-484-105-17	Sequence 17, Appl
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726	56	2.5	2285	3	US-09-127-480-136	Sequence 136, App	799	56	2.5	3334	4	US-09-668-119-2	Sequence 2, Appli
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729	56	2.5	2291	4	US-09-814-915A-95	Sequence 95, Appl	802	56	2.5	3581	2	US-08-738-349-1	Sequence 1, Appli
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733	56	2.5	2301	3	US-09-232-197-8	Sequence 8, Appli	806	56	2.5	3871	3	US-09-137-132-3	Sequence 3, Appli
734	56	2.5	2301	4	US-09-232-195-8	Sequence 8, Appli	807	56	2.5	3871	3	US-08-864-564A-3	Sequence 3, Appli
735	56	2.5	2311	4	US-09-720-317A-19	Sequence 19, Appl	808	56	2.5	3871	4	US-09-094-410-3	Sequence 3, Appli
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737	56	2.5	2312	4	US-08-631-594-45	Sequence 45, Appl	810	56	2.5	3871	4	US-08-583-153A-3	Sequence 3, Appli
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741	56	2.5	2328	3	US-08-802-805D-20	Sequence 20, Appl	814	56	2.5	3994	4	US-09-738-946-7	Sequence 7, Appli
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744	56	2.5	2389	4	US-08-799-875-7	Sequence 7, Appli	817	56	2.5	4064	4	US-09-815-048-1	Sequence 1, Appli
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832	56	2.5	6671	1	US-08-555-678-1	Sequence 1, Appl	905	54	2.4	1013	1	US-08-086-410-23	Sequence 23, Appl
833	56	2.5	6671	5	PCT-US95-02275-1	Sequence 1, Appl	906	54	2.4	1013	1	US-08-314-586-30	Sequence 30, Appl
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837	56	2.5	7859	3	US-07-982-759F-15	Sequence 15, Appl	C 910	54	2.4	1302	4	US-09-322-409-93	Sequence 93, Appl
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839	56	2.5	8638	4	US-10-029-907-6	Sequence 6, Appl	C 912	54	2.4	1302	4	US-09-451-527-93	Sequence 93, Appl
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842	56	2.5	9589	1	US-07-925-695-1	Sequence 1, Appl	915	54	2.4	1395	4	US-09-734-719-1	Sequence 1, Appl
843	56	2.5	9589	1	US-07-925-695-2	Sequence 2, Appl	916	54	2.4	1705	4	US-09-205-258-216	Sequence 216, App
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845	56	2.5	13414	4	US-09-845-917A-28	Sequence 28, Appl	918	54	2.4	2296	3	US-08-496-841C-137	Sequence 137, App
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847	55	2.5	55	4	US-09-621-976-14800	Sequence 14800, A	920	54	2.4	2369	4	US-09-057-996-13	Sequence 13, Appl
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849	55	2.5	135	4	US-09-621-976-11087	Sequence 11087, A	922	54	2.4	2668	4	US-09-370-838-156	Sequence 156, App
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851	55	2.5	184	4	US-09-513-999C-36135	Sequence 36135, A	924	54	2.4	2695	4	US-09-706-197-3	Sequence 3, Appl
852	55	2.5	204	4	US-09-621-976-16458	Sequence 16458, A	C 925	54	2.4	5535	4	US-10-204-708-18	Sequence 18, Appl
853	55	2.5	270	4	US-09-621-976-17927	Sequence 17927, A	926	53	2.4	53	4	US-09-621-976-12332	Sequence 12332, A
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855	55	2.5	326	4	US-09-621-976-16024	Sequence 16024, A	928	53	2.4	56	4	US-09-621-976-13461	Sequence 13461, A
856	55	2.5	339	4	US-09-621-976-16015	Sequence 16015, A	929	53	2.4	82	4	US-09-621-976-11689	Sequence 11689, A
857	55	2.5	375	3	US-08-946-026-23	Sequence 23, Appl	930	53	2.4	82	4	US-09-621-976-11841	Sequence 11841, A
858	55	2.5	474	3	US-08-516-859A-97	Sequence 97, Appl	931	53	2.4	82	4	US-09-621-976-11864	Sequence 11864, A
859	55	2.5	474	3	US-08-586-472-97	Sequence 97, Appl	932	53	2.4	82	4	US-09-621-976-11888	Sequence 11888, A
860	55	2.5	474	3	US-08-528-706-97	Sequence 97, Appl	933	53	2.4	82	4	US-09-621-976-11944	Sequence 11944, A
861	55	2.5	487	4	US-09-257-179-22	Sequence 22, Appl	934	53	2.4	82	4	US-09-621-976-12131	Sequence 12131, A
862	55	2.5	1151	4	US-09-270-767-12633	Sequence 12633, A	935	53	2.4	82	4	US-09-621-976-12015	Sequence 12015, A
863	55	2.5	1181	4	US-09-149-476-310	Sequence 310, App	936	53	2.4	82	4	US-09-621-976-12088	Sequence 12088, A
864	55	2.5	1212	4	US-09-149-476-186	Sequence 186, App	937	53	2.4	82	4	US-09-621-976-12103	Sequence 12103, A
865	55	2.5	1291	4	US-09-524-101D-5	Sequence 5, Appl	938	53	2.4	82	4	US-09-621-976-12127	Sequence 12127, A
866	55	2.5	1653	3	US-09-345-469-2	Sequence 2, Appl	939	53	2.4	82	4	US-09-621-976-12137	Sequence 12137, A
867	55	2.5	1776	3	US-08-655-352-10	Sequence 10, Appl	940	53	2.4	82	4	US-09-621-976-12137	Sequence 12137, A
868	55	2.5	1776	3	US-09-258-016-10	Sequence 10, Appl	941	53	2.4	82	4	US-09-621-976-12332	Sequence 12332, A
869	55	2.5	1776	4	US-09-257-825B-10	Sequence 10, Appl	942	53	2.4	82	4	US-09-621-976-12434	Sequence 12434, A
870	55	2.5	1886	1	US-09-534-506-31	Sequence 31, Appl	943	53	2.4	82	4	US-09-621-976-13499	Sequence 13499, A
871	55	2.5	1897	1	US-08-184-632-1	Sequence 1, Appl	944	53	2.4	82	4	US-09-621-976-13526	Sequence 13526, A
872	55	2.5	1934	3	US-08-776-844-1	Sequence 1, Appl	945	53	2.4	83	4	US-09-621-976-12195	Sequence 12195, A
873	55	2.5	1934	4	US-09-909-325-1	Sequence 1, Appl	946	53	2.4	106	4	US-09-621-976-12079	Sequence 12079, A
874	55	2.5	1934	4	US-09-909-326-1	Sequence 1, Appl	947	53	2.4	140	4	US-09-621-976-17449	Sequence 17449, A
875	55	2.5	2331	4	US-09-866-028-54	Sequence 54, Appl	948	53	2.4	166	4	US-09-621-976-8651	Sequence 8651, Ap
876	55	2.5	2331	4	US-09-944-457-54	Sequence 54, Appl	949	53	2.4	235	4	US-09-621-976-9455	Sequence 9455, Ap
877	55	2.5	2349	4	US-09-805-455-1	Sequence 5, Appl	950	53	2.4	244	4	US-09-621-976-484	Sequence 484, App
878	55	2.5	2797	4	US-09-482-273-74	Sequence 74, Appl	951	53	2.4	351	4	US-09-621-976-17631	Sequence 17631, A
879	55	2.5	2821	4	US-09-702-705-1669	Sequence 1669, Ap	952	53	2.4	443	4	US-09-621-976-17631	Sequence 17631, A
880	55	2.5	2821	4	US-09-736-457-1669	Sequence 1669, Ap	953	53	2.4	685	3	US-09-227-357-66	Sequence 66, Appl
881	55	2.5	2821	4	US-09-671-325-1669	Sequence 1669, Ap	954	53	2.4	872	3	US-09-248-335-63	Sequence 63, Appl
882	55	2.5	2821	4	US-09-658-824-1669	Sequence 1669, Ap	955	53	2.4	882	2	US-08-909-965C-9	Sequence 9, Appl
883	55	2.5	3047	4	US-09-873-737A-1	Sequence 1, Appl	956	53	2.4	1315	3	US-09-721-822A-10	Sequence 10, Appl
884	55	2.5	5503	2	US-08-726-012B-1	Sequence 1, Appl	957	53	2.4	1375	4	US-09-489-847-120	Sequence 120, App
885	55	2.5	5503	4	US-09-023-655-989	Sequence 989, App	958	53	2.4	1376	4	US-09-489-847-66	Sequence 66, Appl
886	55	2.5	15450	4	US-09-470-661A-1	Sequence 1, Appl	959	53	2.4	1619	4	US-09-522-714-11	Sequence 11, Appl
887	54	2.4	54	4	US-09-621-976-14994	Sequence 14994, A	960	53	2.4	1722	4	US-08-482-273-102	Sequence 102, App
888	54	2.4	61	4	US-09-621-976-11967	Sequence 11967, A	961	53	2.4	1858	2	US-08-909-965C-11	Sequence 11, Appl
889	54	2.4	80	3	US-09-284-627-15	Sequence 15, Appl	962	53	2.4	1867	4	US-09-482-273-81	Sequence 81, Appl
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891	54	2.4	83	4	US-09-621-976-12175	Sequence 12175, A	964	53	2.4	1949	4	US-10-012-542-26	Sequence 26, Appl
892	54	2.4	83	4	US-09-621-976-12429	Sequence 12429, A	965	53	2.4	1949	4	US-10-115-123-26	Sequence 26, Appl
893	54	2.4	83	4	US-09-621-976-12450	Sequence 12450, A	966	53	2.4	2327	4	US-10-066-130-20	Sequence 20, Appl
894	54	2.4	91	4	US-09-621-976-12161	Sequence 12161, A	967	53	2.4	2648	3	US-09-417-455-6	Sequence 6, Appl
895	54	2.4	257	2	US-08-520-678A-24	Sequence 24, Appl	968	53	2.4	2648	3	US-09-348-942-6	Sequence 6, Appl
896	54	2.4	257	3	US-08-897-126-24	Sequence 24, Appl	969	53	2.4	2648	4	US-09-457-626-6	Sequence 6, Appl
897	54	2.4	298	4	US-09-621-976-3871	Sequence 3871, Ap	970	53	2.4	2648	4	US-09-576-008-6	Sequence 6, Appl
898	54	2.4	334	4	US-09-513-999C-22131	Sequence 22131, A	971	53	2.4	2674	4	US-10-066-130-19	Sequence 19, Appl
899	54	2.4	365	4	US-09-621-976-14699	Sequence 14699, A	972	53	2.4	2771	4	US-10-066-130-18	Sequence 18, Appl
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902	54	2.4	1001	1	US-08-728-259A-10	Sequence 10, Appl	975	53	2.4	3623	4	US-09-918-909A-23	Sequence 23, Appl
903	54	2.4	1001	2	US-08-473-486-10	Sequence 10, Appl	976	53	2.4	5860	4	US-10-066-130-17	Sequence 17, Appl

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c 978	53	2.4	12980	3	US-09-034-756-5	Sequence 5, Appli	1051	51	2.3	1728	3	US-08-985-950-7	Sequence 7, Appli
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981	52	2.3	62	4	US-09-621-976-14825	Sequence 14825, A	1054	51	2.3	1844	4	US-10-140-002A-75	Sequence 475, App
982	52	2.3	81	4	US-09-621-976-12198	Sequence 12198, A	1055	51	2.3	1865	3	US-09-370-253-5	Sequence 5, Appli
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986	52	2.3	132	4	US-09-621-976-13992	Sequence 13992, A	1059	51	2.3	1998	3	US-09-232-197-68	Sequence 68, Appl
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993	52	2.3	347	4	US-09-621-976-16136	Sequence 16136, A	1066	51	2.3	2087	3	US-09-232-195-6	Sequence 6, Appli
994	52	2.3	427	4	US-09-461-325-107	Sequence 107, App	1067	51	2.3	2087	3	US-09-232-201-6	Sequence 6, Appli
995	52	2.3	427	4	US-10-012-542-107	Sequence 107, App	1068	51	2.3	2087	3	US-09-232-201-6	Sequence 6, Appli
996	52	2.3	427	4	US-10-115-123-107	Sequence 107, App	1069	51	2.3	2087	4	US-09-232-195-6	Sequence 6, Appli
997	52	2.3	472	4	US-09-370-767-12212	Sequence 12212, A	1070	51	2.3	2288	4	US-09-800-729-24	Sequence 24, Appl
998	52	2.3	756	4	US-10-140-002-171	Sequence 171, App	1071	51	2.3	2475	4	US-10-140-002-195	Sequence 195, App
999	52	2.3	1050	4	US-09-482-273-58	Sequence 58, Appl	1072	51	2.3	2581	4	US-09-369-247-51	Sequence 51, Appl
1000	52	2.3	1184	4	US-09-489-847-76	Sequence 76, Appl	1073	51	2.3	3238	3	US-08-123-934A-5	Sequence 5, Appli
1001	52	2.3	1525	4	US-09-461-325-110	Sequence 110, App	1074	51	2.3	3238	4	US-09-874-638-5	Sequence 5, Appli
1002	52	2.3	1525	4	US-10-012-542-110	Sequence 110, App	1075	51	2.3	3238	5	PCT-US94-10080-5	Sequence 5, Appli
1003	52	2.3	1525	4	US-10-115-123-110	Sequence 110, App	1076	51	2.3	3375	3	US-09-511-625B-67	Sequence 67, Appl
1004	52	2.3	1527	4	US-09-344-111-7	Sequence 7, Appli	1077	51	2.3	3842	3	US-09-115-954-7	Sequence 7, Appli
1005	52	2.3	1558	4	US-08-455-550-7	Sequence 7, Appli	1078	51	2.3	3912	3	US-09-115-954-1	Sequence 1, Appli
1006	52	2.3	1810	4	US-09-369-247-11	Sequence 11, Appl	1079	51	2.3	9646	3	US-08-811-566-1	Sequence 1, Appli
1007	52	2.3	1810	4	US-09-800-729-73	Sequence 73, Appl	1080	51	2.3	9646	3	US-09-034-756-1	Sequence 1, Appli
1008	52	2.3	1811	4	US-09-800-729-77	Sequence 77, Appl	1081	51	2.3	13584	4	US-09-991-258-17	Sequence 17, Appl
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1010	52	2.3	2202	4	US-09-396-149-3	Sequence 3, Appli	1083	50	2.2	50	4	US-09-621-976-14715	Sequence 14715, A
1011	52	2.3	2719	3	US-08-706-216-1	Sequence 1, Appli	1084	50	2.2	61	3	US-09-457-959-7	Sequence 7, Appli
1012	52	2.3	2719	4	US-09-650-2848-1	Sequence 1, Appli	1085	50	2.2	61	4	US-10-079-178-7	Sequence 7, Appli
1013	52	2.3	2836	3	US-08-747-221B-24	Sequence 24, Appl	1086	50	2.2	71	1	US-09-816-089A-5	Sequence 5, Appli
c1014	52	2.3	2836	3	US-08-747-221B-26	Sequence 26, Appl	1087	50	2.2	90	1	US-08-677-944-1	Sequence 2, Appli
1015	52	2.3	2836	3	US-09-005-051-24	Sequence 24, Appl	1088	50	2.2	90	1	US-08-677-944-2	Sequence 2, Appli
c1016	52	2.3	2836	3	US-09-005-051-26	Sequence 26, Appl	1089	50	2.2	90	3	US-09-254-048A-1	Sequence 1, Appli
1017	52	2.3	2836	4	US-09-403-942B-24	Sequence 24, Appl	1090	50	2.2	90	4	US-09-921-203-1	Sequence 2, Appli
c1018	52	2.3	2836	4	US-09-403-942B-26	Sequence 26, Appl	1091	50	2.2	90	4	US-09-816-089A-2	Sequence 2, Appli
1019	52	2.3	2837	2	US-08-993-228-11	Sequence 11, Appl	1092	50	2.2	93	4	US-10-106-832-1	Sequence 1, Appli
1020	52	2.3	3136	4	US-09-680-728-1	Sequence 1, Appli	1093	50	2.2	93	4	US-09-816-089A-8	Sequence 8, Appli
1021	51	2.3	61	4	US-09-621-976-12150	Sequence 12150, A	1094	50	2.2	100	3	US-08-991-789A-30	Sequence 30, Appl
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c1025	51	2.3	90	3	US-09-065-058-16	Sequence 16, Appl	1098	50	2.2	104	4	US-09-429-755-30	Sequence 30, Appl
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c1030	51	2.3	356	3	US-08-897-126-22	Sequence 22, Appl	1103	50	2.2	184	4	US-09-621-976-12893	Sequence 29, Appl
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1035	51	2.3	780	2	US-08-540-804-36	Sequence 36, Appl	1108	50	2.2	399	1	US-08-530-797-12	Sequence 12, Appl
1036	51	2.3	780	3	US-08-580-399-36	Sequence 36, Appl	1109	50	2.2	399	2	US-08-298-829-13	Sequence 13, Appl
1037	51	2.3	803	4	US-08-800-729-60	Sequence 60, Appl	1110	50	2.2	399	2	US-08-787-335-12	Sequence 12, Appl
1038	51	2.3	970	2	US-08-504-459-13	Sequence 13, Appl	1111	50	2.2	399	2	US-09-621-976-15107	Sequence 15, Appl
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1040	51	2.3	1212	3	US-09-182-145-34	Sequence 34, Appl	1113	50	2.2	540	4	US-09-149-476-313	Sequence 2, Appli
c1041	51	2.3	1212	3	US-09-182-145-35	Sequence 35, Appl	1114	50	2.2	577	3	US-09-105-542A-2	Sequence 27, Appl
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1043	51	2.3	1332	3	US-09-333-423-1	Sequence 3, Appl	1116	50	2.2	636	4	US-08-975-316-58	Sequence 58, Appl
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1045	51	2.3	1386	2	US-08-897-340-1	Sequence 1, Appli	1118	50	2.2	741	4	US-09-169-789-58	Sequence 9, Appli
1046	51	2.3	1386	3	US-09-252-329-1	Sequence 19, Appl	1119	50	2.2	785	4	US-09-518-036-9	Sequence 9, Appli
1047	51	2.3	1445	4	US-09-697-367-19	Sequence 19, Appl	1120	50	2.2	785	4	US-10-279-130-9	Sequence 96, Appl
1048	51	2.3	1445	4	US-09-918-909A-19	Sequence 59, Appl	1121	50	2.2	788	4	US-09-615-192A-96	
1049	51	2.3	1577	3	US-08-821-994-59	Sequence 59, Appl	1122	50	2.2	788	4		

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1124	50	2.2	873	3	US-09-475-316A-20	Sequence 20, Appl	1197	49	2.2	568	1	US-08-582-257-20	Sequence 20, Appl
1125	50	2.2	873	4	US-09-704-640-20	Sequence 20, Appl	1198	49	2.2	568	2	US-08-582-298-20	Sequence 20, Appl
1126	50	2.2	888	3	US-09-188-930-13	Sequence 13, Appl	1199	49	2.2	619	4	US-09-489-847-58	Sequence 58, Appl
1127	50	2.2	888	4	US-09-312-2830-13	Sequence 13, Appl	1200	49	2.2	728	4	US-09-091-097-5	Sequence 5, Appl
1128	50	2.2	959	4	US-09-578-030-5	Sequence 5, Appl	1201	49	2.2	740	2	US-08-713-000-8	Sequence 8, Appl
1129	50	2.2	1049	4	US-09-800-729-67	Sequence 67, Appl	1202	49	2.2	740	2	US-08-975-316-8	Sequence 8, Appl
1130	50	2.2	1134	3	US-09-248-335-29	Sequence 29, Appl	1203	49	2.2	740	3	US-09-211-710-8	Sequence 8, Appl
1131	50	2.2	1144	4	US-09-904-615-20	Sequence 20, Appl	1204	49	2.2	740	4	US-09-165-192A-8	Sequence 8, Appl
1132	50	2.2	1240	4	US-10-140-002-91	Sequence 91, Appl	1205	49	2.2	740	4	US-09-619-789-8	Sequence 8, Appl
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1134	50	2.2	1242	3	US-08-434-418-1	Sequence 1, Appl	1207	49	2.2	835	4	US-09-800-729-49	Sequence 49, Appl
1135	50	2.2	1242	3	US-08-433-288-1	Sequence 1, Appl	1208	49	2.2	1109	4	US-09-653-778B-1	Sequence 4, Appl
1136	50	2.2	1242	3	US-08-174-739A-1	Sequence 1, Appl	1209	49	2.2	1223	3	US-09-154-874-4	Sequence 4, Appl
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1147	50	2.2	2103	4	US-09-489-847-40	Sequence 40, Appl	1220	49	2.2	1781	1	US-08-481-130-4	Sequence 4, Appl
1148	50	2.2	2114	1	US-07-803-622B-6	Sequence 6, Appl	1221	49	2.2	1781	1	US-08-656-984A-4	Sequence 4, Appl
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1150	50	2.2	2158	2	US-08-602-228-1	Sequence 1, Appl	1223	49	2.2	1781	1	US-08-485-604-4	Sequence 4, Appl
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QY 387 TGAAGGAGTGGGTGGCCATCGAGAGCGACTGTGTCCAGCCTGTGCTTCAGACAAAG 446
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QY 418 AGCTCTTCAGATGATGGCGTGGCTGGCGACACGCTGCAGCGCTGGGGGCCCGTGTGG 477
Db |||||||
QY 447 AGCTCTTCAGATGATGGCGTGGCTGGCGACACGCTGCAGCGCTGGGGGCCCGTGTGG 506
Db |||||||
QY 478 CCTCGGTGACATGGGTCTCTCAGCAGCTGCCGATGCTTCAGAGTCTTCCAAATACCTCCCG 537
Db |||||||
QY 507 CCTCGGTGACATGGGTCTCTCAGCAGCTGCCGATGCTTCAGAGTCTTCCAAATACCTCCCG 566
Db |||||||
QY 538 TCATCTCTGGCCGAAGT 554
Db |||||||
QY 567 TCATCTCTGGCCGAAGT 583
Db |||||||
RESULT 2
US-09-513-999C-13950
; Sequence 13950, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59 US2 REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 13950
; LENGTH: 300
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 7
; OTHER INFORMATION: r=a or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 67
; OTHER INFORMATION: r=a or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 68
; OTHER INFORMATION: w=a or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 69
; OTHER INFORMATION: m=a or c
; US-09-513-999C-13950
Query Match 8.0%; Score 180; DB 4; Length 300;
Best Local Similarity 99.6%; Pred. No. 4.5e-66;
Matches 230; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 66 TTCCTTCGGGGGACACAGCTGGGTGAGGACAGAGATATTAATGTCACCTCTTGG 125
Db |||||||
QY 70 TTCCTTCGGGGGACACAGCTGGGTGAGGACAGAGATATTAATGTCACCTCTTGG 129
Db |||||||
QY 126 GGCTTTTCATGGGACTCCCTCTGTCACATTTTTCGAGGTGGGAAAGTTGCTAGAGGCTT 185
Db |||||||
QY 130 GGCTTTTCATGGGACTCCCTCTGTCACATTTTTCGAGGTGGGAAAGTTGCTAGAGGCTT 189
Db |||||||
QY 186 CAGAACTCCAGCCTAATGGATGCCAAACTCGGGGAGAAATGGCTGCGTCCCTGGCTGTG 245
Db |||||||

Db 190 CAGAACTCCAGCCTAATGGATGCCAAACTCAGGAGATGGCTGCTCCCTGCTGCTGTG 249
QY 246 CTGCTGCTGCTGCTGGAGCGGGCATGTTCTCTCACCCTCCCGCCCCCG 296
Db |||||||
QY 250 CTGCTGCTGCTGCTGGAGCGGGCATGTTCTCTCACCCTCCCGCCCCCG 300
Db |||||||
RESULT 3
US-09-073-569-1
; Sequence 1, Application US/09073569
; Patent No. 6084088
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Grossmann, Angelika
; TITLE OF INVENTION: NOVEL TUMOR ANTIGENS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/073,569
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 97-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1733 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 34...1344
; OTHER INFORMATION:
; US-09-073-569-1
Query Match 2.7%; Score 61; DB 3; Length 1733;
Best Local Similarity 100.0%; Pred. No. 2.9e-16;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2182 CTCCTCAA 2241
Db 1603 CTCCTCAA 1662
QY 2242 A 2242
Db 1663 A 1663
RESULT 4
US-09-621-976-8550
; Sequence 8550, Application US/09621976
; Patent No. 6639063

GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621.976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 8550
; LENGTH: 146
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-8550

Query Match 2.7%; Score 60; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 9.7e-16;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2183 TCCCAAA 2242
Db 58 TCCCAAA 117

RESULT 5

US-09-621-976-8551
; Sequence 8551, Application US/09621976
; Patent No. 6639063
GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621.976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 8551
; LENGTH: 147
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-8551

Query Match 2.7%; Score 60; DB 4; Length 147;
Best Local Similarity 100.0%; Pred. No. 9.7e-16;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2183 TCCCAAA 2242
Db 58 TCCCAAA 117

RESULT 6

US-10-140-002-99
; Sequence 99, Application US/10140002
; Patent No. 6725730
GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C59
; CURRENT APPLICATION NUMBER: US/10/140.002
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 99
; LENGTH: 1904
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-002-99

Query Match 2.7%; Score 60; DB 4; Length 1904;
Best Local Similarity 100.0%; Pred. No. 7.7e-16;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2183 TCCCAAA 2242
Db 1787 TCCCAAA 1846

RESULT 7

US-09-702-705-1801
; Sequence 1801, Application US/09702705
; Patent No. 8504010
GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C14
; CURRENT APPLICATION NUMBER: US/09/702.705
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 1833
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1801
; LENGTH: 4086
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-702-705-1801

Query Match 2.7%; Score 60; DB 4; Length 4086;
Best Local Similarity 100.0%; Pred. No. 7.1e-16;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2183 TCCCAAA 2242
Db 3989 TCCCAAA 4048

RESULT 8

US-09-736-457-1801
; Sequence 1801, Application US/09736457
; Patent No. 6509448
GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc

```

; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aljun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1801
; LENGTH: 4086
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-736-457-1801

Query Match          2.7%; Score 60; DB 4; Length 4086;
Best Local Similarity 100.0%; Pred.No. 7.1e-16;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 2183 TCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2242
Db 3989 TCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4048

RESULT 9
US-09-671-325-1801
; Sequence 1801, Application US/09671325
; Patent No. 6667154
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C12
; CURRENT APPLICATION NUMBER: US/09/671,325
; CURRENT FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 1825
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1801
; LENGTH: 4086
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-671-325-1801

Query Match          2.7%; Score 60; DB 4; Length 4086;
Best Local Similarity 100.0%; Pred.No. 7.1e-16;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 2183 TCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2242
Db 3989 TCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4048

RESULT 10
US-09-621-976-10271
; Sequence 10271, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054FR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21

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; NAME/KEY: SITE
; LOCATION: (1572)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-800-729--41

Query Match          2.6%; Score 59; DB 4; Length 1651;
Best Local Similarity 100.0%; Pred. No. 2e-15;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2184 CCCCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2242
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Db      1586 CCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1644

RESULT 15
US-09-739-455-1
; Sequence 1, Application US/09739455
; Patent No. 6413756
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL000653
; CURRENT APPLICATION NUMBER: US/09/739,455
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1868
; TYPE: DNA
; ORGANISM: Human
US-09-739-455-1

Query Match          2.6%; Score 59; DB 4; Length 1868;
Best Local Similarity 100.0%; Pred. No. 2e-15;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2184 CCCCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2242
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Db      1802 CCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1860

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 16, 2005, 11:19:08 ; Search time 4 Seconds
(without alignments)
4.497 Million cell updates/sec

Title: us-10-036-342-56
Perfect score: 2242
Sequence: 1 gaatgaataacctccgaagcc.....aaaaaaaaaaaaaaaaaaaaa 2242

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Searched: 3 segs, 4012 residues

Total number of hits satisfying chosen parameters: 6

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : 56dba.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2137.1	95.3	2152	1	AAZ65270 Human secreted pro
2	126.6	5.6	127	1	AAZ10638 Human biallelic po
3	62.4	2.8	1733	1	AAV81394 Human tumour antig
4	23.8	1.1	2152	1	AAZ65270 Human secreted pro
5	21.4	1.0	1733	1	AAV81394 Human tumour antig
6	14.6	0.7	127	1	AAZ10638 Human biallelic po

ALIGNMENTS

RESULT 1
AAZ65270
ID AAZ65270 standard; DNA; 2152 BP.

XX AC AAZ65270;

XX DT 23-MAR-2000 (first entry)

XX DE Human secreted protein gene 21.

XX KW Human; secreted protein; cancer; tumour; developmental abnormality;
KW foetal deficiency; blood disorder; immune system disorder; inflammation;
KW autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;
KW schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder;
KW atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;
KW digestive disorder; endocrine disorder; infection; AIDS; leukaemia;
KW therapy; chromosome 18q22-23; ds.

XX OS Homo sapiens.

XX PN W09958660-A1.

XX

PD	18-NOV-1999.	
XX		
PF	06-MAY-1999;	99WO-US009847.
XX		
PR	12-MAY-1998;	98US-0085093P.
PR	12-MAY-1998;	98US-0085094P.
PR	12-MAY-1998;	98US-0085105P.
PR	12-MAY-1998;	98US-0085180P.
PR	18-MAY-1998;	98US-008506P.
PR	18-MAY-1998;	98US-0085920P.
PR	18-MAY-1998;	98US-0085921P.
PR	18-MAY-1998;	98US-0085922P.
PR	18-MAY-1998;	98US-0085923P.
PR	18-MAY-1998;	98US-0085924P.
PR	18-MAY-1998;	98US-0085925P.
PR	18-MAY-1998;	98US-0085927P.
PR	18-MAY-1998;	98US-0085928P.
XX		
PA	(HUMA-) HUMAN GENOME SCI INC.	
XX		
PI	Ruben SM, Florence K, Ni J, Rosen CA, Carter KC, Moore PA;	
PI	Olson HS, Shi Y, Young PE, Wei F, Brewer LA, Soppet DR, Lafleur DW;	
PI	Endress CA, Ebner R;	
XX		
DR	WPI; 2000-062296/05.	
DR	P-PSDB; AAY76144.	
XX		
XX	New isolated human genes and the secreted polypeptides they encode,	
PT	useful for diagnosis and treatment of e.g. cancers, neurological	
PT	disorders, immune diseases, inflammation or blood disorders.	
XX		
PS	Claim 1; Page 309; 475pp; English.	
XX		
CC	AAZ65250 to AAZ65350 represent 97 isolated human secreted protein genes.	
CC	This sequence was found to be present on human chromosome 18q22-23.	
CC	AAZ76124 to AAY76223 represent the secreted proteins encoded by the 97	
CC	human genes. The genes and their corresponding secreted polypeptides are	
CC	useful for preventing, treating or ameliorating medical conditions, e.g.	
CC	by protein or gene therapy. Also pathological conditions can be diagnosed	
CC	by determining the amount of the new polypeptides in a sample or by	
CC	determining the presence of mutations in the new genes. Specific uses are	
CC	described for each of the 97 genes, based on which tissues they are most	
CC	highly expressed in, and include developing products for the diagnosis or	
CC	treatment of cancer, tumours, developmental abnormalities and foetal	
CC	deficiencies, blood disorders, diseases of the immune system, autoimmune	
CC	diseases, inflammation, allergies, Alzheimer's and cognitive disorders,	
CC	schizophrenia, arthritis, asthma, psoriasis, sepsis, skin disorders,	
CC	atherosclerosis, diabetes, cardiovascular disorders, kidney disorders,	
CC	digestive/endocrine disorders, infections and AIDS. The polypeptides are	
CC	also useful for identifying their binding partners. The sequences shown	
CC	in AAY76224 to AAY76424 represent fragments of the secreted proteins	
XX		
SQ	Sequence 2152 BP; 541 A; 526 C; 531 G; 553 T; 0 U; 1 Other;	
	Query Match 95.3%; Score 2137.1; DB 1; Length 2152;	
	Best Local Similarity 99.8%; Pred. No. 4e-11;	
	Matches 2148; Conservative 1; Mismatches 0; Indels 3; Gaps 1;	
Qy	19 CCGCTTTGTTCTCAGATGTGAATAGCTCCACTATACCAGCCTCTTCTTCGGGGG 78	
Db	1 CCGCTTTGTTCTCAGATGTGAATAGCTCCACTATACCAGCCTCTTCTTCGGGGG 60	
Qy	79 ACAACGTGGGTCAAGGCACAGAGAGATATTATGTCCACCTCTTGGGGCTTTCATGGGA 138	
Db	61 ACAACGTGGGTCAAGGCACAGAGAGATATTATGTCCACCTCTTGGGGCTTTCATGGGA 120	
Qy	139 CTCCTCTGTCACATTTTTTTGGAGGTTGGGAAAGTTGTAGAGCTTTCAGAACTCCAGCC 198	
Db	121 CTCCTCTGTCACATTTTTTTGGAGGTTGGGAAAGTTGTAGAGCTTTCAGAACTCCAGCC 180	
Qy	199 TAATGGATCCCAACTCGGGAGAGATGGCTCGCTCCCTGCTGGCTG---TGGTGTCTGTC 255	
Db	181 TAATGGATCCCAACTCGGGAGAGATGGCTCGCTCCCTGCTGGCTGCTGCTGCTGCTGCTG 240	

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QY 256 TCCTGAGCGCGGATGTTCTCCTCACCCTCCCGCCCGCGCTGTAGAGAAAGTCT 315
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QY 241 TGTGAGCGCGGATGTTCTCCTCACCCTCCCGCCCGCGCTGTAGAGAAAGTCT 300
Db |||
QY 316 TCCAGTACATTCACCTCCATCAGGATGATTTGTGACAGCGCTGAAGAGTGGTGCCA 375
Db |||
QY 301 TCAGTACATTTGACCTCCATCAGGATGAAATTTGTGACAGCGCTGAAGAGTGGTGCCA 360
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QY 376 TCGAGAGCGACTCTGTCCAGCGCTGTGCTTCCAGCAAGAGCTCTTCAGAAATGATGG 435
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QY 361 TCGAGAGCGACTCTGTCCAGCGCTGTGCTTCCAGCAAGAGCTCTTCAGAAATGATGG 420
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QY 436 CCGTGTGCGGACAGCGCTGACAGCGCTGCGGCGCGCTGTGCGCTCGGTGAGATGGGTC 495
Db |||
QY 421 CCGTGTGCGGACAGCGCTGACAGCGCTGCGGCGCGCTGTGCGCTCGGTGAGATGGGTC 480
Db |||
QY 496 CTCAGCAGCTGCCCGATGTCAGAGTCTTCCAAATACCTCCCGTCATCTGCGCGCAACTGG 555
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QY 481 CTCAGCAGCTGCCCGATGTCAGAGTCTTCCAAATACCTCCCGTCATCTGCGCGCAACTGG 540
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QY 556 GGAGCGATCCCAGAAAGCACCGTGTCTTCTACCGGCCACTTGGACGTGCGAGCCTGCTG 615
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QY 541 GGAGCGATCCCAGAAAGCACCGTGTCTTCTACCGGCCACTTGGACGTGCGAGCCTGCTG 600
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QY 616 ACCGGGCGATGGTGGCTCAGGACCCCTATGTGCTGACGGAGGTAGACGGAACTTT 675
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QY 601 ACCGGGCGATGGTGGCTCAGGACCCCTATGTGCTGACGGAGGTAGACGGAACTTT 660
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QY 676 ATGACGAGGAGGACCGACCAACAAAGGCCCTGTCTTGGCTTGGATCAATGCTGTGAGCG 735
Db |||
QY 661 ATGACGAGGAGGACCGACCAACAAAGGCCCTGTCTTGGCTTGGATCAATGCTGTGAGCG 720
Db |||
QY 736 CTTTCAGAGCCCTGGAGCAAGATCTTCTGTGTAATCAAAATTCATTCATGAGGGATGG 795
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QY 721 CTTTCAGAGCCCTGGAGCAAGATCTTCTGTGTAATCAAAATTCATTCATGAGGGATGG 780
Db |||
QY 796 AAGAGGCTGCTGTGTGCTCGAGGAACCTGTGGAAAGAAAGGACCGATCTTCT 855
Db |||
QY 781 AAGAGGCTGCTGTGTGCTCGAGGAACCTGTGGAAAGAAAGGACCGATCTTCT 840
Db |||
QY 856 CTGGTGTGACTACATTTGTAATTCAGATAAATCTGTGGATCAGCCAAAGAAAGCAGCAA 915
Db |||
QY 841 CTGGTGTGACTACATTTGTAATTCAGATAAATCTGTGGATCAGCCAAAGAAAGCAGCAA 900
Db |||
QY 916 TCACCTTATGAAACCGGGGGAACAGCTACTTCTATGTTGGAGGTGAAATGCAGAGACAGG 975
Db |||
QY 901 TCACCTTATGAAACCGGGGGAACAGCTACTTCTATGTTGGAGGTGAAATGCAGAGACAGG 960
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QY 976 ATTTTCACTCAGGAACCTTTGTTGGCATCCTTTCATGAACCAATGGCTGATCTGTTGCTC 1035
Db |||
QY 961 ATTTTCACTCAGGAACCTTTGTTGGCATCCTTTCATGAACCAATGGCTGATCTGTTGCTC 1020
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QY 1036 TTCTCGGTAGCCTGGTATAGCTGCTGGTATATCTTGTGCTGCTGCTGCTGCTGCTGCTGCTG 1095
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QY 1021 TTCTCGGTAGCCTGGTATAGCTGCTGGTATATCTTGTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
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QY 1096 TGGTTCCTCTACAGAGAGGAATTAATACATAAAGCCATCCATCTAGACCTAGAAG 1155
Db |||
QY 1081 TGGTTCCTCTACAGAGAGGAATTAATACATAAAGCCATCCATCTAGACCTAGAAG 1140
Db |||
QY 1156 AATACCGGAATAGCAGCGGGTTGAGAAATTTCTGTTTCGATACCTAAGGAGGATTCCTAA 1215
Db |||
QY 1141 AATACCGGAATAGCAGCGGGTTGAGAAATTTCTGTTTCGATACCTAAGGAGGATTCCTAA 1200
Db |||
QY 1216 TGCACCTCTGAGGATACCATCTCTTCTTATTCATGGATCGAGGCGCTTTGATGAGC 1275
Db |||
QY 1201 TGCACCTCTGAGGATACCATCTCTTCTTATTCATGGATCGAGGCGCTTTGATGAGC 1260
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QY 1276 CTGAACTTAAACAGTATACCTGCGCGAGTTATAGGAAATTTTCAATCCGCTAGTCC 1335
Db |||
QY 1261 CTGAACTTAAACAGTATACCTGCGCGAGTTATAGGAAATTTTCAATCCGCTAGTCC 1320
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QY 1336 CTCACATGAATGTCTGTCCGCTGGAAGAAACAGAGTGACACGACATCTTTGAAGATGTGTTCT 1395
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QY 1321 CTCACATGAATGTCTGTCCGCTGGAAGAAACAGAGTGACACGACATCTTTGAAGATGTGTTCT 1380
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QY 1396 CCAAGAGAAATAGTTCCTCAACAAAGATGGTGTTCCTATGACTCTAGGACTACACCGTGGA 1455
Db |||
QY 1381 CCAAGAGAAATAGTTCCTCAACAAAGATGGTGTTCCTATGACTCTAGGACTACACCGTGGA 1440
Db |||
QY 1456 TTGCAAAATATTGATGACACCCAGTATCTCGCAGCAAAAGAGCGATCAGAACAGTGTGTTG 1515
Db |||
QY 1441 TTGCAAAATATTGATGACACCCAGTATCTCGCAGCAAAAGAGCGATCAGAACAGTGTGTTG 1500
Db |||
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QY 1561 AGATCGTCCACAGAGCGTGTCTAATTCGCTGGGAGCTGTGATGATGAGAGAACATT 1620
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Db |||
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QY 1876 TAAATAAATATTTCAAGGCACAGATGTTGGAATGTTTAAAGTCCCGCCACTGCACACC 1935
Db |||
QY 1861 TAAATAAATATTTCAAGGCACAGATGTTGGAATGTTTAAAGTCCCGCCACTGCACACC 1920
Db |||
QY 1936 TTCTCTCAAGTATAGTCTGCTTGCAGCAACTTGTATTTCCCAAGTCTGTGCAATAGCCCC 1995
Db |||
QY 1921 TTCTCTCAAGTATAGTCTGCTTGCAGCAACTTGTATTTCCCAAGTCTGTGCAATAGCCCC 1980
Db |||
QY 1996 AGGATTTGATTCCTTCCAAACCTTTTAGCATATCTCCAACTTTGCAATTTGATTGGCATAA 2055
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QY 1981 AGGATTTGATTCCTTCCAAACCTTTTAGCATATCTCCAACTTTGCAATTTGATTGGCATAA 2040
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QY 2056 TCACTCCGCTTGTCTTCTAGTCTCCTCAAGTCTCGTGACACATATCAATTCATCCATCAAT 2115
Db |||
QY 2041 TCACTCCGCTTGTCTTCTAGTCTCCTCAAGTCTCGTGACACATATCAATTCATCCATCAAT 2100
Db |||
QY 2116 GATCGCTTTGCTTTTACCACTCTTTCTTTTATCTTTATTAATAAATAATGTTG 2167
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QY 2101 GATCGCTTTGCTTTTACCACTCTTTCTTTTATCTTTATTAATAAATAATGTTG 2152
Db |||
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RESULT 2

AA10638/c

ID AAX10638 standard; DNA; 127 BP.

XX AAX10638;

XX 30-MAR-1999 (first entry)

XX Human biallelic polymorphic DNA fragment WI-15225.

XX Polymorphism; biallelic; human; forensic; paternity testing; disease;
XX detection; phenotypic typing; characteristic; infection; hereditary;
XX autoimmune disease; cancer; inflammation; drug; therapy; medicament;
XX treatment; marker; ss.

OS Homo sapiens.

RESULT 5

XX 30-MAR-1999 (first entry)
XX Human biallelic polymorphic DNA fragment WI-15225.
XX Polymorphism: biallelic; human; forensic; paternity testing; disease;
KW detection; phenotypic typing; characteristic; infection; hereditary;
KW autoimmune disease; cancer; inflammation; drug; therapy; medication;
XX treatment; marker; ss.
XX Homo sapiens.
XX WO9820165-A2.
XX 14-MAY-1998.
XX 05-NOV-1997; 97WO-US020313.
XX 06-NOV-1996; 96US-0030455P.
XX (WHED) WHITEHEAD INST BIOMEDICAL RES.
XX Lander ES, Wang D, Hudson T;
XX WPI; 1998-286974/25.
XX New isolated nucleic acid segments from the human genome - used for
PT determining polymorphic forms for use in e.g. forensics, paternity
PT testing or phenotypic typing for disease.
XX
XX Claim 1; Page 67; 310pp; English.
XX AAX10269-X12937 are human DNA fragments which contain biallelic
CC polymorphic markers which have been isolated using the primers
CC represented in AAX09121-X10268. The base occupying the polymorphic site
CC is indicated by the appropriate IUPAC-IUB ambiguity code. These fragments
CC can be used in methods for determining polymorphic forms in an individual
CC for use in e.g. forensics, paternity testing or for phenotypic typing for
CC diseases such as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan
CC syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease,
CC familial hypercholesterolemia, polycystic kidney disease, hereditary
CC spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary
CC haemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos
CC syndrome, osteogenesis imperfecta, acute intermittent porphyria,
CC autoimmune diseases, inflammation, cancer, diseases of the nervous
CC system, infection by pathogenic microorganisms, and characteristics such
CC as longevity, appearance (e.g. baldness, obesity), strength, speed,
CC endurance, fertility, and susceptibility or receptivity to particular
CC drugs or therapeutic treatments. The isolated polymorphic nucleic acid
CC segments can also be used to produce medicaments for the treatment or
CC prophylaxis of such diseases
XX
XX Sequence 127 BP; 47 A; 16 C; 36 G; 27 T; 0 U; 1 Other;
Query Match 0.7%; Score 14.6; DB 1; Length 127;
Best Local Similarity 57.8%; Pred.No. 26;
Matches 26; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
QY 136 GGACTCCCTCTGCCACATTTTTCGAGGTGGGAAGTTCGTACA 180
Db 82 GGAGTGATTATGCCAATCAAAATGCAAGGTGGAGATATGCTAAA 126
Search completed: February 16, 2005, 11:19:14
Job time : 5 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 16, 2005, 11:23:54 ; Search time 553 Seconds
(without alignments)
3.980 Million cell updates/sec

Title: us-10-036-342-56

Perfect score: 2242

Sequence: 1 gaatgaataactccgaagcc.....aaaaaaaaaaaaaaaaaaaaa 2242

Scoring table: IDENTITY NUC

Gapop 10⁻⁷0 , Gapext 0.5

Searched: 13 seqs, 490885 residues

Total number of hits satisfying chosen parameters: 26

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : 56dbb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	614.8	27.4	672	1	AR412460
2	614.8	27.4	672	1	AX969294
3	614.8	27.4	672	1	BD108013
4	567.5	25.3	3755	1	AK131263
c	524.6	23.4	164394	1	AC116904
	292.8	13.1	300	1	AX898087
	292.8	13.1	300	1	BD033620
7	279	12.4	279	1	CQ715367
8	225	10.0	178691	1	AC009704
9	203.4	9.1	64201	1	AC117833
10	203.4	9.1	64201	1	AC117833
11	169.4	7.6	73476	1	AC123772
12	169.4	6.9	2006	1	BC047599
c	154.4	6.8	73476	1	AC123772
14	153	6.8	1467	1	BC065925
c	152.8	6.8	1467	1	BC065925
16	46.6	2.1	178691	1	AC009704
17	34.4	1.5	164394	1	AC116904
18	32	1.4	2006	1	BC047599
c	25	1.1	300	1	AX898087
19	25	1.1	300	1	BD033620
c	20	1.1	300	1	BD033620
21	23.8	1.1	672	1	AR412460
c	23.8	1.1	672	1	AX969294
23	23.8	1.1	672	1	BD108013
c	24	1.0	3755	1	AK131263
25	21.6	0.9	1467	1	BC065925
c	20.4	0.9	1467	1	BC065925
26	19.4	0.9	279	1	CQ715367

ALIGNMENTS

RESULT 1
AR412460

LOCUS	AR412460	Sequence 97 from patent US 6639063.	672 bp	DNA	linear	PAT 18-DEC-2003
DEFINITION	Sequence 97 from patent US 6639063.					
ACCESSION	AR412460					
VERSION	AR412460.1	GI:40167570				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 672)					
AUTHORS	Edwards,J.-B.D.M., Jobert,S. and Giordano,J.-Y.					
TITLE	EST's and encoded human proteins					
JOURNAL	Patent: US 6639063-A 97 28-OCT-2003;					
FEATURES	Location/Qualifiers					
source	1..672					
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	/mol_type="genomic DNA"					
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Best Local Similarity	98.1%;	Pred. No. 5.7;				
Matches	635;	Conservative 5;	Mismatches 3;	Indels 4;	Gaps 2;	
Qy	1	GAATGAATACCTCCGAAGCCGCTTTGTTCTCCAGATGTGAATAGTCCACTATACCAAGCC	60			
Db	27	GAATGAATACCTCCGAAGCCGCTTTGTTCTCCAGATGTGAATAGTCCACTATACCAAGCC	86			
Qy	61	TCGTCTTCTTCCCGGGGACAACTGGGTGAGGCACAGAGATATTTAATGTCAACCT	120			
Db	87	TCGTCTTCTTCCCGGGGACAACTGGGTGAGGCACAGAGATATTTAATGTCAACCT	146			
Qy	121	CTTGGGGCTTTCATGGGACTCCCTCTGCCACATTTTGGAGGTGGGAAAGTTGCTAGA	180			
Db	147	CTTGGGGCTTTCATGGGACTCCCTCTGCCACATTTTGGAGGTGGGAAAGTTGCTAGA	206			
Qy	181	GGCTTCAGAACTCCAGCTTAATGATCCCAAACTCGGGAGAAATGGCTGCGTCCCTGCTGG	240			
Db	207	GGCTTCAGAACTCCAGCTTAATGATCCCAAACTCGGGAGAAATGGCTGCGTCCCTGCTGG	266			
Qy	241	CTG---TGCTGTGCTGCTCTGGAGCGCGGCAATGTTCTCTCACCTCCCGCCCCCGG	297			
Db	267	CTGTGCTGCTGCTGCTGCTGGAGCGGCAATGTTCTCTCACCTCCCGCCCCCGG	326			
Qy	298	CGCTGTAGAGAAAGTCTTCAGTACATTCACCTCCATCAGGATGAATTTGTGCAGACGC	357			
Db	327	CGCTGTAGAGAAAGTCTTCAGTACATTCACCTCCATCAGGATGAATTTGTGCAGACGC	386			
Qy	358	TGAAGGAGTGGTGGCCATCGAGAGCGACTCTGTCCAGCCTGTGCTTCAGACAAG	417			
Db	387	TGAAGGAGTGGTGGCCATCGAGAGCGACTCTGTCCAGCCTGTGCTTCAGACAAG	446			
Qy	418	AGCTCTTCAGAAATGATGGCGTGGCTGCGGACACGCTGCAGCGCTGGGGGGCCCGTGG	477			
Db	447	AGCTCTTCAGAAATGATGGCGTGGCTGCGGACACGCTGCAGCGCTGGGGGGCCCGTGG	506			
Qy	478	CCTCGGTGACATGGGTCTCTCAGAGCTGCCGATGGTTCAGAGTCTTTCATACCTCCCG	537			
Db	507	CCTCGGTGACATGGGTCTCTCAGAGCTGCCGATGGTTCAGAGTCTTTCATACCTCCCG	566			
Qy	538	TCATCTCGCCGAACCTGGGAGCGATCCCAAGAACCGGTGTGCTTCTACGGCCACT	597			
Db	567	TCATCTCGCCGAACCTGGGAGCGATCCCAAGAACCGGTGTGCTTCTACGGCCACT	625			
Qy	598	TGACACGTGACAGCTGTGACCGGGGGGATGGGTGGCTTCACGGACCCCC	644			
Db	626	TGACACGTGACAGCTGTGACCGGGGGGATGGGTGGCTTCACGGACCCCC	672			
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LOCUS	AX969294					
DEFINITION	Sequence 97 from Patent EP1104808.					
ACCESSION	AX969294					
VERSION	AX969294.1	GI:40975507				
KEYWORDS						

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Dumas Milne Edwards, J.B., Jobert, S. and Giordano, J.Y.
ESTs and encoded human proteins
TITLE Patent: EP 1104808-A 97 06-JUN-2001;
JOURNAL Genset (FR)
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227..307
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Best Local Similarity 98.1%; Pred. No. 5.7;
Matches 635; Conservative 5; Mismatches 3; Indels 4; Gaps 2;
Qy 1 GAATGAATACCTCCGAGCGCTTTGTTCTCCAGATGTGAATAGCTCCACTATACCAGCC 60
Db 27 GAATGAATACCTCCGAGCGCTTTGTTCTCCAGATGTGAATAGCTCCACTATACCAGCC 86
Qy 61 TCGTCTTCCCTCCGGGGGACAACTGGGTGAGGACAGAGAGATATTTAATGTCAACCT 120
Db 87 TCGTCTTCCCTCCGGGGGACAACTGGGTGAGGACAGAGAGATATTTAATGTCAACCT 146
Qy 121 CTTGGGGCTTTCATGGGACTCCCTCTGCGACATTTTGGAGTTGGGAAAGTTGCTAGA 180
Db 147 CTTGGGGCTTTCATGGGACTCCCTCTGCGACATTTTGGAGTTGGGAAAGTTGCTAGA 206
Qy 298 CGCTGTTAGAAAAGTCTTCAGTACATTCAGCTCCATCAGGATGAATTTGTGACAGCG 357
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Qy 358 TGAAGGAGTGGGTGGCCATCGAGAGCGACTCTGTCAGCGCTGTCCTCGCTTCAGACAAG 417
Db 387 TGAAGGAGTGGGTGGCCATCGAGAGCGACTCTGTCAGCGCTGTCCTCGCTTCAGACAAG 446
Qy 418 AGCTCTTCAGAAATGATGGCCGTGGCTGGGACACGCTGACGCGCTGGGGCCCGGTGG 477
Db 447 AGCTCTTCAGAAATGATGGCCGTGGCTGGGACACGCTGACGCGCTGGGGCCCGGTGG 506
Qy 478 CCTGGTGGACATGGGTCTTCAGAGCTGCCGATGGTTCAGAGTCTTCAGTACCTCCCG 537
Db 507 CCTGGTGGACATGGGTCTTCAGAGCTGCCGATGGTTCAGAGTCTTCAGTACCTCCCG 566
Qy 538 TCATCTGGCGGAACTGGGGGCGGATCCCAAGGACCGCTGTGCTTTCAGCGCACT 597
Db 567 TCATCTGGCGGAACTGGGGGCGGATCCCAAGGACCGCTGTGCTTTCAGCGCACT 625
Qy 598 TGGAGTGGAGCTGCTGACCGGGCGGATGGGTGGCTCACGGAGCCC 644
Db 626 TGGAGTGGAGCTGCTGACCGGGCGGATGGGTGGCTCACGGAGCCC 672

RESULT 3
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LOCUS
DEFINITION
EST and encoded human protein.
ACCESSION
BD108013
VERSION
BD108013.1 GI:23202831
KEYWORDS
JP 2002010789-A/90.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 672)
AUTHORS
Edwards, J.B.D.M., Jobert, S. and Giordano, J.E.
TITLE
EST and encoded human protein
JOURNAL
Patent: JP 2002010789-A 90 15-JAN-2002;
GENSET CORP
COMMENT
OS Homo sapiens (human)
PN JP 2002010789-A/90
PD 15-JAN-2002
PF 07-AUG-2000 JP 2000280989
PR 03-AUG-1999 US 60/147499
PI JEAN BAPTISTE DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE PI
GIORDANO
PC C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, PC
C12N1/21,
PC C12N5/10, C12P21/02, C12P21/08, C12Q1/68, C12N15/00, C12N5/00, PC
C12N15/00
CC Von Heijne matrix
CC score 7.09999990463257
CC seq VLLLLLLRGMFSS/SP
CC n=a, g, c or t
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FT sig_peptide 227..307
FT misc feature 586
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Query Match 27.4%; Score 614.8; DB 1; Length 672;
Best Local Similarity 98.1%; Pred. No. 5.7;
Matches 635; Conservative 5; Mismatches 3; Indels 4; Gaps 2;
Qy 1 GAATGAATACCTCCGAGCGCTTTGTTCTCCAGATGTGAATAGCTCCACTATACCAGCC 60
Db 27 GAATGAATACCTCCGAGCGCTTTGTTCTCCAGATGTGAATAGCTCCACTATACCAGCC 86
Qy 61 TCGTCTTCCCTCCGGGGGACAACTGGGTGAGGACAGAGAGATATTTAATGTCAACCT 120
Db 87 TCGTCTTCCCTCCGGGGGACAACTGGGTGAGGACAGAGAGATATTTAATGTCAACCT 146
Qy 121 CTTGGGGCTTTCATGGGACTCCCTCTGCGACATTTTGGAGTTGGGAAAGTTGCTAGA 180
Db 147 CTTGGGGCTTTCATGGGACTCCCTCTGCGACATTTTGGAGTTGGGAAAGTTGCTAGA 206
Qy 181 GGCTTTCAGAACTCTTCAGTACATTCAGCTCCATCAGGATGAATTTGTGACAGCG 240
Db 207 GGCTTTCAGAACTCTTCAGTACATTCAGCTCCATCAGGATGAATTTGTGACAGCG 326
Qy 241 TGAAGGAGTGGGTGGCCATCGAGAGCGACTCTGTCAGCGCTGTCCTCGCTTCAGACAAG 417
Db 327 TGAAGGAGTGGGTGGCCATCGAGAGCGACTCTGTCAGCGCTGTCCTCGCTTCAGACAAG 446
Qy 418 AGCTCTTCAGAAATGATGGCCGTGGCTGGGACACGCTGACGCGCTGGGGCCCGGTGG 477
Db 447 AGCTCTTCAGAAATGATGGCCGTGGCTGGGACACGCTGACGCGCTGGGGCCCGGTGG 506
Qy 478 CCTGGTGGACATGGGTCTTCAGAGCTGCCGATGGTTCAGAGTCTTCAGTACCTCCCG 537
Db 507 CCTGGTGGACATGGGTCTTCAGAGCTGCCGATGGTTCAGAGTCTTCAGTACCTCCCG 566
Qy 538 TCATCTGGCGGAACTGGGGGCGGATCCCAAGGACCGCTGTGCTTTCAGCGCACT 597
Db 567 TCATCTGGCGGAACTGGGGGCGGATCCCAAGGACCGCTGTGCTTTCAGCGCACT 625
Qy 598 TGGAGTGGAGCTGCTGACCGGGCGGATGGGTGGCTCACGGAGCCC 644
Db 626 TGGAGTGGAGCTGCTGACCGGGCGGATGGGTGGCTCACGGAGCCC 672

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Qy      CCTCGGTGGACATGGGTCTCAGCAGCTGCCGATGGTTCAGAGTCTTCCAAATACCTCCCG 537
Db      CCTCGGTGGACATGGGTCTCAGCAGCTGCCGATGGTTCAGAGTCTTCCAAATACCTCCCG 566
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Db      TGGACGTGACGCTGTGACCGGGCGATGGTGGCTCAGCGACCCC 672

RESULT 4
LOCUS   AK131263 3755 bp mRNA linear PRI 07-MAY-2004
DEFINITION Homo sapiens cDNA FLJ16195 fis, clone BRTHA3000296.
ACCESSION AK131263
VERSION   AK131263.1 GI:47077013
KEYWORDS  oligo capping; fis (full insert sequence).
SOURCE   Homo sapiens
ORGANISM Homo sapiens
REFERENCE
AUTHORS Ota, T., Nakagawa, S., Senoh, A., Mizuguchi, H., Inagaki, H., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagabari, K., Masuho, Y., Nagai, K. and Isogai, T.
TITLE    NEDO human cDNA sequencing project
JOURNAL  Unpublished
REFERENCE 2 (bases 1 to 3755)
AUTHORS   Isogai, T. and Yamamoto, J.
TITLE     Direct Submission
JOURNAL   Submitted (01-MAR-2004) Takao Isogai, FLJ Project (HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan (E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.
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CDS

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Query Match 25.3%; Score 567.5; DB 1; Length 3755;
Best Local Similarity 55.2%; Pred. No. 2.1;
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Qy 1321 CAATCCGCTAGTCCCTCACAATGATGTCTGCGGTGGAAAAACAGGTGACACGACATC 1380
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Db 2772 TATTTATCTCTCCAGGCCCTGTCTCCAAATACACAGACACTGGGGGTTTAGGGTTCAAC 2831
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DEFINITION AC116904
ACCESSION AC116904
VERSION AC116904.7 GI:22655819
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 164394)
AUTHORS Birren,B., Nussbaum,C. and Lander,E.
TITLE Homo sapiens chromosome 18, clone RP11-1112M8
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 164394)
AUTHORS Birren,B., Linton,L., Nussbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavsky,L.,
Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,
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Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
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Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission
Submitted (02-APR-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 164394)
Birren,B., Nussbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
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Zembek,L., Zimmer,A. and Zody,M.

Direct Submission
Submitted (28-AUG-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
4 (bases 1 to 164394)
Birren,B., Nussbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
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Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
Zembek,L., Zimmer,A. and Zody,M.

Direct Submission
Submitted (03-SEP-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Sep 3, 2002 this sequence version replaced gi:22532750.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L26198
 Center clone name: 1112_M_8

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 VERSION AX898087.1 GI:40053000
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 ORGANISM
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
 AUTHORS Dumas Milne Edwards, J.B., Duclert, A. and Giordano, J.Y.
 TITLE Expressed sequence tags and encoded human proteins
 JOURNAL Patent: EP 1033401-A 13950 06-SEP-2000;
 Genset (FR)

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 ORGANISM Homo sapiens
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
 AUTHORS Edwards, J.B.D.M., Duclair, E. and Jordan, J.Y.
 TITLE Sequence tag and encoded human protein
 JOURNAL Patent: JP 2001269182-A 9866 02-OCT-2001;
 GENSET

COMMENT
 OS Homo sapiens (human)
 PN JP 2001269182-A/9866
 PD 02-OCT-2001
 PR 24-FEB-2000 JP 2000118773
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* NOTE: This record contains 80 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
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* 1563: contig of 718 bp in length
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* 2471: gap of 100 bp
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* 3992: contig of 710 bp in length
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* 4795: contig of 703 bp in length
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* 19412: gap of 100 bp
* 19413
* 20124: contig of 712 bp in length
* 20125
* 20224: gap of 100 bp
* 20225
* 20902: contig of 678 bp in length
* 20903
* 21002: gap of 100 bp
* 21003
* 21707: contig of 705 bp in length
* 21708
* 21807: gap of 100 bp
* 21808
* 22510: contig of 703 bp in length
* 22511
* 22610: gap of 100 bp
* 22611
* 23325: contig of 715 bp in length
* 23326
* 23425: gap of 100 bp
* 23426
* 24136: contig of 711 bp in length
* 24137
* 24236: gap of 100 bp
* 24237
* 24928: contig of 692 bp in length
* 24929
* 25029
* 25735: contig of 707 bp in length
* 25736
* 25835: gap of 100 bp
* 25836
* 26535: contig of 700 bp in length
* 26536
* 26635: gap of 100 bp
* 26636
* 27347: contig of 712 bp in length
* 27348
* 27447: gap of 100 bp
* 27448
* 28154: contig of 707 bp in length
* 28155
* 28254: gap of 100 bp
* 28255
* 28963: contig of 709 bp in length
* 28964
* 29063: gap of 100 bp
* 29064
* 29774: contig of 711 bp in length
* 29775
* 29874: gap of 100 bp
* 29875
* 30587: contig of 713 bp in length
* 30588
* 31398: gap of 100 bp
* 31399
* 31498: gap of 100 bp
* 31499
* 32122: contig of 714 bp in length
* 32123
* 32312: gap of 100 bp
* 32313
* 32992: contig of 680 bp in length
* 32993
* 33092: gap of 100 bp
* 33093
* 33780: contig of 688 bp in length
* 33781
* 33880: gap of 100 bp
* 33881
* 34582: contig of 702 bp in length
* 34583
* 34682: gap of 100 bp
* 34683
* 35351: contig of 669 bp in length
* 35352
* 35451: gap of 100 bp
* 35452
* 36126: contig of 675 bp in length
* 36127
* 36226: gap of 100 bp
* 36227
* 36940: contig of 714 bp in length
* 36941
* 37040: gap of 100 bp
* 37041
* 37759: contig of 719 bp in length
* 37760
* 37859: gap of 100 bp
* 37860
* 38574: contig of 715 bp in length
* 38575
* 38674: gap of 100 bp
* 38675
* 39348: contig of 674 bp in length
* 39349
* 39448: gap of 100 bp
* 39449
* 40151: contig of 703 bp in length
* 40152
* 40251: gap of 100 bp
* 40252
* 40932: contig of 681 bp in length
* 40933
* 41032: gap of 100 bp
* 41033
* 41714: contig of 682 bp in length
* 41715
* 41814: gap of 100 bp
* 41815
* 42522: contig of 708 bp in length
* 42523
* 42622: gap of 100 bp
* 42623
* 43322: contig of 700 bp in length
* 43323
* 43422: gap of 100 bp
* 43423
* 44114: contig of 692 bp in length
* 44115
* 44214: gap of 100 bp
* 44215
* 44919: contig of 705 bp in length
* 44920
* 45019: gap of 100 bp
* 45020
* 45734: contig of 715 bp in length
* 45735
* 45834: gap of 100 bp
* 45835
* 46541: contig of 707 bp in length
* 46542
* 46641: gap of 100 bp
* 46642
* 47332: contig of 691 bp in length
* 47333
* 47432: gap of 100 bp
* 47433
* 48081: contig of 649 bp in length
* 48082
* 48181: gap of 100 bp
* 48182
* 48898: contig of 717 bp in length
* 48899
* 48998: gap of 100 bp
* 48999
* 49706: contig of 708 bp in length
* 49707
* 49806: gap of 100 bp
* 49807
* 50517: contig of 711 bp in length
* 50518
* 50617: gap of 100 bp
* 50618
* 51305: contig of 688 bp in length
* 51306
* 51405: gap of 100 bp
* 51406
* 52112: contig of 707 bp in length
* 52113
* 52212: gap of 100 bp
* 52213
* 52907: contig of 695 bp in length
* 52908
* 53007: gap of 100 bp
* 53008
* 53725: contig of 718 bp in length
* 53726
* 53825: gap of 100 bp
* 24928: gap of 100 bp
* 25029
* 25735: contig of 707 bp in length
* 25736
* 25835: gap of 100 bp
* 25836
* 26535: contig of 700 bp in length
* 26635: gap of 100 bp
* 27347: contig of 712 bp in length
* 27447: gap of 100 bp
* 28154: contig of 707 bp in length
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* 28963: contig of 709 bp in length
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* 29774: contig of 711 bp in length
* 29874: gap of 100 bp
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* 31398: gap of 100 bp
* 31498: gap of 100 bp
* 32122: contig of 714 bp in length
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* 32992: contig of 680 bp in length
* 33092: gap of 100 bp
* 33780: contig of 688 bp in length
* 33880: gap of 100 bp
* 34582: contig of 702 bp in length
* 34682: gap of 100 bp
* 35351: contig of 669 bp in length
* 35451: gap of 100 bp
* 36126: contig of 675 bp in length
* 36226: gap of 100 bp
* 36940: contig of 714 bp in length
* 37040: gap of 100 bp
* 37759: contig of 719 bp in length
* 37859: gap of 100 bp
* 38574: contig of 715 bp in length
* 38674: gap of 100 bp
* 39348: contig of 674 bp in length
* 39448: gap of 100 bp
* 40151: contig of 703 bp in length
* 40251: gap of 100 bp
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* 41032: gap of 100 bp
* 41714: contig of 682 bp in length
* 41814: gap of 100 bp
* 42522: contig of 708 bp in length
* 42622: gap of 100 bp
* 43322: contig of 700 bp in length
* 43422: gap of 100 bp
* 44114: contig of 692 bp in length
* 44214: gap of 100 bp
* 44919: contig of 705 bp in length
* 45019: gap of 100 bp
* 45734: contig of 715 bp in length
* 45834: gap of 100 bp
* 46541: contig of 707 bp in length
* 46641: gap of 100 bp
* 47332: contig of 691 bp in length
* 47432: gap of 100 bp
* 48081: contig of 649 bp in length
* 48181: gap of 100 bp
* 48898: contig of 717 bp in length
* 48998: gap of 100 bp
* 49706: contig of 708 bp in length
* 49806: gap of 100 bp
* 50517: contig of 711 bp in length
* 50617: gap of 100 bp
* 51305: contig of 688 bp in length
* 51405: gap of 100 bp
* 52112: contig of 707 bp in length
* 52212: gap of 100 bp
* 52907: contig of 695 bp in length
* 53007: gap of 100 bp
* 53725: contig of 718 bp in length
* 53825: gap of 100 bp

```

* 53926 54536: contig of 711 bp in length
* 54537 54636: gap of 100 bp
* 54637 55339: contig of 703 bp in length

Query Match          9.1%; Score 203.4; DB 1; Length 64201;
Best Local Similarity 99.5%; Pred. No. 6.5;
Matches 204; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 754 AGATCTTCTGTGAATATCAAAATCATATGAGGGATGAAGAGGCTGCTGTG 813
Db 10669 AGGATCTTCTGTGAATATCAAAATCATATGAGGGATGAAGAGGCTGCTGTG 10728
QY 814 CCTGGAGGACTGTGGAAAAGAAAGACCGATTCTCTCTGTGTGGACTACATTG 873
Db 10729 CCTGGAGGACTGTGGAAAAGAAAGACCGATTCTCTCTGTGTGGACTACATTG 10788
QY 874 TAATTTTCAGATAACCTGTGGATCAGCAAGGAGGACCAATCATTTATGAACCCGGG 933
Db 10789 TAATTTTCAGATAACCTGTGGATCAGCAAGGAGGACCAATCATTTATGAACCCGGG 10848
QY 934 GGAACAGCTACTTCATGTTGGAGGT 958
Db 10849 GGAACAGCTACTTCATGTTGGAGGT 10873

RESULT 11
AC117833 64201 bp DNA linear HTG 10-APR-2002
LOCUS Homo sapiens chromosome 18 clone CTD-2088C24 map 18, LOW-PASS
DEFINITION SEQUENCE SAMPLING.
AC117833
VERSION AC117833.1 GI:20128630
KEYWORDS HTG; HTGS_PHASE0.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 64201)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavsky,L.,
Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,
Chazaro,B., Chospel,Y., Colangelo,M., Collins,S., Collymore,A.,
Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Fierre,N.,
Hagos,B., Horton,L., Hulme,W., Illiev,I., Johnson,R., Jones,C.,
Kanat,A., Karatas,A., Kells,C., LaRocque,K., Lamazares,R.,
Landers,T., Lehoczyk,J., Levine,R., Lindblad-Toh,K., Liu,G.,
Maclean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
McCarthy,M., McEwan,P., McKernan,K., Meldrim,J., Meneus,L.,
Mihova,T., Mienga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R.,
Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,
Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
Raymond,C., Retta,R., Roy,A., Santos,R., Schauer,S., Schupback,R.,
Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (10-APR-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit,A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
```

```

Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L26228
Center clone name: 2088_C_24

* NOTE: This record contains 80 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
* 1 745: contig of 745 bp in length
* 746 845: gap of 100 bp
* 846 1563: contig of 718 bp in length
* 1564 1663: gap of 100 bp
* 1664 2371: contig of 708 bp in length
* 2372 2471: gap of 100 bp
* 2472 3182: contig of 711 bp in length
* 3183 3282: gap of 100 bp
* 3283 3992: contig of 710 bp in length
* 3993 4092: gap of 100 bp
* 4093 4795: contig of 703 bp in length
* 4796 4895: gap of 100 bp
* 4896 5605: contig of 710 bp in length
* 5606 5705: gap of 100 bp
* 5706 6419: contig of 714 bp in length
* 6420 6519: gap of 100 bp
* 6520 7222: contig of 703 bp in length
* 7223 7322: gap of 100 bp
* 7323 8029: contig of 707 bp in length
* 8030 8129: gap of 100 bp
* 8130 8444: contig of 715 bp in length
* 8445 8544: gap of 100 bp
* 8545 9640: contig of 696 bp in length
* 9641 9740: gap of 100 bp
* 9741 10442: contig of 702 bp in length
* 10443 10542: gap of 100 bp
* 10543 11247: contig of 705 bp in length
* 11248 11347: gap of 100 bp
* 11348 12138: contig of 691 bp in length
* 12039 12138: gap of 100 bp
* 12139 12818: contig of 680 bp in length
* 12819 12918: gap of 100 bp
* 12919 13633: contig of 715 bp in length
* 13634 13733: gap of 100 bp
* 13734 14450: contig of 717 bp in length
* 14451 14550: gap of 100 bp
* 14551 15261: contig of 711 bp in length
* 15262 15361: gap of 100 bp
* 15362 16099: contig of 738 bp in length
* 16100 16199: gap of 100 bp
* 16200 16911: contig of 712 bp in length
* 17011 17011: gap of 100 bp
* 17012 17687: contig of 676 bp in length
* 17688 17787: gap of 100 bp
* 17788 18507: contig of 720 bp in length
* 18508 18607: gap of 100 bp
* 18608 19312: contig of 705 bp in length
* 19313 19412: gap of 100 bp
* 19413 20124: contig of 712 bp in length
* 20125 20224: gap of 100 bp
* 20225 20902: contig of 678 bp in length
* 20903 21002: gap of 100 bp
* 21003 21707: contig of 705 bp in length
* 21708 21807: gap of 100 bp
* 21808 22510: contig of 703 bp in length
* 22511 22610: gap of 100 bp
```

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* 22611 23325: contig of 715 bp in length
* 23326 23425: gap of 100 bp
* 23426 24136: contig of 711 bp in length
* 24137 24236: gap of 100 bp
* 24237 24928: contig of 692 bp in length
* 24929 25028: gap of 100 bp
* 25029 25735: contig of 707 bp in length
* 25736 25835: gap of 100 bp
* 25836 26535: contig of 700 bp in length
* 26536 27247: contig of 712 bp in length
* 27248 27444: gap of 100 bp
* 27445 28154: contig of 707 bp in length
* 28155 28254: gap of 100 bp
* 28255 28963: contig of 709 bp in length
* 28964 29063: gap of 100 bp
* 29064 29775: contig of 711 bp in length
* 29776 29874: gap of 100 bp
* 29875 30587: contig of 713 bp in length
* 30588 30687: gap of 100 bp
* 30688 31398: contig of 711 bp in length
* 31399 31498: gap of 100 bp
* 31499 32212: contig of 714 bp in length
* 32213 32312: gap of 100 bp
* 32313 32992: contig of 680 bp in length
* 32993 33092: gap of 100 bp
* 33093 33780: contig of 688 bp in length
* 33781 33880: gap of 100 bp
* 33881 34582: contig of 702 bp in length
* 34583 34682: gap of 100 bp
* 34683 35351: contig of 669 bp in length
* 35352 35451: gap of 100 bp
* 35452 36126: contig of 675 bp in length
* 36127 36226: gap of 100 bp
* 36227 36940: contig of 714 bp in length
* 36941 37040: gap of 100 bp
* 37041 37759: contig of 719 bp in length
* 37760 37859: gap of 100 bp
* 37860 38574: contig of 715 bp in length
* 38575 38674: gap of 100 bp
* 38676 39348: contig of 674 bp in length
* 39349 39448: gap of 100 bp
* 39449 40151: contig of 703 bp in length
* 40152 40251: gap of 100 bp
* 40252 40932: contig of 681 bp in length
* 40933 41032: gap of 100 bp
* 41033 41714: contig of 682 bp in length
* 41715 41814: gap of 100 bp
* 41815 42522: contig of 708 bp in length
* 42523 42622: gap of 100 bp
* 42623 43322: contig of 700 bp in length
* 43323 43422: gap of 100 bp
* 43423 44114: contig of 692 bp in length
* 44115 44214: gap of 100 bp
* 44215 44919: contig of 705 bp in length
* 44920 45019: gap of 100 bp
* 45020 45734: contig of 715 bp in length
* 45735 45834: gap of 100 bp
* 45835 46541: contig of 707 bp in length
* 46542 46641: gap of 100 bp
* 46642 47332: contig of 691 bp in length
* 47333 47432: gap of 100 bp
* 47433 48081: contig of 649 bp in length
* 48082 48181: gap of 100 bp
* 48182 48898: contig of 717 bp in length
* 48899 48998: gap of 100 bp
* 48999 49708: contig of 708 bp in length
* 49707 49806: gap of 100 bp
* 49807 50517: contig of 711 bp in length
* 50518 50617: gap of 100 bp
* 50618 51305: contig of 688 bp in length
* 51306 51405: gap of 100 bp
* 51406 52112: contig of 707 bp in length

Query Match          9.1%; Score 203.4; DB 1; Length 64201;
Best Local Similarity 99.5%; Pred. No. 6.5;
Matches 204; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 754 AAGATCTTCTGTCATATCAATTCATCATTCAGGGGATGGAAGAGCGTCTCTGTTG 813
|
|
|
Db 8825 AGGATCTTCTGTCATATCAATTCATCATTCAGGGGATGGAAGAGCGTCTCTGTTG 8766
|
|
|
Qy 814 CCTGGAGGAACCTGTGGAAAAAGAAAGACCGATTCTTCTGTGTGGACTACATTG 873
|
|
|
Db 8765 CCCTGGAGGAACCTGTGGAAAAAGAAAGACCGATTCTTCTGTGTGGACTACATTG 8706
|
|
|
Qy 874 TAATTTTCAGATAACCTGTGGATCAGCCAAAGGAAGCAGCAATCATTATGGAACCCGGG 933
|
|
|
Db 8705 TAATTTTCAGATAACCTGTGGATCAGCCAAAGGAAGCAGCAATCATTATGGAACCCGGG 8646
|
|
|
Qy 934 GGAACAGCTACTTTCATGCTGGAGGT 958
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|
Db 8645 GGAACAGCTACTTTCATGCTGGAGGT 8621

RESULT 12
AC123772
LOCUS          73476 bp      DNA      linear      HTG 01-JUN-2002
DEFINITION    Homo sapiens chromosome 18 clone RP11-911e16 map 18, LOW-PASS
               SEQUENCE SAMPLING.
AC123772
VERSION        AC123772.1 GI:21307335
KEYWORDS       HTG; HTGS PHASE0.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 73476)
AUTHORS        Birren, B., Linton, L., Nusbaum, C. and Lander, E.
TITLE          Homo sapiens chromosome 18, clone RP11-911e16
JOURNAL         Unpublished
REFERENCE      2 (bases 1 to 73476)
AUTHORS        Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
               Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L.,
               Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J.,
               Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A.,
               Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J. S., Dodge, S.,
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               Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I.,
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               Nicol, R., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P.,
               O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,
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               Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Testaye, S.,
               Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J.,
               Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J.,
               Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
               Direct Submission
TITLE          Submitted (01-JUN-2002) Whitehead Institute/MIT Center for Genome
               Research, 320 Charles Street, Cambridge, MA 02141, USA
JOURNAL
COMMENT        All repeats were identified using RepeatMasker:
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Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L27294
Center clone name: 911_E_16

* NOTE: This record contains 89 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

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832
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1654: gap of 100 bp
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1655
2374
2473: gap of 100 bp
3190: contig of 717 bp in length
3191
3290: gap of 100 bp
4026: contig of 736 bp in length
4027
4126: gap of 100 bp
4845: contig of 719 bp in length
4846
4946: gap of 100 bp
5666: contig of 721 bp in length
5667
5766: gap of 100 bp
6496: contig of 730 bp in length
6497
6596: gap of 100 bp
7320: contig of 724 bp in length
7321
7420: gap of 100 bp
8143: contig of 729 bp in length
8150
8249: gap of 100 bp
8250
9086: contig of 737 bp in length
9087
9817: contig of 731 bp in length
9818
9917: gap of 100 bp
10643: contig of 732 bp in length
10650
10749: gap of 100 bp
11474: contig of 725 bp in length
11475
11574: gap of 100 bp
12313: contig of 739 bp in length
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12413: gap of 100 bp
13146: contig of 733 bp in length
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13246: gap of 100 bp
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13982: contig of 736 bp in length
13983
14082: gap of 100 bp
14798: contig of 716 bp in length
14799
14898: gap of 100 bp
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15624
15723: gap of 100 bp
16453: contig of 730 bp in length
16454
16553: gap of 100 bp
16554
17279: contig of 726 bp in length
17280
17379: gap of 100 bp
18106: contig of 727 bp in length
18206: gap of 100 bp
18207
18915: contig of 709 bp in length
18916
19742: contig of 727 bp in length
19743
19842: gap of 100 bp
20580: contig of 738 bp in length
20581
20680: gap of 100 bp
21384: contig of 704 bp in length
20681

21385
21485
2205: contig of 721 bp in length
22305: gap of 100 bp
23029: contig of 724 bp in length
23129: gap of 100 bp
233030
23855: contig of 726 bp in length
23955: gap of 100 bp
24675: contig of 720 bp in length
24676
24775: gap of 100 bp
25500: contig of 725 bp in length
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25601
26314: contig of 714 bp in length
26315
26414: gap of 100 bp
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27144
27243: gap of 100 bp
27244
27976: contig of 733 bp in length
28076: gap of 100 bp
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28801: contig of 725 bp in length
28802
28901: gap of 100 bp
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29635
29734: gap of 100 bp
30473: contig of 739 bp in length
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30573: gap of 100 bp
31305: contig of 732 bp in length
31306
31405: gap of 100 bp
32138: contig of 733 bp in length
32139
32238: gap of 100 bp
32977: contig of 739 bp in length
33077: gap of 100 bp
33078
33801: contig of 724 bp in length
33802
33901: gap of 100 bp
34631: contig of 730 bp in length
34731: gap of 100 bp
34732
35453: contig of 722 bp in length
35454
35553: gap of 100 bp
36291: contig of 738 bp in length
36391: gap of 100 bp
36292
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37115
37214: gap of 100 bp
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40496: gap of 100 bp
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41319: gap of 100 bp
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43784
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44611: gap of 100 bp
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47008: contig of 737 bp in length
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47942: gap of 100 bp
48665: contig of 723 bp in length
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48765: gap of 100 bp
49500: contig of 735 bp in length
49501
49600: gap of 100 bp
49601
50337: contig of 737 bp in length
50338
50437: gap of 100 bp
51156: contig of 719 bp in length
51157
51256: gap of 100 bp

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 * 51986: gap of 100 bp
 * 52086 52812: contig of 727 bp in length
 * 52813 52912: gap of 100 bp
 * 52913 53627: contig of 715 bp in length
 * 53628 53722: gap of 100 bp
 * 53723 54459: contig of 732 bp in length
 * 54460 54559: gap of 100 bp
 * 54560 55288: contig of 729 bp in length
 * 55289 55388: gap of 100 bp
 * 55389 56104: contig of 716 bp in length
 * 56105 56204: gap of 100 bp
 * 56205 56922: contig of 718 bp in length

Query Match 7.6%; Score 169.4; DB 1; Length 73476;

Best Local Similarity 99.4%; Pred. No. 7.4; Indels 0; Gaps 0;
 Matches 170; Conservative 0; Mismatches 1;

Qy 497 TCAGCAGTCCCGATGTCAGAGTCTTCCAAATACCTCCCGTCATCTCTGCGCGAATCGGG 556
 Db 11159 TCTGCGATGCCCGATGTCAGAGTCTTCCAAATACCTCCCGTCATCTCTGCGCGAATCGGG 11218
 Qy 557 GAGCGATCCCAAGACGACCGTGTCTTCTAGCGCACTTGCAGCTGCAGCTGCTGTA 616
 Db 11219 GAGCGATCCCAAGACGACCGTGTCTTCTAGCGCACTTGCAGCTGCAGCTGCTGTA 11278
 Qy 617 CCGGGGCGATGGTGGCTCAGCGACCCCTATGTCTGACGGAGGTAGACGG 667
 Db 11279 CCGGGGCGATGGTGGCTCAGCGACCCCTATGTCTGACGGAGGTAGACGG 11329

RESULT 13
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 LOCUS BC047599 2006 bp mRNA linear PRI 25-AUG-2003
 DEFINITION Homo sapiens cDNA clone IMAGE:5528129, partial cds.

ACCESSION BC047599
 VERSION BC047599.2 GI:34192884
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 2006)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
 Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
 Diatchenko, L., Marusik, K., Farmer, A.A., Rubin, G.M., Hong, L.,
 Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
 Scheetz, T.E., Brownstein, M.J., Uedin, T.B., Toshiyuki, S.,
 Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
 Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
 McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
 Worley, K.C., Hale, S., Garcia, A.M., Gay, D.J., Hulyk, S.W.,
 Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
 Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,
 Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
 Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D.,
 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
 Butlerfield, Y.S., Krzywicki, M.I., Skalska, U., Smalios, D.E.,
 Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

22388257

JOURNAL MEDLINE

REFERENCE 2 (bases 1 to 2006)

12477932

Strausberg, R.

Direct Submission

Submitted (03-MAR-2003) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

REMARK
 COMMENT

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 On Aug 25, 2003 this sequence version replaced gi:28838418.
 Contact: MGC help desk
 Email: cgapbe-r@mail.nih.gov
 Tissue Procurement: ATCC/DCTP/DRP
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome
 Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www-shgc.stanford.edu>
 Contact: (Dickson, Mark) med@paxil.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
 R. M.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAC Plate: 88 Row: d Column: 4.

FEATURES
 source

1. 2006
 /location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5528129"
 /tissue_type="Skin, melanotic melanoma."
 /clone_lib="NIH MGC_72"
 /lab_host="DH10B"
 /note="Vector: pCMV-SPORT6"

Query Match 6.9%; Score 154.4; DB 1; Length 2006;
 Best Local Similarity 99.4%; Pred. No. 2.3e+02;
 Matches 155; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 352 AGACGCTGAAGGAGTGGTGGCCATCGAGAGCGACTCTGCCAGCCTGTGCTCGCTTCA 411
 Db 1071 AGACGCTGAAGGAGTGGTGGCCATCGAGAGCGACTCTGCCAGCCTGTGCTCGCTTCA 1012
 Qy 412 GACAAGAGCTCTTTCAGAAATGATGGCGTGGCTCGGACACGCTGCAGCGCTGGGGGCC 471
 Db 1011 GACAAGAGCTCTTTCAGAAATGATGGCGTGGCTCGGACACGCTGCAGCGCTGGGGGCC 952
 Qy 472 GTGTGGCTCGGTGGACATGGTCTTCCTCAGCAGCTGC 507
 Db 951 GTGTGGCTCGGTGGACATGGTCTTCCTCAGCAGCTGC 916

RESULT 14
 AC123772/c

LOCUS AC123772 73476 bp DNA linear HTG 01-JUN-2002
 DEFINITION Homo sapiens chromosome 18 clone RP11-911E16 map 18, LOW-PASS
 SEQUENCE SAMPLING.

ACCESSION AC123772

VERSION AC123772.1 GI:21307335

KEYWORDS HTG; HTGS PHASE0.

SOURCE Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 73476)

Birken, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens chromosome 18, clone RP11-911E16

Unpublished

2 (bases 1 to 73476)

Birken, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,

Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L.,

Boukhalter, B., Brown, A., Camarata, J., Campiano, A., Chang, J.,

Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A.,

Cook, A., Cooke, P., DeArillano, K., Dewar, K., Diaz, J.S., Dodge, S.,

Faro, S., Ferreira, P., FitzGerald, M., FitzHugh, W., Gage, D.,

Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L.,

Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I.,

Johnson, R., Jones, C., Kamat, A., Karatas, A., Kellis, C., LaRoque, K.,

Lamaze, R., Lander, E., Lehotzky, J., Levine, R., Lindblad-Toh, K.,

Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N.,

Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrum, J.,
 Meneus, L., Mihova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C.,
 Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P.,
 O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,
 Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C.,
 Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S.,
 Schupbach, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N.,
 Stojanovic, N., Straus, K., Subramanian, A., Talamas, J., Tesfaye, S.,
 Theodore, J., Topham, K., Travers, M., Travis, N., Trigglio, J.,
 Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
 Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

Submitted (01-JUN-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA

All repeats were identified using RepeatMasker:

Snit, A.F.A. & Green, P. (1996-1997)

<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L27294

Center clone name: 911_E_16

* NOTE: This record contains 89 individual
 * sequencing reads that have not been assembled into
 * contigs. Runs of N are used to separate the reads
 * and the order in which they appear is completely
 * arbitrary. Low-pass sequence sampling is useful for
 * identifying clones that may be gene-rich and allows
 * overlap relationships among clones to be deduced.
 * However, it should not be assumed that this clone
 * will be sequenced to completion. In the event that
 * the record is updated, the accession number will
 * be preserved.

1 731: contig of 731 bp in length
 732 831: gap of 100 bp
 832 1554: contig of 723 bp in length
 1555 1654: gap of 100 bp
 1655 2373: contig of 719 bp in length
 2374 2474: gap of 100 bp
 2474 3190: contig of 717 bp in length
 3191 3290: gap of 100 bp
 3291 4026: contig of 736 bp in length
 4027 4126: gap of 100 bp
 4127 4845: contig of 719 bp in length
 4846 4945: gap of 100 bp
 4946 5666: contig of 721 bp in length
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 8987 9086: gap of 100 bp
 9087 9817: contig of 731 bp in length
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 13247 13982: contig of 736 bp in length
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Dy 51951 CAGTGTGGAGACAGACGATGATCCGGGATGATCCACCATTCATTCGCAAAA 51992

Qy 1567 TGTTCAGGAGATCGTCCACAGAGCGTGGTGCTAAATTCCTCGGAGCTGTGATGATG 1626
Dy 51891 TGTTCAGGAGATCGTCCACAGAGCGTGGTGCTAAATTCCTCGGAGCTGTGATGATG 51932

Qy 1627 GAGAACATTCGAGAAATGAGAAATCAACAGGT 1659
Dy 51831 GAGAACATTCGAGAAATGAGAAATCAACAGGT 51799

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RESULT 15
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LOCUS      Homo sapiens cDNA clone IMAGE:6157986, partial cds.
DEFINITION BC065925
ACCESSION  BC065925
VERSION    BC065925.1 GI:41943841
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1467)
Strausberg,R.L., Feingold,B.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altshul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Heieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Schaeetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Frange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J.J., Helton,E., Kettunen,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,

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TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
REMARK
COMMENT

Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalek,U., Smallos,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 1467)
Strausberg,R.
Direct Submission
Submitted (02-FEB-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DRP
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhri.nih.gov
Akhter,N., Ayale,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantropop,S., Thomas,P.J., Touchman,J.W.,
Teurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.

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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 140 Row: m Column: 2
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.

FEATURES

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/db_xref="taxon:9606"
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/note="Vector: pCMV-SPORT6"

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Qy 352 AGACGCTGAAGGAGTGGTGGCCATCGAGACGACTCTGCCAGCCTGTGCTTCCTCA 411
Dy 544 AGACGCTGAAGGAGTGGTGGCCATCGAGACGACTCTGTCCAGCCTGTGCTTCCTCA 485

Qy 412 GACAAGAGCTCTTCAGAAATGATGGCTGGCTGGGACACGCTGCAGCGCTGGGGGCC 471
Dy 484 GACAAGAGCTCTTCAGAAATGATGGCTGGCTGGGACACGCTGCAGCGCTGGGGGCC 425

Qy 472 GTGTGGCTCGGTGGACATGGTCTTCAGAGCTGC 507
Dy 424 GTGTGGCTCGGTGGACATGGTCTTCAGAGCTGC 389

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RESULT 16
AC009704/c
LOCUS      Homo sapiens chromosome 18, clone RP11-231E4, complete sequence.
DEFINITION AC009704
ACCESSION  AC009704

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23431..23531
/rpt_family="MER46A"
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/rpt_family="LiMBa"
23727..24031
/rpt_family="AluSx"
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complement(25849..25806)
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25928..26079
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Query Match      2.1%; Score 46.6; DB 1; Length 178691;
Best Local Similarity 83.9%; Pred. NO. 5.3;
Matches 52; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 2177 ACTGCTCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2236
|||
Db 99161 ACTCGTCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2236

Qy 2237 AA 2238
|||
Db 99101 AA 99100

RESULT 17
AC116904
LOCUS AC116904 164394 bp DNA linear PRI 03-SEP-2002
DEFINITION Homo sapiens chromosome 18, clone RP11-1112M8, complete sequence.
ACCESSION AC116904
VERSION AC116904.7 GI:22655819
KEYWORDS HTG.
SOURCE Homo sapiens (human)

```

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

1 (bases 1 to 164394)

Birren,B., Nusbaum,C. and Lander,E.

Homo sapiens chromosome 18, clone RP11-1112M8

Unpublished

2 (bases 1 to 164394)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,

Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavsky,L.,

Boukhalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,

Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A.,

Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S.,

Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,

Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,

Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,

Kamat,A., Karatas,A., Kells,C., Larocque,K., Lamazares,R.,

Landers,T., Lehoczy,J., Levine,R., Lindblad-Toh,K., Liu,G.,

MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,

McCarthy,M., McEwan,P., McKernan,K., Meldrim,J., Meneus,L.,

Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R.,

Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D.,

Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,

Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,

Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R.,

Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,

Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,

Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,

Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,

Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission

Submitted (02-APR-2002) Whitehead Institute/MIT Center for Genome

Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 164394)

Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,

Barna,N., Bastien,V., Bloom,T., Boguslavsky,L., Boukhalter,B.,

Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,

Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S.,

Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J.,

Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B.,

Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.,

Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K.,

Liu,G., Maclean,C., Macdonald,P., Major,J., Matthews,C.,

McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,

Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,

O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K.,

Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P.,

Roman,J., Roy,A., Schauer,S., Schupback,R., Seaman,S., Severy,P.,

Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J.,

Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,

Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,

Zembek,L., Zimmer,A. and Zody,M.

Direct Submission

Submitted (28-AUG-2002) Whitehead Institute/MIT Center for Genome

Research, 320 Charles Street, Cambridge, MA 02141, USA

4 (bases 1 to 164394)

Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,

Barna,N., Bastien,V., Bloom,T., Boguslavsky,L., Boukhalter,B.,

Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,

Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S.,

Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J.,

Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B.,

Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.,

Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K.,

Liu,G., Maclean,C., Macdonald,P., Major,J., Matthews,C.,

McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,

Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,

O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K.,

Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P.,

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Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J.,

Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,

Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,

Zembek,L., Zimmer,A. and Zody,M.

Direct Submission

Submitted (28-AUG-2002) Whitehead Institute/MIT Center for Genome

Research, 320 Charles Street, Cambridge, MA 02141, USA


```

REFERENCE
AUTHORS
1 (bases 1 to 2006)
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Scapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.D.,
Schetzl,E., Brownstein,M.J., Uedin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whitting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalios,D.E.,
Schnurch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
2388257
MEDLINE
2477932
REFERENCE
2 (bases 1 to 2006)
Strausberg,R.
Direct Submission
Submitted (03-MAR-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK
COMMENT
NIH-MGC Project URL: http://mgc.nci.nih.gov
On Aug 25, 2003 this sequence version replaced gi:28838418.
Contact: MGC help desk
Email: cgaps-remail.nih.gov
Tissue Procurement: ATCC/DCTP
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/ILNL at: http://image.llnl.gov
Series: IRAC Plate: 88 Row: d Column: 4.
Location/Qualifiers
1. .2006
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Query Match 1.4%; Score 32; DB 1; Length 2006;
Best Local Similarity 85.4%; Pred. No. 4.4e+02;
Matches 35; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 2173 CACCACGTGCTCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2213
Db 1966 CAAGACTCCATCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2006
REFERENCE
AUTHORS
19
AX898087/c
LOCUS
DEFINITION
ACCESSION
AX898087
Sequence 13950 from Patent EP1033401.
PAT 18-DEC-2003

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VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS
Dumas Milne Edwards,J.B., Duclert,A. and Giordano,J.Y.
Expressed sequence tags and encoded human proteins
Patent: EP 1033401-A 13950 06-SEP-2000;
GENSET (FR)
FEATURES
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Best Local Similarity 48.9%; Pred. No. 2.8e+03;
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Qy 159 GGAGGTTGGGAAAGTTGCTAGAGGCTTCAGAACTCCAGACCTAATGGATCCCAACTCGGG 218
Db 299 GGGGGGGGGAGGGTGAGGAGAACATGCCCGCTCCAGCAGCAGCAGCCAGC 240
Qy 219 AGAATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 278
Db 239 AGGAGCGCAGCCATCTCTGAGTTGGATTCATTAGGCTGGAGTTCTGAAGCCTCTAG 180
Qy 279 TCACCTTCCCGCCCCC 295
Db 179 CAACCTTCCCAACCTCC 163
RESULT 20
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LOCUS
DEFINITION
Sequence tag and encoded human protein.
ACCESSION
BD033620
VERSION
BD033620.1 GI:22575362
KEYWORDS
JP 2001269182-A/9866.
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 300)
Edwards,J.B.D.M., Duclair,E. and Jordan,J.Y.
Sequence tag and encoded human protein
Patent: JP 2001269182-A 9866 02-OCT-2001;
GENSET
COMMENT
OS Homo sapiens (human)
PN JP 2001269182-A/9866
PD 02-OCT-2001
PF 24-FEB-2000 JP 2000118773
PI 26-FEB-1999 US 60/122487
PI JEAN BAPTISTE DUMAS MILNE EDWARDS,EIMERIC DUCLAIR,JEAN YVES
PI JORDAN
PC C12N15/09,C07K14/435,C07K16/18,C12N1/15,C12N1/19,C12N1/21, PC
C12N5/10,
PC C12P21/02,C12P21/08,C12Q1/68//G06F17/30,C12N15/00,C12N5/00, PC
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Query Match 1.1%; Score 25; DB 1; Length 300;
Best Local Similarity 48.9%; Pred. No. 2.8e+03;
Matches 67; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

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QY 159 GGAGGTTGGGAAGTTGCTAGAGGCTTCAGAACTCAGCCTAATGATCCCAAACTCGGG 218
Db 299 GGGGGGGGGAGGGTGAGGAGAACATGCCCGCTCCAGCAGCAGCAGCAGCAGCAGCAGC 240
QY 219 AGAATGGCTGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 278
Db 239 AGGAGCGAGCCATTCTCTGAGTTGGATCCATTAGCTGGAGTTCTGAAGCCTCTAG 180
QY 279 TCACCCCTCCCGCCCCC 295
Db 179 CAACTTCCCAACCTCC 163

RESULT 21
AR412460/c
LOCUS AR412460 672 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 97 from patent US 6639063.
ACCESSION AR412460
VERSION AR412460.1 GI:40167570
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 672)
AUTHORS Edwards,J.-B.D.M., Jobert,S. and Giordano,J.-Y.
TITLE EST's and encoded human proteins
JOURNAL Patent: US 6639063-A 97 28-OCT-2003;
FEATURES
Location/Qualifiers
source 1..672
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Matches 46; Conservative 0; Mismatches 37;

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Db 551 GACTCTGACCATCGGCAGCTGCTGAGGACCCATGTCCACCGAGGCCACACGCGGCCCA 492

QY 500 GCAGCTGCCCGATGGTCAGAGTC 522
Db 491 GGCCTGCAGCGTGTCCGAGCC 469

RESULT 22
AX969294/c
LOCUS AX969294 672 bp DNA linear PAT 15-JAN-2004
DEFINITION Sequence 97 from Patent EP1104808.
ACCESSION AX969294
VERSION AX969294.1 GI:40975507
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Dumas Milne Edwards,J.B., Jobert,S. and Giordano,J.Y.
TITLE ESTs and encoded human proteins
JOURNAL Patent: EP 1104808-A 97 06-JUN-2001;
GENSET Genset (FR)
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227..307
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Best Local Similarity 55.4%; Pred. No. 1.3e+03; Indels 0; Gaps 0;
Matches 46; Conservative 0; Mismatches 37;

QY 440 GGCTGCGGACACGCTGCAGCGCCTGGGGGCCGCTGTGGCTCGGTGGACATGGGTCTCTCA 499
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QY 500 GCAGCTGCCCGATGGTCAGAGTC 522
Db 491 GGCCTGCAGCGTGTCCGAGCC 469

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BD108013/c
LOCUS BD108013 672 bp DNA linear PAT 18-SEP-2002
DEFINITION EST and encoded human protein.
ACCESSION BD108013
VERSION BD108013.1 GI:23202831
KEYWORDS JP 2002010789-A/90.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 672)
AUTHORS Edwards,J.B.D.M., Jobert,S. and Giordano,J.E.
TITLE EST and encoded human protein
JOURNAL Patent: JP 2002010789-A 90 15-JAN-2002;
GENSET GENSET CORP
COMMENT
OS Homo sapiens (human)
PN JP 2002010789-A/90
PD 15-JAN-2002
PF 07-AUG-2000 JP 2000280989
PR 05-AUG-1999 US 60/147499
PI JEAN BAPTISTE DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE
GIORDANO
PC C12N15/09,C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,PC
C12N1/21,
PC C12N5/10,C12P21/02,C12P21/08,C12Q1/68,C12N15/00,C12N5/00,PC
C12N15/00
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CC score 7.09999990463257
CC seq VLLLLLLRGMFS/SP
CC n=a, g, c or t
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FT sig_peptide 227..307
FT misc feature 586
FT misc feature 602..603.
FT Location/Qualifiers
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Query Match 1.1%; Score 23.8; DB 1; Length 672;
Best Local Similarity 55.4%; Pred. No. 1.3e+03; Indels 0; Gaps 0;
Matches 46; Conservative 0; Mismatches 37;

QY 440 GGCTGCGGACACGCTGCAGCGCCTGGGGGCCGCTGTGGCTCGGTGGACATGGGTCTCTCA 499
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QY 500 GCAGCTGCCCGATGGTCAGAGTC 522
Db 491 GGCCTGCAGCGTGTCCGAGCC 469
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RESULT 24
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LOCUS          AK131263          3755 bp          mRNA          linear          PRI 07-MAY-2004
DEFINITION     Homo sapiens cDNA FLJ16195 fis, clone BRTHA3000296.
ACCESSION      AK131263
VERSION        AK131263.1 GI:47077013
KEYWORDS       oligo capping; fis (full insert sequence).
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1
AUTHORS        Ota, T., Nakagawa, S., Senoh, A., Mizuguchi, H., Inagaki, H.,
               Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S.,
               Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T.,
               Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M.,
               Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K.,
               Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y.,
               Sugano, S., Nagahara, K., Masuho, Y., Nagai, K. and Isogai, T.
               NEDO human cDNA sequencing project
TITLE          Unpublished
JOURNAL        2 (bases 1 to 3755)
REFERENCE      2
AUTHORS        Isogai, T. and Yamamoto, J.
TITLE          Direct Submission
JOURNAL        Submitted (01-MAR-2004) Takao Isogai, FLJ Project (HRI Team); 2-6-7
               Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan
               (E-mail: genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT        NEDO human cDNA sequencing project supported by Ministry of
               Economy, Trade and Industry of Japan; cDNA full insert sequencing:
               Research Association for Biotechnology (RAB); cDNA library
               construction: Helix Research Institute (HRI) (supported by Japan
               Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
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               Evaluation; clone selection for full insert sequencing: HRI and
               RAB; annotation: HRI and RAB.
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               Db 2239 GTGTAGTCTAGAGTCATGGAACACCATCTTGTGGACATATTCTTTTGGAGAACAC 2180
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               ACCESSION      BC065925
               VERSION        BC065925.1 GI:41943841
               KEYWORDS
               SOURCE         Homo sapiens (human)
               ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1
AUTHORS        Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
               Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
               Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
               Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heieh, F.,
               Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
               Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
               Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
               Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J.,
               McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
               Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
               Fahy, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,
               Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
               Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D.,
               Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
               Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Smalilus, D.E.,
               Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
               Generation and initial analysis of more than 15,000 full-length
               human and mouse cDNA sequences
               Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
               12477932
               2 (bases 1 to 1467)
               Strausberg, R.
               Direct Submission
               Submitted (02-FEB-2004) National Institutes of Health, Mammalian
               Gene Collection (MGC), Cancer Genomics Office, National Cancer
               Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
               USA
               NTH-MGC Project URL: http://mgc.nci.nih.gov
               Contact: MGC help desk
               Email: gcgaps@mail.nih.gov
               Tissue Procurement: ATCC/DCTP/DTP
               cDNA Library Preparation: Life Technologies, Inc.
               CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
               DNA Sequencing by: National Institutes of Health Intramural
               Sequencing Center (NISC),
               Gaithersburg, Maryland:
               Web site: http://www.nisc.nih.gov/
               Contact: nisc.mgc@hri.nih.gov
               Akhter, N., Ayelle, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
               Blakeley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
               Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
               Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
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               Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
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               Clone distribution: MGC clone distribution information can be found
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Thu Feb 17 18:38:12 2005

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RESULT 26
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VERSION CQ715367.1 GI:42276224
KEYWORDS
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ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 1301 06-SEP-2002;
PE Corporation (NY) (US)
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QY 522 C 522
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Search completed: February 16, 2005, 11:33:14
Job time : 560 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 13, 2005, 19:10:01 ; Search time 822 Seconds

(without alignment)
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Total number of hits satisfying chosen parameters: 8780412

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Listing first 1500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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6	2241	100.0	2242	9	ACD42296
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8	2241	100.0	2242	10	AAD59237
9	2241	100.0	2242	10	ADC29812
10	2241	100.0	2242	10	ACA06168
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26	1531.6	68.3	1587	4	AAS43075
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94	121.8	5.4	512	6	AAD333905	Aad333905 Human car	c 167	69.4	3.1	563	13	ACN58977	Acn58977 Cotton gy
95	120.2	5.4	402	6	AAD33899	Aad33899 Human car	c 168	69.2	3.1	543	13	ACN56816	Acn56816 Cotton gy
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98	118.2	5.3	386	6	AAD33898	Aad33898 Human car	c 171	68.8	3.1	392	5	ADI70087	Adi70087 Human ova
99	118	5.3	715	13	ADQ55638	Adq55638 Novel can	c 172	68.8	3.1	392	5	ADI76417	Adi76417 Human ova
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102	103.6	4.6	465	5	ADL44322	Adl44322 Human ova	c 175	68.8	3.1	1086	3	ACN59534	Acn59534 Human sec
103	103.6	4.6	465	5	ADL37938	Adl37938 Human ova	c 176	68.8	3.1	1499	10	ADC38712	Adc38712 Human cdn
104	99.2	4.4	1390	4	AAS80064	Aas80064 Human adu	c 177	68.6	3.1	291	8	ABX36078	Abx36078 Bovine ES
105	98.8	4.4	403	9	ACH17246	Ach17246 Human adu	c 178	68.6	3.1	380	10	ADK61481	Adk61481 Ovarian c
106	96.4	4.3	273	8	ACA98664	Aca98664 Tr22-GSE.	c 179	68.6	3.1	411	4	AAI87378	Aai87378 Human pol
107	95	4.2	1320	8	ACA24244	Aca24244 Prokaryot	c 180	68.6	3.1	492	5	ADL43533	Adl43533 Human ova
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111	85.8	3.8	1371	12	ADM91824	Adm91824 S. pneumo	c 184	68.4	3.1	396	6	ABL48775	Abt03092 Human ova
112	85.8	3.8	1389	8	ABZ421150	Abz421150 Streptoco	c 185	68.4	3.1	396	11	ADM10685	Adm10685 Human ova
113	85.8	3.8	3766	2	AAV523358	Aav523358 Streptoco	c 186	68.4	3.1	396	12	ADJ11015	Adj11015 Represent
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115	85.2	3.8	1455	9	ADB08961	Adb08961 Alloiooc	c 188	68.4	3.1	647	5	ADI72227	Adi72227 Human ova
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118	79.8	3.6	26309	4	ACF59535	Acf59535 Propionib	c 191	68.4	3.1	2805	3	AZ24487	Aaz24487 Wheat sol
119	79.8	3.6	26309	8	ACF64464	Acf64464 Propionib	c 192	68.4	3.1	3232	10	ADD18806	Adi18806 Human dis
120	79.4	3.5	582	12	ACH80302	Ach80302 Human gen	c 193	68.4	3.1	327	5	ADI76313	Adi76313 Human ova
121	79.4	3.5	912	13	ADR92406	Adr92406 Novel S.	c 194	68.2	3.0	327	5	ADI69980	Adi69980 Human ova
122	79.4	3.5	24788	4	AAK85123	Aak85123 Human imm	c 195	68.2	3.0	617	11	ACN87667	Acn87667 Breast ca
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124	79.4	3.5	24788	4	AAK77849	Aak77849 Human imm	c 197	68.2	3.0	402	4	AAI84805	Aai84805 Human pol
125	76.8	3.4	409	3	AAK01627	Aak01627 Human sec	c 198	68	3.0	517	13	ACN56273	Acn56273 Cotton an
126	76.8	3.4	464	3	AAK01626	Aak01626 Human sec	c 199	68	3.0	549	13	ACN52303	Acn52303 Cotton an
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128	75.4	3.4	650	3	AAFI1970	Aafi1970 Aspergill	c 201	68	3.0	850	6	AD42252	Ad42252 Soybean F
129	75	3.3	540	13	ACN55464	Acn55464 Cotton an	c 202	68	3.0	850	6	AD42252	Ad42252 Soybean F
130	73	3.3	202	12	ACH94002	Ach94002 Human gen	c 203	68	3.0	850	6	AD42252	Ad42252 Soybean F
131	73	3.3	216	10	ACD94023	Acn94023 Human col	c 204	68	3.0	1630	10	ADL08408	Adl08408 Human can
132	72.8	3.2	411	13	ACN52913	Acn52913 Cotton an	c 205	68	3.0	1630	10	ADL08408	Adl08408 Human can
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135	72	3.2	467	5	ADL37255	Adl37255 Human ova	c 208	67.8	3.0	429	5	ABV56874	Abv56874 Human pro
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138	71	3.2	480	13	ACN51787	Acn51787 Cotton an	c 211	67.8	3.0	556	5	ABV40063	Abv40063 Human pro
139	71	3.2	593	13	ACN52339	Acn52339 Cotton an	c 212	67.8	3.0	556	5	ABV42105	Abv42105 Human pro
140	71	3.2	638	11	ACN87410	Acn87410 Breast ca	c 213	67.8	3.0	556	5	ABV43601	Abv43601 Human pro
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142	70.6	3.1	499	4	AAI93507	Aai93507 Human pol	c 215	67.8	3.0	588	13	ACN46068	Acn46068 Cotton pr
143	70.4	3.1	428	4	AAI89008	Aai89008 Human pol	c 216	67.8	3.0	690	13	ADR63575	Adr63575 Cotton CD
144	70.4	3.1	580	5	ABV58017	Abv58017 Human pro	c 217	67.8	3.0	810	4	AAS27002	Aas27002 cDNA enco
145	70.4	3.1	1095	4	AAAL35667	Aal35667 Human mus	c 218	67.8	3.0	810	4	AAS27002	Aas27002 cDNA enco
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147	70.4	3.1	1095	8	ABX58655	Abx58655 cDNA enco	c 220	67.8	3.0	1274	5	ADM19285	Adm19285 Novel, hum
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150	70.2	3.1	408	4	AAI83619	Aai83619 Human pol	c 223	67.6	3.0	553	13	ACN62578	Acn62578 Cotton de
151	70.2	3.1	464	13	ACN51998	Acn51998 Cotton an	c 224	67.6	3.0	575	3	AAAC59682	Aac59682 Human sec
152	70.2	3.1	594	13	ACN60993	Acn60993 Cotton gy	c 225	67.6	3.0	575	8	ADA43897	Ada43897 Human sec
153	70.2	3.1	616	13	ACN50609	Acn50609 Cotton ma	c 226	67.6	3.0	575	8	ADA43897	Ada43897 Human sec
154	70.2	3.1	1527	3	AAA16633	Aaa16633 Human sec	c 227	67.6	3.0	575	10	ADP10596	Adp10596 Human sec
155	70.2	3.1	1580	5	ABV04355	Abv04355 Human pro	c 228	67.6	3.0	575	10	ADP10596	Adp10596 Human sec
156	70	3.1	381	4	AAI80552	Aai80552 Human pol	c 229	67.6	3.0	575	10	ABZ67037	Abz67037 Human sec
157	70	3.1	448	4	AAI80552	Aai80552 Human pol	c 230	67.6	3.0	575	10	ABZ67037	Abz67037 Human sec
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159	69.8	3.1	491	5	ADL72087	Adl72087 Human ova	c 232	67.6	3.0	896	4	AAH33168	Aah33168 Human col
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161	69.8	3.1	560	13	ACN48235	Acn48235 Cotton pr	c 234	67.6	3.0	1639	2	AAAC98202	Aac98202 Human col
162	69.8	3.1	1792	3	AAAC59834	Aac59834 Human sec	c 235	67.6	3.0	3899	6	ABQ92042	Abq92042 cDNA from
163	69.8	3.1	287	4	AAI14832	Aai14832 Human bre	c 236	67.6	3.0	5625	12	ABQ2042	Abq2042 Human pol
164	69.4	3.1	421	11	ACN84857	Acn84857 Breast ca	c 237	67.4	3.0	453	5	ABV56723	Abv56723 Human pro
165	69.4	3.1	516	13	ACN62215	Acn62215 Cotton gy	c 238	67.4	3.0	545	4	AAH70126	Aah70126 Human cer
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c 241	67.4	3.0	4397	5	ABV30288	Abv30288 Human pro	314	66.6	3.0	2846	8	ACF00184	Human sec
c 242	67.2	3.0	376	5	ABV56400	Abv56400 Human pro	315	66.6	3.0	2846	8	ACA60381	Novel hum
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c 247	67.2	3.0	557	13	ACN47785	Acn47785 Cotton pr	320	66.6	3.0	2846	8	ACA88667	Novel hum
c 248	67.2	3.0	680	3	AAC79893	Aac79893 Human sec	321	66.6	3.0	2846	8	ACA70109	Human sec
c 249	67.2	3.0	749	3	AAC77999	Aac77999 Human can	322	66.6	3.0	2846	8	ACD12331	Novel hum
c 250	67.2	3.0	743	6	ABQ54165	Abq54165 Human ova	323	66.6	3.0	2846	8	ACC74246	Human sec
c 251	67.2	3.0	1043	4	AAH72615	Aah72615 Human cer	324	66.6	3.0	2846	8	ACD15874	Human sec
c 252	67.2	3.0	1058	6	ABQ54594	Abq54594 Human ova	325	66.6	3.0	2846	8	ACD25442	Novel hum
c 253	67.2	3.0	1091	4	ACH89723	Aac89723 Maize Zmg	326	66.6	3.0	2846	8	ACD17919	Human sec
c 254	67.2	3.0	1091	8	ABX95035	Abx95035 cDNA enco	327	66.6	3.0	2846	8	ACC88206	Human sec
c 255	67.2	3.0	2007	12	ADQ23886	Adq23886 Human sof	328	66.6	3.0	2846	8	ACD21560	Human sec
c 256	67	3.0	346	5	ADL37542	Adl37542 Human ova	329	66.6	3.0	2846	8	ACD18627	Human sec
c 257	67	3.0	346	5	ADI72399	Adi72399 Human ova	330	66.6	3.0	2846	8	ACA58828	cDNA enco
c 258	67	3.0	404	5	ABV56394	Abv56394 Human pro	331	66.6	3.0	2846	8	ABX98237	Human CDN
c 259	67	3.0	461	5	ADL43889	Adl43889 Human ova	332	66.6	3.0	2846	8	ACD13988	Human PRO
c 260	67	3.0	508	67	ACN50622	Acn50622 Cotton ma	333	66.6	3.0	2846	8	ACD09768	Human sec
c 261	67	3.0	528	13	ACN47028	Acn47028 Cotton pr	334	66.6	3.0	2846	8	ACC88513	Human sec
c 262	67	3.0	768	4	AAI08093	Aai08093 Human bre	335	66.6	3.0	2846	8	ACD21253	Human sec
c 263	67	3.0	976	4	AAI08093	Aai08093 Human bre	336	66.6	3.0	2846	8	ABX75625	Human CDN
c 264	67	3.0	1925	2	AAV34271	Aav34271 Human sec	337	66.6	3.0	2846	8	ACA64004	cDNA enco
c 265	67	3.0	1925	8	ACD08142	Adc08142 cDNA enco	338	66.6	3.0	2846	8	ABX97828	Human PRO
c 266	66.8	3.0	330	5	ADL43756	Adl43756 Human ova	339	66.6	3.0	2846	8	ACA97304	Novel hum
c 267	66.8	3.0	411	4	AAI93716	Aai93716 Human pol	340	66.6	3.0	2846	8	ACA57767	Human PRO
c 268	66.8	3.0	445	5	ADI76334	Adi76334 Human ova	341	66.6	3.0	2846	8	ACD14295	Human PRO
c 269	66.8	3.0	445	5	ADI70001	Adi70001 Human ova	342	66.6	3.0	2846	8	ACC91078	Human sec
c 270	66.8	3.0	553	13	ACN53206	Acn53206 Cotton an	343	66.6	3.0	2846	8	ACC88820	Human sec
c 271	66.8	3.0	610	5	ADL37504	Adl37504 Human ova	344	66.6	3.0	2846	8	ACD07017	Human PRO
c 272	66.8	3.0	610	5	ADI72360	Adi72360 Human ova	345	66.6	3.0	2846	8	ACA67468	Human PRO
c 273	66.8	3.0	705	6	ABQ54208	Abq54208 Human ova	346	66.6	3.0	2846	8	ACC81523	Human sec
c 274	66.8	3.0	1365	4	AAI02661	Aai02661 Human sec	347	66.6	3.0	2846	8	ACA91268	cDNA enco
c 275	66.8	3.0	1365	8	ABZ73522	Abz73522 Secreted	348	66.6	3.0	2846	8	ACC89127	Human sec
c 276	66.8	3.0	1365	10	ABZ67119	Abz67119 Human sec	349	66.6	3.0	2846	8	ACC86483	Human sec
c 277	66.8	3.0	2187	10	ADQ79073	Adq79073 Human pro	350	66.6	3.0	2846	8	ACC89741	Human sec
c 278	66.8	3.0	2329	5	AAI07661	Aai07661 Human sec	351	66.6	3.0	2846	8	ACC92920	Human sec
c 279	66.8	3.0	2343	6	ABQ54904	Abq54904 Human ova	352	66.6	3.0	2846	8	ABX80775	Human sec
c 280	66.8	3.0	2755	6	ABQ54342	Abq54342 Human ova	353	66.6	3.0	2846	8	ACA72548	Human PRO
c 281	66.8	3.0	3144	3	AAI18172	Aai18172 Lung canc	354	66.6	3.0	2846	8	ACA89006	Human sec
c 282	66.8	3.0	6155	6	ABK28362	Abk28362 DNA trans	355	66.6	3.0	2846	8	ACA69802	Human sec
c 283	66.6	3.0	2951	5	ADI73348	Adi73348 Human ova	356	66.6	3.0	2846	8	ACA96945	Novel hum
c 284	66.6	3.0	291	5	ADL38479	Adl38479 Human ova	357	66.6	3.0	2846	8	ACA90941	Novel hum
c 285	66.6	3.0	310	6	ABK09625	Abk09625 Human ova	358	66.6	3.0	2846	8	ACA70723	Human sec
c 286	66.6	3.0	390	5	ADL43918	Adl43918 Human ova	359	66.6	3.0	2846	8	ACA95233	Novel hum
c 287	66.6	3.0	445	5	ADL43518	Adl43518 Human ova	360	66.6	3.0	2846	8	ACD44284	cDNA enco
c 288	66.6	3.0	458	13	ACN50953	Acn50953 Cotton an	361	66.6	3.0	2846	8	ACC86176	Human sec
c 289	66.6	3.0	498	13	ACN56190	Acn56190 Cotton an	362	66.6	3.0	2846	8	ACD45167	Human sec
c 290	66.6	3.0	591	13	ACN58226	Acn58226 Cotton gy	363	66.6	3.0	2846	8	ACC90048	Human sec
c 291	66.6	3.0	688	4	AAI15556	Aai15556 Human bre	364	66.6	3.0	2846	8	ACD12656	Human sec
c 292	66.6	3.0	912	11	ACN85543	Acn85543 Breast ca	365	66.6	3.0	2846	8	ACF19886	Human sec
c 293	66.6	3.0	936	2	AAZ06226	Aaz06226 Human sec	366	66.6	3.0	2846	8	ABX76830	Human PRO
c 294	66.6	3.0	2022	6	AAI33261	Aai33261 Human sec	367	66.6	3.0	2846	8	ACA73162	Novel hum
c 295	66.6	3.0	2311	7	ADR41309	Adr41309 Human CD-	368	66.6	3.0	2846	8	ACA68705	Novel hum
c 296	66.6	3.0	2843	9	ADA00368	Ada00368 Human sec	369	66.6	3.0	2846	8	ACA74549	cDNA enco
c 297	66.6	3.0	2846	3	AAZ65034	Aaz65034 Membrane-	370	66.6	3.0	2846	8	ACA70416	Human sec
c 298	66.6	3.0	2846	4	AAZ46009	Aaz46009 Human DNA	371	66.6	3.0	2846	8	ACD14602	Human PRO
c 299	66.6	3.0	2846	4	AAI92076	Aai92076 Human PRO	372	66.6	3.0	2846	8	ACA93715	Human CDN
c 300	66.6	3.0	2846	5	AAI44180	Aai44180 Human PRO	373	66.6	3.0	2846	8	ACA68274	Novel hum
c 301	66.6	3.0	2846	6	ABE74396	AbE74396 Human CDN	374	66.6	3.0	2846	8	ABX98739	Novel hum
c 302	66.6	3.0	2846	8	ACA89459	AcA89459 cDNA enco	375	66.6	3.0	2846	8	ACC81216	Human sec
c 303	66.6	3.0	2846	8	ACA73469	AcA73469 Human sec	376	66.6	3.0	2846	8	ACA95540	Novel hum
c 304	66.6	3.0	2846	8	ACA05784	AcA05784 Human sec	377	66.6	3.0	2846	8	ACD04458	Human hum
c 305	66.6	3.0	2846	8	ACA66618	AcA66618 cDNA enco	378	66.6	3.0	2846	8	ACC87899	Human sec
c 306	66.6	3.0	2846	8	ACA64316	AcA64316 Novel hum	379	66.6	3.0	2846	8	ACF12561	Human sec
c 307	66.6	3.0	2846	8	ACA91182	AcA91182 Novel hum	380	66.6	3.0	2846	8	ACH6262	Novel hum
c 308	66.6	3.0	2846	8	ACD81559	AcD81559 Human CDN	381	66.6	3.0	2846	8	ABX79455	Human sec
c 309	66.6	3.0	2846	8	ACF20193	AcF20193 Human sec	382	66.6	3.0	2846	8	ACA96276	Human PRO
c 310	66.6	3.0	2846	8	ACF19579	AcF19579 Human sec	383	66.6	3.0	2846	8	ACA65050	Human PRO
c 311	66.6	3.0	2846	8	ACD21867	AcD21867 Human sec	384	66.6	3.0	2846	8	ACA73776	Human sec
c 312	66.6	3.0	2846	8	ACF13032	AcF13032 Human sec	385	66.6	3.0	2846	8	ACA74188	Novel hum

386	66.6	3.0	2846	8	ACA96583	Human PRO	459	66.6	3.0	2846	9	ACD41572	Human sec
387	66.6	3.0	2846	8	ACD10689	CDNA enco	460	66.6	3.0	2846	9	ADA37741	Human CDN
388	66.6	3.0	2846	8	ACC91385	Human sec	461	66.6	3.0	2846	9	Adf31985	Human sec
389	66.6	3.0	2846	8	ACA93476	Novel hum	462	66.6	3.0	2846	9	Adf23263	Human sec
390	66.6	3.0	2846	8	ACD02720	CDNA enco	463	66.6	3.0	2846	9	Adf39953	Human sec
391	66.6	3.0	2846	8	ACC87285	Human sec	464	66.6	3.0	2846	9	Adf5475	Human sec
392	66.6	3.0	2846	8	ACC85869	Human sec	465	66.6	3.0	2846	9	Adf53132	Human sec
393	66.6	3.0	2846	8	ABX81158	Human sec	466	66.6	3.0	2846	9	Adf53132	Human sec
394	66.6	3.0	2846	8	ACA65357	Human PRO	467	66.6	3.0	2846	9	Adf53132	Human sec
395	66.6	3.0	2846	8	ACA94174	Human sec	468	66.6	3.0	2846	9	Adf53132	Human sec
396	66.6	3.0	2846	8	ACA97918	Human PRO	469	66.6	3.0	2846	9	Adf53132	Human sec
397	66.6	3.0	2846	8	ACA91420	Novel hum	470	66.6	3.0	2846	9	Adf53132	Human sec
398	66.6	3.0	2846	8	ACA90634	Novel hum	471	66.6	3.0	2846	9	Adf53132	Human sec
399	66.6	3.0	2846	8	ACD16181	Human sec	472	66.6	3.0	2846	9	Adf53132	Human sec
400	66.6	3.0	2846	8	ACD17342	Human sec	473	66.6	3.0	2846	9	Adf53132	Human sec
401	66.6	3.0	2846	8	ACC91999	Human sec	474	66.6	3.0	2846	9	Adf53132	Human sec
402	66.6	3.0	2846	8	ACD02316	Novel hum	475	66.6	3.0	2846	9	Adf53132	Human sec
403	66.6	3.0	2846	8	ACA74856	CDNA enco	476	66.6	3.0	2846	9	Adf53132	Human sec
404	66.6	3.0	2846	8	ACA91727	Human PRO	477	66.6	3.0	2846	9	Adf53132	Human sec
405	66.6	3.0	2846	8	ACA89307	Novel hum	478	66.6	3.0	2846	9	Adf53132	Human sec
406	66.6	3.0	2846	8	ACA71371	Human sec	479	66.6	3.0	2846	9	Adf53132	Human sec
407	66.6	3.0	2846	8	ACA90771	Human sec	480	66.6	3.0	2846	9	Adf53132	Human sec
408	66.6	3.0	2846	8	ACA65781	CDNA enco	481	66.6	3.0	2846	9	Adf53132	Human sec
409	66.6	3.0	2846	8	ACA68944	Novel hum	482	66.6	3.0	2846	9	Adf53132	Human sec
410	66.6	3.0	2846	8	ACA92974	Novel hum	483	66.6	3.0	2846	9	Adf53132	Human sec
411	66.6	3.0	2846	8	ACA94926	CDNA enco	484	66.6	3.0	2846	9	Adf53132	Human sec
412	66.6	3.0	2846	8	ACD16488	Human sec	485	66.6	3.0	2846	9	Adf53132	Human sec
413	66.6	3.0	2846	8	ACD15567	Human sec	486	66.6	3.0	2846	9	Adf53132	Human sec
414	66.6	3.0	2846	8	ACA98466	Human PRO	487	66.6	3.0	2846	9	Adf53132	Human sec
415	66.6	3.0	2846	8	ABX17058	Human PRO	488	66.6	3.0	2846	9	Adf53132	Human sec
416	66.6	3.0	2846	8	ABX16670	Human CDN	489	66.6	3.0	2846	9	Adf53132	Human sec
417	66.6	3.0	2846	8	ACA67913	Novel hum	490	66.6	3.0	2846	9	Adf53132	Human sec
418	66.6	3.0	2846	9	ACA63391	CDNA enco	491	66.6	3.0	2846	9	Adf53132	Human sec
419	66.6	3.0	2846	9	ACA97611	Human PRO	492	66.6	3.0	2846	9	Adf53132	Human sec
420	66.6	3.0	2846	9	ACA99060	Novel hum	493	66.6	3.0	2846	9	Adf53132	Human sec
421	66.6	3.0	2846	9	ACC91692	Human sec	494	66.6	3.0	2846	9	Adf53132	Human sec
422	66.6	3.0	2846	9	ACD11103	Novel hum	495	66.6	3.0	2846	9	Adf53132	Human sec
423	66.6	3.0	2846	9	ACD14953	Human sec	496	66.6	3.0	2846	9	Adf53132	Human sec
424	66.6	3.0	2846	9	ACA88362	Human sec	497	66.6	3.0	2846	9	Adf53132	Human sec
425	66.6	3.0	2846	9	ACD81869	CDNA enco	498	66.6	3.0	2846	9	Adf53132	Human sec
426	66.6	3.0	2846	9	ACD11717	Human sec	499	66.6	3.0	2846	9	Adf53132	Human sec
427	66.6	3.0	2846	9	ACC95846	Human sec	500	66.6	3.0	2846	9	Adf53132	Human sec
428	66.6	3.0	2846	9	ACF16409	Human sec	501	66.6	3.0	2846	9	Adf53132	Human sec
429	66.6	3.0	2846	9	ACF02527	Human sec	502	66.6	3.0	2846	9	Adf53132	Human sec
430	66.6	3.0	2846	9	ACF02834	Human sec	503	66.6	3.0	2846	9	Adf53132	Human sec
431	66.6	3.0	2846	9	ACF21421	Human sec	504	66.6	3.0	2846	9	Adf53132	Human sec
432	66.6	3.0	2846	9	ACF10105	Human sec	505	66.6	3.0	2846	9	Adf53132	Human sec
433	66.6	3.0	2846	9	ACF77998	Human sec	506	66.6	3.0	2846	9	Adf53132	Human sec
434	66.6	3.0	2846	9	ACD46703	Human sec	507	66.6	3.0	2846	9	Adf53132	Human sec
435	66.6	3.0	2846	9	ACD49466	Human sec	508	66.6	3.0	2846	9	Adf53132	Human sec
436	66.6	3.0	2846	9	ACF28233	Human sec	509	66.6	3.0	2846	9	Adf53132	Human sec
437	66.6	3.0	2846	9	ACD88923	Human sec	510	66.6	3.0	2846	9	Adf53132	Human sec
438	66.6	3.0	2846	9	ACD84318	Human sec	511	66.6	3.0	2846	9	Adf53132	Human sec
439	66.6	3.0	2846	9	ADAF77921	Human sec	512	66.6	3.0	2846	9	Adf53132	Human sec
440	66.6	3.0	2846	9	ACF48834	Human sec	513	66.6	3.0	2846	9	Adf53132	Human sec
441	66.6	3.0	2846	9	ACD09154	Human sec	514	66.6	3.0	2846	9	Adf53132	Human sec
442	66.6	3.0	2846	9	ACF11947	Human sec	515	66.6	3.0	2846	9	Adf53132	Human sec
443	66.6	3.0	2846	9	ACF41181	Human sec	516	66.6	3.0	2846	9	Adf53132	Human sec
444	66.6	3.0	2846	9	ACF15795	Human sec	517	66.6	3.0	2846	9	Adf53132	Human sec
445	66.6	3.0	2846	9	ACF16102	Human sec	518	66.6	3.0	2846	9	Adf53132	Human sec
446	66.6	3.0	2846	9	ACF16102	Human sec	519	66.6	3.0	2846	9	Adf53132	Human sec
447	66.6	3.0	2846	9	ADB17094	Human CDN	520	66.6	3.0	2846	9	Adf53132	Human sec
448	66.6	3.0	2846	9	ACD31929	Human sec	521	66.6	3.0	2846	9	Adf53132	Human sec
449	66.6	3.0	2846	9	ACF18737	Human sec	522	66.6	3.0	2846	9	Adf53132	Human sec
450	66.6	3.0	2846	9	ACF09184	Human sec	523	66.6	3.0	2846	9	Adf53132	Human sec
451	66.6	3.0	2846	9	ACF78305	Human sec	524	66.6	3.0	2846	9	Adf53132	Human sec
452	66.6	3.0	2846	9	ACF51904	Human sec	525	66.6	3.0	2846	9	Adf53132	Human sec
453	66.6	3.0	2846	9	ACF26391	Human sec	526	66.6	3.0	2846	9	Adf53132	Human sec
454	66.6	3.0	2846	9	ACF26391	Human sec	527	66.6	3.0	2846	9	Adf53132	Human sec
455	66.6	3.0	2846	9	ACF26391	Human sec	528	66.6	3.0	2846	9	Adf53132	Human sec
456	66.6	3.0	2846	9	ACF63495	Human sec	529	66.6	3.0	2846	9	Adf53132	Human sec
457	66.6	3.0	2846	9	ACH07840	Human sec	530	66.6	3.0	2846	9	Adf53132	Human sec
458	66.6	3.0	2846	9	ACF13646	Human sec	531	66.6	3.0	2846	9	Adf53132	Human sec

532	66.6	3.0	2846	9	ACD90458 Human sec	605	66.6	3.0	2846	9	ACF32599 Human sec
533	66.6	3.0	2846	9	ACD91071 Human sec	606	66.6	3.0	2846	9	ACF40260 Human sec
534	66.6	3.0	2846	9	ACF30382 Human sec	607	66.6	3.0	2846	9	ACF48220 Human sec
535	66.6	3.0	2846	9	ACD87081 Human sec	608	66.6	3.0	2846	9	ACF38169 Human sec
536	66.6	3.0	2846	9	ACF60135 Human sec	609	66.6	3.0	2846	9	ACF25105 Human sec
537	66.6	3.0	2846	9	ACF46685 Human sec	610	66.6	3.0	2846	9	ACF27005 Human sec
538	66.6	3.0	2846	9	ACF75542 Human sec	611	66.6	3.0	2846	9	ACF29461 Human sec
539	66.6	3.0	2846	9	ADA79713 Human sec	612	66.6	3.0	2846	9	ACD87695 Human sec
540	66.6	3.0	2846	9	ACF17202 Human sec	613	66.6	3.0	2846	9	ACF76156 Human sec
541	66.6	3.0	2846	9	ACF22956 Human sec	614	66.6	3.0	2846	9	ACF49448 Human sec
542	66.6	3.0	2846	9	ACF07956 Human sec	615	66.6	3.0	2846	9	ACF43905 Human sec
543	66.6	3.0	2846	9	ACF08263 Human sec	616	66.6	3.0	2846	9	ACH06250 cDNA enco
544	66.6	3.0	2846	9	ACF40567 Human sec	617	66.6	3.0	2846	9	ACH06557 cDNA enco
545	66.6	3.0	2846	9	ACF53746 Human sec	618	66.6	3.0	2846	9	ADA83238 Human sec
546	66.6	3.0	2846	9	ACD47010 Human sec	619	66.6	3.0	2846	9	ACC92613 Human sec
547	66.6	3.0	2846	9	ACF47913 Human sec	620	66.6	3.0	2846	9	ACC93227 Human sec
548	66.6	3.0	2846	9	ACF47299 Human sec	621	66.6	3.0	2846	9	ACF19272 Human sec
549	66.6	3.0	2846	9	ACF46071 Human sec	622	66.6	3.0	2846	9	ACD12963 Human sec
550	66.6	3.0	2846	9	ACD86160 Human sec	623	66.6	3.0	2846	9	ACF06421 Human sec
551	66.6	3.0	2846	9	ACF52518 Human sec	624	66.6	3.0	2846	9	ACC94455 Human sec
552	66.6	3.0	2846	9	ACF52825 Human sec	625	66.6	3.0	2846	9	ACC97883 Human sec
553	66.6	3.0	2846	9	ACF64818 Human sec	626	66.6	3.0	2846	9	ACC94148 Human sec
554	66.6	3.0	2846	9	ACF78463 Human sec	627	66.6	3.0	2846	9	ACF42102 Human sec
555	66.6	3.0	2846	9	ACF61363 Human sec	628	66.6	3.0	2846	9	ACD31008 Human sec
556	66.6	3.0	2846	9	ACF61670 Human sec	629	66.6	3.0	2846	9	ACD43037 cDNA enco
557	66.6	3.0	2846	9	ACD30701 Human sec	630	66.6	3.0	2846	9	ACD43344 cDNA enco
558	66.6	3.0	2846	9	ACD31622 Human sec	631	66.6	3.0	2846	9	ACF14874 Human sec
559	66.6	3.0	2846	9	ACD32543 Human sec	632	66.6	3.0	2846	9	ADA22792 Human sec
560	66.6	3.0	2846	9	ADA20071 Novel hum	633	66.6	3.0	2846	9	ACF01606 Human sec
561	66.6	3.0	2846	9	ACD82108 Human sec	634	66.6	3.0	2846	9	ACF31678 Human sec
562	66.6	3.0	2846	9	ACF17509 Human sec	635	66.6	3.0	2846	9	ACD67355 cDNA enco
563	66.6	3.0	2846	9	ADA94446 Human sec	636	66.6	3.0	2846	9	ACD48545 Human sec
564	66.6	3.0	2846	9	ACF07342 Human sec	637	66.6	3.0	2846	9	ACD48852 Human sec
565	66.6	3.0	2846	9	ACF20500 Human sec	638	66.6	3.0	2846	9	ACF51290 Human sec
566	66.6	3.0	2846	9	ACF20807 Human sec	639	66.6	3.0	2846	9	ACF54053 Human sec
567	66.6	3.0	2846	9	ACD21114 Human sec	640	66.6	3.0	2846	9	ACF25777 Human sec
568	66.6	3.0	2846	9	ACD47624 Human sec	641	66.6	3.0	2846	9	ACF39090 Human sec
569	66.6	3.0	2846	9	ACF47606 Human sec	642	66.6	3.0	2846	9	ACF28847 Human sec
570	66.6	3.0	2846	9	ACF53439 Human sec	643	66.6	3.0	2846	9	ACD90764 Human sec
571	66.6	3.0	2846	9	ACD86774 Human sec	644	66.6	3.0	2846	9	ACD86467 Human sec
572	66.6	3.0	2846	9	ACH05022 cDNA enco	645	66.6	3.0	2846	9	ACH05329 cDNA enco
573	66.6	3.0	2846	9	ACF44519 Human sec	646	66.6	3.0	2846	9	ACF65125 Human sec
574	66.6	3.0	2846	9	ADA81440 Human sec	647	66.6	3.0	2846	9	ADB20281 Human sec
575	66.6	3.0	2846	9	ACD22174 Human sec	648	66.6	3.0	2846	9	ACF43598 Human sec
576	66.6	3.0	2846	9	ACD24521 Human sec	649	66.6	3.0	2846	9	ACH09068 Human sec
577	66.6	3.0	2846	9	ACD39724 cDNA enco	650	66.6	3.0	2846	9	ACH09375 Human sec
578	66.6	3.0	2846	9	ACD40031 cDNA enco	651	66.6	3.0	2846	9	ADA78533 Human sec
579	66.6	3.0	2846	9	ACF13339 Human sec	652	66.6	3.0	2846	9	ACH10603 Human sec
580	66.6	3.0	2846	9	ACF03141 Human sec	653	66.6	3.0	2846	9	ACF09798 Human sec
581	66.6	3.0	2846	9	ACF78612 Human sec	654	66.6	3.0	2846	9	ACF50983 Human sec
582	66.6	3.0	2846	9	ACF11333 Human sec	655	66.6	3.0	2846	9	ACF23877 Human sec
583	66.6	3.0	2846	9	ACF50676 Human sec	656	66.6	3.0	2846	9	ACH09682 Human sec
584	66.6	3.0	2846	9	ACF34171 Human sec	657	66.6	3.0	2846	9	ACH10603 Human sec
585	66.6	3.0	2846	9	ACD46396 Human sec	658	66.6	3.0	2846	9	ACH11410 Human sec
586	66.6	3.0	2846	9	ACD48238 Human sec	659	66.6	3.0	2846	9	ACC96460 Human sec
587	66.6	3.0	2846	9	ACF27619 Human sec	660	66.6	3.0	2846	9	ACC98490 Human sec
588	66.6	3.0	2846	9	ACF24491 Human sec	661	66.6	3.0	2846	9	ACF41795 Human sec
589	66.6	3.0	2846	9	ACD85546 Human sec	662	66.6	3.0	2846	9	ACF16716 Human sec
590	66.6	3.0	2846	9	ACD90151 Human sec	663	66.6	3.0	2846	9	ACD32236 Human sec
591	66.6	3.0	2846	9	ACD83704 Human sec	664	66.6	3.0	2846	9	ACD30394 Human sec
592	66.6	3.0	2846	9	ACF49141 Human sec	665	66.6	3.0	2846	9	ACD41265 Human sec
593	66.6	3.0	2846	9	ACH07226 Human sec	666	66.6	3.0	2846	9	ACF07649 Human sec
594	66.6	3.0	2846	9	ACH07533 Human sec	667	66.6	3.0	2846	9	ACF31064 Human sec
595	66.6	3.0	2846	9	ACH08147 Human sec	668	66.6	3.0	2846	9	ACF77384 Human sec
596	66.6	3.0	2846	9	ACH11338 Human sec	669	66.6	3.0	2846	9	ACF11026 Human sec
597	66.6	3.0	2846	9	ACH11645 Human sec	670	66.6	3.0	2846	9	ACF32906 Human sec
598	66.6	3.0	2846	9	ACH10296 Human sec	671	66.6	3.0	2846	9	ACF26084 Human sec
599	66.6	3.0	2846	9	ACH01299 Human sec	672	66.6	3.0	2846	9	ACD83397 Human sec
600	66.6	3.0	2846	9	ACF40874 Human sec	673	66.6	3.0	2846	9	ACF23570 Human sec
601	66.6	3.0	2846	9	ACD24214 Human sec	674	66.6	3.0	2846	9	ACF42984 Human sec
602	66.6	3.0	2846	9	ACD31315 Human sec	675	66.6	3.0	2846	9	ACF43291 Human sec
603	66.6	3.0	2846	9	ACF17816 Human sec	676	66.6	3.0	2846	9	ACH05943 cDNA enco
604	66.6	3.0	2846	9	ADA38671 Human sec	677	66.6	3.0	2846	9	ACH08761 Human sec

824	66.6	3.0	2846	10	ADH98069	Novel	hum	Adh98069	Novel	hum	897	66.6	3.0	2846	12	ADH33721	Human	PRO
825	66.6	3.0	2846	10	ABX78612	Human	PRO	Abx78612	Human	PRO	898	66.6	3.0	2846	12	ADG82818	Human	PRO
826	66.6	3.0	2846	10	ACA75584	Novel	hum	AcA75584	Novel	hum	899	66.6	3.0	2846	12	ADH02364	Human	PRO
827	66.6	3.0	2846	10	ACA71064	Human	sec	AcA71064	Human	sec	900	66.6	3.0	2846	12	ADH07971	Novel	hum
828	66.6	3.0	2846	10	ACC87592	Human	sec	Acc87592	Human	sec	901	66.6	3.0	2846	12	ADG69368	Novel	hum
829	66.6	3.0	2846	10	ACC86978	Human	sec	Acc86978	Human	sec	902	66.6	3.0	2846	12	ADH39189	Novel	hum
830	66.6	3.0	2846	10	ACD04151	Human	sec	AcD04151	Human	sec	903	66.6	3.0	2846	12	ADH26099	Novel	hum
831	66.6	3.0	2846	10	ABX77859	Human	PRO	Abx77859	Human	PRO	904	66.6	3.0	2846	12	ADG83929	Human	PRO
832	66.6	3.0	2846	10	ABX80271	Human	sec	Abx80271	Human	sec	905	66.6	3.0	2846	12	ADH19476	Human	CDN
833	66.6	3.0	2846	10	ACA69177	Human	CDN	AcA69177	Human	CDN	906	66.6	3.0	2846	12	ADG85473	Novel	hum
834	66.6	3.0	2846	10	ACA69482	cDNA	enco	AcA69482	cDNA	enco	907	66.6	3.0	2846	12	ADH06267	Novel	hum
835	66.6	3.0	2846	10	ACA90327	Novel	hum	AcA90327	Novel	hum	908	66.6	3.0	2846	12	ADH30097	Novel	hum
836	66.6	3.0	2846	10	ACC89434	Human	sec	Acc89434	Human	sec	909	66.6	3.0	2846	12	ADH24409	Novel	hum
837	66.6	3.0	2846	10	ABX90248	Human	sec	Abx90248	Human	sec	910	66.6	3.0	2846	12	ADH33068	Human	PRO
838	66.6	3.0	2846	10	ACA98225	Novel	hum	AcA98225	Novel	hum	911	66.6	3.0	2846	12	ADG69538	Novel	hum
839	66.6	3.0	2846	10	ACA93867	Human	sec	AcA93867	Human	sec	912	66.6	3.0	2846	12	ADH07801	Novel	hum
840	66.6	3.0	2846	10	ACD15260	Human	sec	AcD15260	Human	sec	913	66.6	3.0	2846	12	ADG85813	Novel	hum
841	66.6	3.0	2846	10	ACD08847	Human	sec	AcD08847	Human	sec	914	66.6	3.0	2846	12	ADH39359	Novel	hum
842	66.6	3.0	2846	10	ACC96767	Human	sec	Acc96767	Human	sec	915	66.6	3.0	2846	12	ADH33551	Human	PRO
843	66.6	3.0	2846	10	ACF15488	Human	sec	AcF15488	Human	sec	916	66.6	3.0	2846	12	ADH33891	Human	PRO
844	66.6	3.0	2846	10	ABX64094	cDNA	enco	Abx64094	cDNA	enco	917	66.6	3.0	2846	12	ADH01101	Human	PRO
845	66.6	3.0	2846	10	ACA72855	Human	PRO	AcA72855	Human	PRO	918	66.6	3.0	2846	12	ADG69708	Novel	hum
846	66.6	3.0	2846	10	ACD03027	Novel	hum	AcD03027	Novel	hum	919	66.6	3.0	2846	12	ADH20969	Human	CDN
847	66.6	3.0	2846	10	ACD01842	Novel	hum	AcD01842	Novel	hum	920	66.6	3.0	2846	12	ADH02194	Human	PRO
848	66.6	3.0	2846	10	ACA92034	Novel	hum	AcA92034	Novel	hum	921	66.6	3.0	2846	12	ADG69198	Novel	hum
849	66.6	3.0	2846	10	ADIO0507	Novel	hum	Adi05057	Novel	hum	922	66.6	3.0	2846	12	ADG85983	Novel	hum
850	66.6	3.0	2846	10	ADIO3407	Novel	hum	Adi03407	Novel	hum	923	66.6	3.0	2846	12	ADH24919	Novel	hum
851	66.6	3.0	2846	10	ADIO4802	Novel	hum	Adi04802	Novel	hum	924	66.6	3.0	2846	12	ADH39536	Novel	hum
852	66.6	3.0	2846	10	ADH78256	Human	PRO	Adh78256	Human	PRO	925	66.6	3.0	2846	12	ADH20009	Human	CDN
853	66.6	3.0	2846	10	ADH119600	Novel	hum	Adh119600	Novel	hum	926	66.6	3.0	2846	12	ADH02534	Human	PRO
854	66.6	3.0	2846	10	ADH90348	Novel	hum	Adh90348	Novel	hum	927	66.6	3.0	2846	12	ADG69028	Novel	hum
855	66.6	3.0	2846	10	ADIO3067	Novel	hum	Adi03067	Novel	hum	928	66.6	3.0	2846	12	ADH07631	Novel	hum
856	66.6	3.0	2846	10	ADH77916	Human	PRO	Adh77916	Human	PRO	929	66.6	3.0	2846	12	ADG86153	Novel	hum
857	66.6	3.0	2846	10	ADH97899	Novel	hum	Adh97899	Novel	hum	930	66.6	3.0	2846	12	ADH24749	Novel	hum
858	66.6	3.0	2846	10	ADIO1284	Novel	hum	Adi01284	Novel	hum	931	66.6	3.0	2846	12	ADH25797	Novel	hum
859	66.6	3.0	2846	10	ADIO1979	Novel	hum	Adi01979	Novel	hum	932	66.6	3.0	2846	12	ADH38363	Novel	hum
860	66.6	3.0	2846	10	ADIO3237	Novel	hum	Adi03237	Novel	hum	933	66.6	3.0	2846	12	ADH57202	Novel	hum
861	66.6	3.0	2846	10	ADII1424	Human	PRO	Adi11424	Human	PRO	934	66.6	3.0	2846	12	ADH52190	Novel	hum
862	66.6	3.0	2846	10	ADIO2326	Novel	hum	Adi02326	Novel	hum	935	66.6	3.0	2846	12	ADH49556	Novel	hum
863	66.6	3.0	2846	10	ADII1764	Human	PRO	Adi11764	Human	PRO	936	66.6	3.0	2846	12	ADH90518	Novel	hum
864	66.6	3.0	2846	10	ADIO5401	Novel	hum	Adi05401	Novel	hum	937	66.6	3.0	2846	12	ADH11254	Novel	hum
865	66.6	3.0	2846	10	ADH79473	Novel	hum	Adh79473	Novel	hum	938	66.6	3.0	2846	12	ADH98919	Novel	hum
866	66.6	3.0	2846	10	ADII19430	Novel	hum	Adi119430	Novel	hum	939	66.6	3.0	2846	12	ADH02149	Novel	hum
867	66.6	3.0	2846	10	ADIO5231	Novel	hum	Adi05231	Novel	hum	940	66.6	3.0	2846	12	ADH90688	Novel	hum
868	66.6	3.0	2846	10	ADH79643	Novel	hum	Adh79643	Novel	hum	941	66.6	3.0	2846	12	ADJ54807	Human	PRO
869	66.6	3.0	2846	10	ADIO1469	Novel	hum	Adi01469	Novel	hum	942	66.6	3.0	2846	12	ADJ98563	Novel	hum
870	66.6	3.0	2846	10	ADIO1639	Novel	hum	Adi01639	Novel	hum	943	66.6	3.0	2846	12	ADJ98733	Novel	hum
871	66.6	3.0	2846	10	ADIO1809	Novel	hum	Adi01809	Novel	hum	944	66.6	3.0	2846	12	ADJ78892	Novel	hum
872	66.6	3.0	2846	10	ADH79813	Novel	hum	Adh79813	Novel	hum	945	66.6	3.0	2846	12	ADJ99126	Novel	hum
873	66.6	3.0	2846	10	ADIO4631	Novel	hum	Adi04631	Novel	hum	946	66.6	3.0	2846	12	ADJ99296	Novel	hum
874	66.6	3.0	2846	10	ADIO2767	Novel	hum	Adi02767	Novel	hum	947	66.6	3.0	2846	12	ADJ98914	Novel	hum
875	66.6	3.0	2846	10	ADH78086	Human	PRO	Adh78086	Human	PRO	948	66.6	3.0	2846	12	ADH79062	Novel	hum
876	66.6	3.0	2846	10	ADJ25725	Novel	hum	Adi25725	Novel	hum	949	66.6	3.0	2846	12	ADK00922	Human	PRO
877	66.6	3.0	2846	10	ADJ25895	Novel	hum	Adi25895	Novel	hum	950	66.6	3.0	2846	12	ADK14443	Novel	hum
878	66.6	3.0	2846	10	ADK65407	Novel	hum	Adk65407	Novel	hum	951	66.6	3.0	2846	12	ADJ64578	Human	PRO
879	66.6	3.0	2846	10	ADH98749	Novel	hum	Adh98749	Novel	hum	952	66.6	3.0	2846	12	ADM31474	Novel	hum
880	66.6	3.0	2846	10	ADH79990	Novel	hum	Adh79990	Novel	hum	953	66.6	3.0	2846	12	ADM36521	Novel	hum
881	66.6	3.0	2846	11	ADM32775	Novel	hum	Adm32775	Novel	hum	954	66.6	3.0	2846	12	ADM40326	Novel	hum
882	66.6	3.0	2846	11	ADM30309	Novel	hum	Adm30309	Novel	hum	955	66.6	3.0	2846	12	ADM80892	Human	PRO
883	66.6	3.0	2846	11	ADL93721	Novel	hum	Adl93721	Novel	hum	956	66.6	3.0	2846	12	ADN37934	Novel	hum
884	66.6	3.0	2846	12	ADC52175	Novel	hum	Adc52175	Novel	hum	957	66.6	3.0	2848	8	ACA67289	cDNA	enco
885	66.6	3.0	2846	12	ADL74306	Human	sec	Adl74306	Human	sec	c 958	66.4	3.0	228	5	ADL43698	Human	ova
886	66.6	3.0	2846	12	ADL74918	Human	sec	Adl74918	Human	sec	c 959	66.4	3.0	255	5	AAH82206	Rat	diffe
887	66.6	3.0	2846	12	ADF35356	cDNA	enco	Adf35356	cDNA	enco	c 960	66.4	3.0	266	5	ABV07596	Human	pro
888	66.6	3.0	2846	12	ADG11606	Novel	hum	Adg11606	Novel	hum	c 961	66.4	3.0	300	5	ABV04310	Human	pro
889	66.6	3.0	2846	12	ADG96131	Novel	hum	Adg96131	Novel	hum	c 962	66.4	3.0	489	13	ACN49736	Cotton	pr
890	66.6	3.0	2846	12	ADG04402	Novel	hum	Adg04402	Novel	hum	c 963	66.4	3.0	522	5	ABV39211	Human	pro
891	66.6	3.0	2846	12	ADG00562	Novel	hum	Adg00562	Novel	hum	c 964	66.4	3.0	550	13	ACN47393	Cotton	pr
892	66.6	3.0	2846	12	ADH06607	Novel	hum	Adh06607	Novel	hum	965	66.4	3.0	823	4	AAI02457	Human	rep
893	66.6	3.0	2846	12	ADH06437	Novel	hum	Adh06437	Novel	hum	966	66.4	3.0	823	4	ABA07664	Human	ova
894	66.6	3.0	2846	12	ADG68858	Novel	hum	Adg68858	Novel	hum	967	66.4	3.0	1781	8	ABX15518	cDNA	enco
895	66.6	3.0	2846	12	ADH27748	Novel	hum	Adh27748	Novel	hum	968	66.4	3.0	1781	10	AAI47901	Human	tra
896	66.6	3.0	2846	12	ADH25089	Novel	hum	Adh25089	Novel	hum	969	66.4	3.0	1874	10	ADI62940	Human	apo

970	66.4	3.0	1927	4	AA44987	Aaf44987 Human Gen	1043	2.9	2291	13	ADR25949	Adr25949 Breast ca
971	66.4	3.0	4816	10	AD615662	Ad615662 Human str	1044	2.9	2988	12	ADQ23141	Adq23141 Human sof
c 972	66.2	3.0	379	4	AAU20476	Aal20476 Human bre	1045	2.9	3116	3	AAZ52568	Aaz52568 Human sec
973	66.2	3.0	388	4	AAI189390	Aai189390 Human pol	1046	2.9	4824	12	ADQ22371	Adq22371 Human sof
974	66.2	3.0	433	13	ACN15900	Acn15900 Cotton an	1047	65.8	216	5	ADL37402	Adl37402 Human ova
975	66.2	3.0	470	5	ABV55159	Abv55159 Human pro	c1048	65.8	216	5	ADI72258	Adi72258 Human ova
c 976	66.2	3.0	476	5	ADL37109	Adl37109 Human ova	1049	65.8	391	4	AAI83087	Aai83087 Human pol
c 977	66.2	3.0	476	5	ADL171958	Adl171958 Human ova	1050	65.8	398	4	AAI85290	Aai85290 Human pol
c 978	66.2	3.0	486	13	ACN46735	Acn46735 Cotton pr	c1051	65.8	425	4	AA650450	Aa650450 Human can
c 979	66.2	3.0	499	13	ACN46935	Acn46935 Cotton pr	1052	65.8	522	3	AAA60770	Aaa60770 Pig SENR
980	66.2	3.0	526	13	ACN59983	Acn59983 Cotton gy	1053	65.8	522	6	ABK50023	Abk50023 Pig senso
c 981	66.2	3.0	532	13	ACN61789	Acn61789 Cotton gy	c1054	65.8	608	5	ADL37588	Adl37588 Human ova
c 982	66.2	3.0	560	13	ACN51599	Acn51599 Cotton an	c1055	65.8	608	5	ADI72448	Adi72448 Human ova
c 983	66.2	3.0	693	4	AAI14804	Aai14804 Human bre	1056	65.8	638	3	AA60768	Aa60768 Pig SENR
c 984	66.2	3.0	723	5	ADL71984	Adl71984 Human ova	1057	65.8	638	3	AAK50021	Aak50021 Pig senso
c 985	66.2	3.0	723	5	ADL371134	Adl371134 Human ova	1058	65.8	711	12	ADN05332	Adn05332 Antipsori
c 986	66.2	3.0	810	5	ADL38237	Adl38237 Human ova	1059	65.8	1383	12	ADQ23192	Adq23192 Human sof
c 987	66.2	3.0	810	5	ADL731104	Adl731104 Human ova	1060	65.8	1475	10	ADC38959	Adc38959 Human cDN
c 988	66.2	3.0	874	11	ACN84830	Acn84830 Breast ca	1061	65.8	1635	3	AAF21664	Aaf21664 Human bre
989	66.2	3.0	878	8	ACC62513	Acc62513 Human sec	1062	65.8	1883	3	AAA77670	Aaa77670 Human PRO
990	66.2	3.0	1153	13	ADP55850	Adp55850 Human PRO	1063	65.8	1883	3	AAA37066	Aaa37066 Human PRO
991	66.2	3.0	1315	4	AAF81788	Aaf81788 Human sec	1064	65.8	1883	3	AA54302	Aa54302 DNA enco
992	66.2	3.0	1315	8	ADMA40552	Adma40552 Human sec	1065	65.8	1883	4	AA521494	Aa521494 Human cDN
993	66.2	3.0	1315	8	ACC50854	Acc50854 Human sec	1066	65.8	1883	8	ACA03853	ACA03853 cDNA enco
994	66.2	3.0	1315	10	ADC73986	Adc73986 Human sec	1067	65.8	1883	8	ABX89391	Abx89391 DNA enco
995	66.2	3.0	1315	10	ADD37810	Add37810 Human sec	1068	65.8	1883	8	ACD42045	AcD42045 Human sec
996	66.2	3.0	1315	10	ADA56701	Ada56701 Gene enco	1069	65.8	1883	8	ACA04274	ACA04274 Human cDN
997	66.2	3.0	1317	8	ADMA40234	Adma40234 Human sec	1070	65.8	1883	9	ADA46020	Ada46020 Novel hum
998	66.2	3.0	1317	8	ACC50674	Acc50674 Human sec	1071	65.8	1883	9	ADA16451	Ada16451 Human PRO
999	66.2	3.0	1317	10	ADC73758	Adc73758 Human sec	1072	65.8	1883	9	ADA19101	Ada19101 Human PRO
1000	66.2	3.0	1317	10	ADD37713	Add37713 Human sec	1073	65.8	1883	9	ADA61724	Ada61724 Homo sapi
1001	66.2	3.0	1317	10	ADA56395	Ada56395 Gene enco	1074	65.8	1883	9	ADB19509	Adb19509 Novel hum
1002	66.2	3.0	1321	3	AA982225	Aac982225 Human col	1075	65.8	1883	9	ADB28050	Adb28050 cDNA enco
1003	66.2	3.0	1337	12	AD142582	Adi42582 Plant tra	1076	65.8	1883	9	AD86529	Ad86529 Novel hum
1004	66.2	3.0	1337	12	AD002883	Ado02883 Soybean o	1077	65.8	1883	9	ADB16093	Adb16093 Human PRO
1005	66.2	3.0	1378	2	AAV59706	Aav59706 Human sec	1078	65.8	1883	9	ADA47879	Ada47879 Human PRO
1006	66.2	3.0	1378	6	AB573695	Ab573695 Human cDN	1079	65.8	1883	9	ACD68339	AcD68339 Novel hum
1007	66.2	3.0	1378	9	ACD82838	Adc82838 cDNA sequ	1080	65.8	1883	9	AD67674	Ad67674 Human PRO
1008	66.2	3.0	1378	10	AD122923	Adi22923 cDNA enco	1081	65.8	1883	9	ADB30681	Adb30681 cDNA enco
1009	66.2	3.0	1378	12	ADH73325	Adh73325 Human sec	1082	65.8	1883	9	ADA85977	Ada85977 Novel hum
1010	66.2	3.0	1856	8	ACC69466	Acc69466 Human mal	1083	65.8	1883	9	ADA97189	Ada97189 Human PRO
1011	66.2	3.0	1867	10	ACA92442	ACA92442 DNA enco	1084	65.8	1883	9	ADA79493	Ada79493 Human PRO
1012	66.2	3.0	2323	2	AAV59524	Aav59524 Human sec	1085	65.8	1883	9	AD87632	Ad87632 Novel hum
1013	66.2	3.0	2323	6	AB573511	Ab573511 Human cDN	1086	65.8	1883	9	AD16834	Ad16834 Human PRO
1014	66.2	3.0	2323	9	ACD82654	Adc82654 cDNA sequ	1087	65.8	1883	9	ADA91926	Ada91926 Novel hum
1015	66.2	3.0	2323	10	ADH72739	Adh72739 cDNA enco	1088	65.8	1883	9	ADB14989	Adb14989 Human PRO
1016	66.2	3.0	2323	12	ADH73741	Adh73741 Human sec	1089	65.8	1883	9	ADB18950	Adb18950 Novel hum
c1017	66	2.9	375	5	ABV44911	Abv44911 Human pro	1090	65.8	1883	9	ADA94165	Ada94165 Human PRO
c1018	66	2.9	384	5	ADI69792	Adi69792 Human ova	1091	65.8	1883	9	AD20061	Ad20061 Novel hum
c1019	66	2.9	384	5	ADI76128	Adi76128 Human ova	1092	65.8	1883	9	AD13373	Ad13373 Human PRO
1020	66	2.9	403	4	AAI82937	Aai82937 Human pol	1093	65.8	1883	9	ACD98674	AcD98674 Novel hum
c1021	66	2.9	464	5	ABV03810	Abv03810 Human pro	1094	65.8	1883	9	ADA74627	Ada74627 Human PRO
c1022	66	2.9	483	13	ACN61841	Acn61841 Cotton gy	1095	65.8	1883	9	AD24860	Ad24860 Human PRO
1023	66	2.9	516	12	ACN59785	Acn59785 Cotton gy	1096	65.8	1883	9	ADA82384	Ada82384 Human PRO
1024	66	2.9	940	12	ADQ62500	Ado62500 Transcript	1097	65.8	1883	9	ADA75347	Ada75347 Human PRO
1025	66	2.9	1181	6	AAV59803	Aav59803 Human sec	1098	65.8	1883	9	AD85425	Ad85425 Novel hum
1026	66	2.9	1181	6	AB573757	Ab573757 Human cDN	1099	65.8	1883	9	AD84873	Ad84873 Novel hum
1027	66	2.9	1181	9	ACD82940	Adc82940 cDNA sequ	1100	65.8	1883	9	AD30129	Ad30129 cDNA enco
1028	66	2.9	1181	10	AD123025	Adi23025 cDNA enco	1101	65.8	1883	9	ADA80657	Ada80657 Human PRO
1029	66	2.9	1181	12	ADH74027	Adh74027 Human sec	1102	65.8	1883	9	ADA75899	Ada75899 Human PRO
1030	66	2.9	1212	2	AAV59686	Aav59686 Human sec	1103	65.8	1883	9	ADA7124	Ada7124 Human PRO
1031	66	2.9	1212	6	ABQ54333	Abq54333 Human ova	1104	65.8	1883	9	AD25420	Ad25420 Human PRO
1032	66	2.9	1212	6	AB573673	Ab573673 Human cDN	1105	65.8	1883	9	ADA93596	Ada93596 Human PRO
1033	66	2.9	1212	9	ACD82816	Adc82816 cDNA sequ	1106	65.8	1883	9	AD26946	Ad26946 cDNA enco
1034	66	2.9	1212	10	AD122901	Adi22901 cDNA enco	1107	65.8	1883	9	AD31233	Ad31233 cDNA enco
1035	66	2.9	1212	12	ADH73903	Adh73903 Human sec	1108	65.8	1883	9	ADA61161	Ada61161 Homo sapi
1036	66	2.9	1447	5	ABX71274	Abx71274 Human bra	1109	65.8	1883	9	AD24308	Ad24308 Human PRO
1037	66	2.9	1453	2	AAQ50573	Aaq50573 Asparagin	1110	65.8	1883	9	ADA96637	Ada96637 Human PRO
1038	66	2.9	1585	12	ADQ25305	Adq25305 Human sof	1111	65.8	1883	9	ADA81209	Ada81209 Human PRO
1039	66	2.9	1640	2	AAQ50575	Aaq50575 Asparagin	1112	65.8	1883	9	ADA96085	Ada96085 Human PRO
1040	66	2.9	1793	3	AAQ77949	Aaq77949 Human can	1113	65.8	1883	9	AD26394	Ad26394 cDNA enco
1041	66	2.9	1910	2	AAQ50579	Aaq50579 Asparagin	1114	65.8	1883	9	AD21879	Ad21879 Novel hum
1042	66	2.9	2291	9	AAI62477	Aai62477 Human oxl	1115	65.8	1883	9	ADA77658	Ada77658 Human PRO

1116	65.8	2.9	1883	9	ADB18398	Adb18398 cDNA enco	1189	65.8	2.9	1883	10	ADB50435	Ade50435 Human cDN
1117	65.8	2.9	1883	9	ADA87081	Ada87081 Novel hum	1190	65.8	2.9	1883	10	ADD92635	Add92635 Human PRO
1118	65.8	2.9	1883	9	ACH04441	Ach04441 Human cDN	1191	65.8	2.9	1883	10	ADD91531	Add91531 Human PRO
1119	65.8	2.9	1883	9	ADA88184	Ada88184 Novel hum	1192	65.8	2.9	1883	10	ADE04145	Ade04145 Human PRO
1120	65.8	2.9	1883	9	ADA46572	Ada46572 Novel hum	1193	65.8	2.9	1883	10	ADE00447	Ade00447 Human cDN
1121	65.8	2.9	1883	9	ADB28602	Adb28602 cDNA enco	1194	65.8	2.9	1883	10	ADE32442	Ade32442 Novel hum
1122	65.8	2.9	1883	9	ADB29154	Adb29154 cDNA enco	1195	65.8	2.9	1883	10	ADE22374	Ade22374 cDNA enco
1123	65.8	2.9	1883	9	ADA77106	Ada77106 Human PRO	1196	65.8	2.9	1883	10	ADD79598	Add79598 cDNA enco
1124	65.8	2.9	1883	9	ACD67985	Acd67985 Novel hum	1197	65.8	2.9	1883	10	ADE42134	Ade42134 Human PRO
1125	65.8	2.9	1883	9	ADA88736	Ada88736 Novel hum	1198	65.8	2.9	1883	10	ADE17951	Ade17951 Human PRO
1126	65.8	2.9	1883	9	ADA97741	Ada97741 Human PRO	1199	65.8	2.9	1883	10	ADD92083	Add92083 Human PRO
1127	65.8	2.9	1883	9	ADB27498	Adb27498 cDNA enco	1200	65.8	2.9	1883	10	ADE33546	Ade33546 Novel hum
1128	65.8	2.9	1883	9	ADB22431	Adb22431 Novel hum	1201	65.8	2.9	1883	10	ADE34098	Ade34098 Novel hum
1129	65.8	2.9	1883	9	ADA67122	Ada67122 Human PRO	1202	65.8	2.9	1883	10	ADD80150	Add80150 cDNA enco
1130	65.8	2.9	1883	9	ADB22983	Adb22983 Human PRO	1203	65.8	2.9	1883	10	ADE49958	Ade49958 Human cDN
1131	65.8	2.9	1883	9	ADB23756	Adb23756 Human PRO	1204	65.8	2.9	1883	10	ADD93187	Add93187 Human PRO
1132	65.8	2.9	1883	9	ADA92478	Ada92478 Novel hum	1205	65.8	2.9	1883	10	ADE19607	Ade19607 Human PRO
1133	65.8	2.9	1883	9	ADB15541	Adb15541 Human PRO	1206	65.8	2.9	1883	10	ADE21516	Ade21516 Human cDN
1134	65.8	2.9	1883	9	ADB38793	Adb38793 Novel hum	1207	65.8	2.9	1883	10	ADE19055	Ade19055 Human PRO
1135	65.8	2.9	1883	9	ADB38241	Adb38241 Novel hum	1208	65.8	2.9	1883	10	ADE43251	Ade43251 Human PRO
1136	65.8	2.9	1883	9	ADB66713	Adb66713 Novel hum	1209	65.8	2.9	1883	10	ADD96040	Add96040 Human PRO
1137	65.8	2.9	1883	10	ADB89793	Adb89793 Human PRO	1210	65.8	2.9	1883	10	ADE22926	Ade22926 cDNA enco
1138	65.8	2.9	1883	10	ADB90525	Adb90525 Human PRO	1211	65.8	2.9	1883	10	ADD79044	Add79044 cDNA enco
1139	65.8	2.9	1883	10	ADB39626	Adb39626 Novel hum	1212	65.8	2.9	1883	10	ADE32994	Ade32994 Novel hum
1140	65.8	2.9	1883	10	ADB47249	Adb47249 Novel hum	1213	65.8	2.9	1883	10	ADE42686	Ade42686 Human PRO
1141	65.8	2.9	1883	10	ADB86856	Adb86856 Human PRO	1214	65.8	2.9	1883	10	ADD80702	Add80702 cDNA enco
1142	65.8	2.9	1883	10	ADB77461	Adb77461 Novel hum	1215	65.8	2.9	1883	10	ADD89730	Add89730 Human PRO
1143	65.8	2.9	1883	10	ADB34618	Adb34618 Human PRO	1216	65.8	2.9	1883	10	ADE41014	Ade41014 Human PRO
1144	65.8	2.9	1883	10	ADB35722	Adb35722 Human PRO	1217	65.8	2.9	1883	10	ADE04813	Ade04813 Human PRO
1145	65.8	2.9	1883	10	ADB34066	Adb34066 Human PRO	1218	65.8	2.9	1883	10	ADE92942	Ade92942 Human PRO
1146	65.8	2.9	1883	10	ADB35170	Adb35170 Human PRO	1219	65.8	2.9	1883	10	ADF29941	Adf29941 Human cDN
1147	65.8	2.9	1883	10	ADB36274	Adb36274 Human PRO	1220	65.8	2.9	1883	10	ADF55834	Adf55834 Human cDN
1148	65.8	2.9	1883	10	ADB46669	Adb46669 Novel hum	1221	65.8	2.9	1883	10	ADG21651	Adg21651 Novel hum
1149	65.8	2.9	1883	10	ADC18014	Adc18014 Human PRO	1222	65.8	2.9	1883	10	ADG23292	Adg23292 Novel hum
1150	65.8	2.9	1883	10	ADC50542	Adc50542 Novel hum	1223	65.8	2.9	1883	10	ADF97627	Adf97627 Human PRO
1151	65.8	2.9	1883	10	ADC72089	Adc72089 Novel hum	1224	65.8	2.9	1883	10	ADG80691	Adg80691 Human PRO
1152	65.8	2.9	1883	10	ADC60068	Adc60068 Novel hum	1225	65.8	2.9	1883	10	ADG80139	Adg80139 Human PRO
1153	65.8	2.9	1883	10	ADC53075	Adc53075 Novel hum	1226	65.8	2.9	1883	10	ADH55431	Adh55431 Novel hum
1154	65.8	2.9	1883	10	ADC57429	Adc57429 Novel hum	1227	65.8	2.9	1883	10	ADH55983	Adh55983 Novel hum
1155	65.8	2.9	1883	10	ADC60620	Adc60620 Novel hum	1228	65.8	2.9	1883	10	ADH99338	Adh99338 Human cDN
1156	65.8	2.9	1883	10	ADC51095	Adc51095 Novel hum	1229	65.8	2.9	1883	10	ADI64202	Adi64202 Novel hum
1157	65.8	2.9	1883	10	ADC65622	Adc65622 Human PRO	1230	65.8	2.9	1883	10	ADI65151	Adi65151 Novel hum
1158	65.8	2.9	1883	10	ADC54720	Adc54720 Novel hum	1231	65.8	2.9	1883	10	ADI63650	Adi63650 Novel hum
1159	65.8	2.9	1883	10	ADC53681	Adc53681 Novel hum	1232	65.8	2.9	1883	10	ADH82064	Adh82064 Novel hum
1160	65.8	2.9	1883	10	ADC59204	Adc59204 Novel hum	1233	65.8	2.9	1883	10	ADH81512	Adh81512 Novel hum
1161	65.8	2.9	1883	10	ADC56082	Adc56082 Novel hum	1234	65.8	2.9	1883	10	ACD24103	Acd24103 Novel hum
1162	65.8	2.9	1883	10	ADC58652	Adc58652 Novel hum	1235	65.8	2.9	1883	10	ACA67244	ACA67244 cDNA enco
1163	65.8	2.9	1883	10	ADP03326	Adp03326 Novel hum	1236	65.8	2.9	1883	11	ADM82681	Adm82681 Novel hum
1164	65.8	2.9	1883	10	ADC90318	Adc90318 Novel hum	1237	65.8	2.9	1883	11	ADN16080	Adn16080 Novel hum
1165	65.8	2.9	1883	10	ADC69737	Adc69737 cDNA enco	1238	65.8	2.9	1883	11	ADN16709	Adn16709 Novel hum
1166	65.8	2.9	1883	10	ADC48626	Adc48626 Human PRO	1239	65.8	2.9	1883	11	ADN15528	Adn15528 Novel hum
1167	65.8	2.9	1883	10	ADD10195	Add10195 Human PRO	1240	65.8	2.9	1883	11	ADN14976	Adn14976 Novel hum
1168	65.8	2.9	1883	10	ADP04730	Adp04730 Novel hum	1241	65.8	2.9	1883	12	ADC81238	Adc81238 Novel hum
1169	65.8	2.9	1883	10	ADC80686	Adc80686 Novel hum	1242	65.8	2.9	1883	12	ADD76686	Add76686 Human PRO
1170	65.8	2.9	1883	10	ADP11193	Adp11193 Human PRO	1243	65.8	2.9	1883	12	ADP88050	Adp88050 Human PRO
1171	65.8	2.9	1883	10	ADC48074	Adc48074 Human PRO	1244	65.8	2.9	1883	12	ADD86454	Add86454 Human PRO
1172	65.8	2.9	1883	10	ADC80134	Adc80134 Novel hum	1245	65.8	2.9	1883	12	ADP86454	Adp86454 Human PRO
1173	65.8	2.9	1883	10	ADD09603	Add09603 Human PRO	1246	65.8	2.9	1883	12	ADE75902	Ade75902 Human PRO
1174	65.8	2.9	1883	10	ADP41316	Adp41316 Novel hum	1247	65.8	2.9	1883	12	ADE23478	Ade23478 cDNA enco
1175	65.8	2.9	1883	10	ADP52455	Adp52455 cDNA enco	1248	65.8	2.9	1883	12	ADE24030	Ade24030 cDNA enco
1176	65.8	2.9	1883	10	ADP70660	Adp70660 Human cDN	1249	65.8	2.9	1883	12	ADE24673	Ade24673 cDNA enco
1177	65.8	2.9	1883	10	ADP39737	Adp39737 Human cDN	1250	65.8	2.9	1883	12	ADD87498	Add87498 Human PRO
1178	65.8	2.9	1883	10	ADP53195	Adp53195 cDNA enco	1251	65.8	2.9	1883	12	ADP89164	Adp89164 Human PRO
1179	65.8	2.9	1883	10	ADP53747	Adp53747 Novel hum	1252	65.8	2.9	1883	12	ADP18503	Adp18503 Human PRO
1180	65.8	2.9	1883	10	ADP70183	Adp70183 Human cDN	1253	65.8	2.9	1883	12	ADP88812	Adp88812 Human PRO
1181	65.8	2.9	1883	10	ADP38304	Adp38304 Human cDN	1254	65.8	2.9	1883	12	ADP96518	Ade96518 Human cDN
1182	65.8	2.9	1883	10	ADP39260	Adp39260 Human cDN	1255	65.8	2.9	1883	12	ADP94832	Ade94832 cDNA enco
1183	65.8	2.9	1883	10	ADP51903	Adp51903 cDNA enco	1256	65.8	2.9	1883	12	ADP91243	Adp91243 Human PRO
1184	65.8	2.9	1883	10	ADD02702	Add02702 Human PRO	1257	65.8	2.9	1883	12	ADP25829	Adp25829 Human cDN
1185	65.8	2.9	1883	10	ADD02136	Add02136 Human PRO	1258	65.8	2.9	1883	12	ADP95384	Ade95384 cDNA enco
1186	65.8	2.9	1883	10	ADP54318	Adp54318 Novel hum	1259	65.8	2.9	1883	12	ADP24728	Adp24728 Human cDN
1187	65.8	2.9	1883	10	ADP38783	Adp38783 Human cDN	1260	65.8	2.9	1883	12	ADP29464	Adp29464 Human cDN
1188	65.8	2.9	1883	10	ADD40214	Add40214 Human cDN	1261	65.8	2.9	1883	12	ADF35075	Adf35075 cDNA enco

1262	65.8	2.9	1883	12	ADG96995	Adg96995 Human cDN	cl335	65.6	2.9	319	5	ADL38504	Adl38504 Human ova
1263	65.8	2.9	1883	12	ADG92390	Novel hum	cl336	65.6	2.9	319	5	ADI73373	Adi73373 Human ova
1264	65.8	2.9	1883	12	ADG90691	Novel hum	cl337	65.6	2.9	361	11	ACN87469	Acn87469 Breast ca
1265	65.8	2.9	1883	12	ADG91838	Novel hum	cl338	65.6	2.9	372	5	ABV37528	Abv37528 Human pro
1266	65.8	2.9	1883	12	ADG02417	Human PRO	cl339	65.6	2.9	394	5	ADL44065	Adl44065 Human ova
1267	65.8	2.9	1883	12	ADG22203	Novel hum	cl340	65.6	2.9	429	5	ABV58465	Abv58465 Human pro
1268	65.8	2.9	1883	12	ADG20273	Novel hum	cl341	65.6	2.9	442	5	ABV54422	Abv54422 Human pro
1269	65.8	2.9	1883	12	ADG98179	Human PRO	cl342	65.6	2.9	458	4	AAI88397	Aai88397 Human pol
1270	65.8	2.9	1883	12	ADG24396	Novel hum	cl343	65.6	2.9	464	4	AAH33341	Aah33341 Human col
1271	65.8	2.9	1883	12	ADG98750	Human PRO	cl344	65.6	2.9	545	13	ACN51318	Acn51318 Cotton an
1272	65.8	2.9	1883	12	ADG03581	Human PRO	cl345	65.6	2.9	604	3	ACG59787	Acg59787 Human sec
1273	65.8	2.9	1883	12	ADG99302	Human PRO	cl346	65.6	2.9	639	13	ADR59449	Adr59449 Cotton cD
1274	65.8	2.9	1883	12	ADG16887	Novel hum	cl347	65.6	2.9	1180	2	AAV84347	Aav84347 Human Apo
1275	65.8	2.9	1883	12	ADG05346	Human PRO	cl348	65.6	2.9	1180	6	ABSS3571	Abss3571 cDNA enco
1276	65.8	2.9	1883	12	ADG19613	Novel hum	cl349	65.6	2.9	1180	6	ABSS3570	Abss3570 cDNA enco
1277	65.8	2.9	1883	12	ADG13450	Novel hum	cl350	65.6	2.9	1180	10	AAAD64037	Aaad64037 Human Apo
1278	65.8	2.9	1883	12	ADG08507	Novel hum	cl351	65.6	2.9	1180	10	AAAD64038	Aaad64038 Human Apo
1279	65.8	2.9	1883	12	ADG15677	Novel hum	cl352	65.6	2.9	1285	3	ACG59828	Acg59828 Human sec
1280	65.8	2.9	1883	12	ADG97075	Human PRO	cl353	65.6	2.9	1342	3	AAA26424	Aaa26424 Human sec
1281	65.8	2.9	1883	12	ADG06260	Human PRO	cl354	65.6	2.9	1342	12	ADL71485	Adl71485 Novel hum
1282	65.8	2.9	1883	12	ADG23844	Novel hum	cl355	65.6	2.9	1401	3	AACT78016	Aact78016 Human can
1283	65.8	2.9	1883	12	ADG04133	Human PRO	cl356	65.6	2.9	2652	9	ACA98920	Ac98920 cDNA enco
1284	65.8	2.9	1883	12	ADG25034	Novel hum	cl357	65.6	2.9	5059	12	ACQ223993	Acq223993 Human sof
1285	65.8	2.9	1883	12	ADG07331	Novel hum	cl358	65.6	2.9	5216	6	ABL32347	Abi32347 Human imm
1286	65.8	2.9	1883	12	ADG07883	Novel hum	cl359	65.6	2.9	5216	6	ABL34459	Abi34459 Human met
1287	65.8	2.9	1883	12	ADG55378	Novel hum	cl360	65.6	2.9	5216	7	ADS99720	Adsg99720 Complemen
1288	65.8	2.9	1883	12	ADG61042	Novel hum	cl361	65.4	2.9	330	4	AAH69540	Aah69540 Human cer
1289	65.8	2.9	1883	12	ADG62146	Novel hum	cl362	65.4	2.9	373	8	ABX35671	Abx35671 Bovine ES
1290	65.8	2.9	1883	12	ADH03033	Human cDN	cl363	65.4	2.9	373	13	ACN50919	Acn50919 Cotton an
1291	65.8	2.9	1883	12	ADG82347	Human PRO	cl364	65.4	2.9	408	4	AAI83697	Aai83697 Human pol
1292	65.8	2.9	1883	12	ADG57586	Novel hum	cl365	65.4	2.9	413	4	AAI19684	Aai19684 Human bre
1293	65.8	2.9	1883	12	ADG57034	Novel hum	cl366	65.4	2.9	430	9	ACH41045	Ach41045 Human fo
1294	65.8	2.9	1883	12	ADG55930	Novel hum	cl367	65.4	2.9	433	4	AAI82080	Aai82080 Human pol
1295	65.8	2.9	1883	12	ADG58690	Novel hum	cl368	65.4	2.9	457	4	AAI85461	Aai85461 Human pol
1296	65.8	2.9	1883	12	ADG71056	Novel hum	cl369	65.4	2.9	525	13	ACN54429	Acn54429 Cotton pr
1297	65.8	2.9	1883	12	ADH03987	Human cDN	cl370	65.4	2.9	536	13	ACN55415	Acn55415 Cotton an
1298	65.8	2.9	1883	12	ADH033510	Human cDN	cl371	65.4	2.9	563	13	ACN47476	Acn47476 Cotton pr
1299	65.8	2.9	1883	12	ADG58138	Novel hum	cl372	65.4	2.9	578	3	AACT79470	Aact79470 cDNA sequ
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1301	65.8	2.9	1883	12	ADG71608	Novel hum	cl374	65.4	2.9	578	6	ABK29014	Abk29014 Human bre
1302	65.8	2.9	1883	12	ADG81795	Human PRO	cl375	65.4	2.9	600	11	ACN87284	Acn87284 Breast ca
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1304	65.8	2.9	1883	12	ADH12124	Novel hum	cl377	65.4	2.9	1312	6	AAD24774	Aad24774 Glycine m
1305	65.8	2.9	1883	12	ADG52546	Novel hum	cl378	65.4	2.9	1626	4	AAO21160	Aao21160 Fertiliza
1306	65.8	2.9	1883	12	ADG54274	Novel hum	cl379	65.4	2.9	1626	10	ADC29845	Adc29845 Fertiliza
1307	65.8	2.9	1883	12	ADG81243	Human PRO	cl380	65.4	2.9	1663	3	AACT59302	Acact59302 Human sec
1308	65.8	2.9	1883	12	ADG56482	Novel hum	cl381	65.4	2.9	1663	8	ABZ73679	Abz73679 Secreted
1309	65.8	2.9	1883	12	ADH12748	Novel hum	cl382	65.4	2.9	1663	8	ADA98154	Ada98154 Human sec
1310	65.8	2.9	1883	12	ADG61594	Novel hum	cl383	65.4	2.9	1663	10	ABT16860	Abt16860 Human sec
1311	65.8	2.9	1883	12	ADH28681	Human PRO	cl384	65.4	2.9	1663	10	ABZ67274	Abz67274 Human sec
1312	65.8	2.9	1883	12	ADG54826	Novel hum	cl385	65.4	2.9	1691	4	AAO33892	Aao33892 Human sec
1313	65.8	2.9	1883	12	ADG59866	Novel hum	cl386	65.4	2.9	2069	12	ADQ67271	Adq67271 Novel hum
1314	65.8	2.9	1883	12	ADH04464	Human cDN	cl387	65.4	2.9	2435	12	ADQ22529	Adq22529 Human sof
1315	65.8	2.9	1883	12	ADH04464	Human cDN	cl388	65.4	2.9	2435	12	ADQ22529	Adq22529 Human sof
1316	65.8	2.9	1883	12	ADH61465	Human cDN	cl389	65.4	2.9	2785	12	ADQ22627	Adq22627 Human sof
1317	65.8	2.9	1883	12	ADG10033	Novel hum	cl390	65.4	2.9	2785	12	ADQ22627	Adq22627 Human sof
1318	65.8	2.9	1883	12	ADL15504	Novel hum	cl391	65.4	2.9	3021	3	AACT7541	Aact7541 Human ORF
1319	65.8	2.9	1883	12	ADG09381	Novel hum	cl392	65.4	2.9	3021	3	AACT7541	Aact7541 Human ORF
1320	65.8	2.9	1883	12	ADL14836	Novel hum	cl393	65.4	2.9	3034	8	ABZ73661	Abz73661 Secreted
1321	65.8	2.9	1883	12	ADL18431	Novel hum	cl394	65.4	2.9	3034	8	ADA98146	Ada98146 Human sec
1322	65.8	2.9	1883	12	ADJ63712	Novel hum	cl395	65.4	2.9	3034	10	ABT16854	Abt16854 Human sec
1323	65.8	2.9	1883	12	ADJ77607	Human PRO	cl396	65.4	2.9	3034	10	ABZ67255	Abz67255 Human sec
1324	65.8	2.9	1883	12	ADJ65729	Novel hum	cl397	65.4	2.9	4777	9	AAI62016	Aai62016 Human cel
1325	65.8	2.9	1883	12	ADM27865	Novel hum	cl398	65.4	2.9	7295	5	AAAS85462	Aaas85462 Human cel
1326	65.8	2.9	1883	12	ADM42589	Novel hum	cl399	65.2	2.9	7295	5	AAI34678	Aai34678 Human mus
1327	65.8	2.9	1883	12	ADL94664	Human cDN	cl400	65.2	2.9	181	4	AAI34678	Aai34678 Human mus
1328	65.8	2.9	1883	12	ADM28451	Novel hum	cl401	65.2	2.9	181	8	ABX57666	Abx57666 cDNA enco
1329	65.8	2.9	1883	13	ADL95933	cDNA enco	cl402	65.2	2.9	181	8	ABX57666	Abx57666 cDNA enco
1330	65.8	2.9	1883	13	ADL95933	cDNA enco	cl403	65.2	2.9	273	12	ADL10902	Adl10902 Cat flea
1331	65.8	2.9	1883	13	ADL96485	Novel hum	cl404	65.2	2.9	273	12	ADL10902	Adl10902 Cat flea
1332	65.8	2.9	1883	13	ADL94370	Human PRO	cl405	65.2	2.9	287	11	ADL98155	Adl98155 Human tum
1333	65.8	2.9	1883	13	ADL94370	Human PRO	cl406	65.2	2.9	287	11	ADL98155	Adl98155 Human tum
1334	65.8	2.9	1883	13	ADL94370	Human PRO	cl407	65.2	2.9	318	5	ADL73647	Adl73647 Human ova
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1337	65.8	2.9	1883	13	ADL94370	Human PRO	cl410	65.2	2.9	318	5	ADL73647	Adl73647 Human ova
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1340	65.8	2.9	1883	13	ADL94370	Human PRO	cl413	65.2	2.9	318	5	ADL73647	Adl73647 Human ova
1341	65.8	2.9	1883	13	ADL94370	Human PRO	cl414	65.2	2.9	318	5	ADL73647	Adl73647 Human ova
1342	65.8	2.9	1883	13	ADL94370	Human PRO	cl415	65.2	2.9	318	5	ADL73647	Adl73647 Human ova
1343	65.8	2.9	1883	13	ADL94370	Human PRO	cl416	65.2	2.9	318	5	ADL73647	Adl73647 Human ova
1344	65.8	2.9	1883	13	ADL94370	Human PRO	cl417	65.2	2.9	318	5	ADL73647	Adl73647 Human ova
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1347	65.8	2.9	1883	13	ADL94370	Human PRO	cl420	65.2	2.9	318	5	ADL73647	Adl73647 Human ova
1348	65.8	2.9	1883	13	ADL94370	Human PRO	cl421	65.2	2.9	318	5	ADL73647	Adl73647 Human ova
1349	65.8	2.9	1883	13	ADL94370	Human PRO	cl422	65.2	2.9	318	5	ADL73647	Adl73647 Human ova
1350	65.8	2.9	1883	13	ADL94370	Human PRO	cl423	65.2	2.9	318	5	ADL73647	Adl73647 Human ova
1351	65.8	2.9	1883	13	ADL94370	Human PRO	cl424	65.2	2.9	318	5	ADL73647	Adl73647 Human ova
1352	65.8	2.9	1883	13	ADL94370	Human PRO	cl425	65.2	2.9	318	5	ADL73647	Adl73647 Human ova
1353	65.8	2.9	1883	13	ADL94370	Human PRO	cl426	65.2	2.9				

1408	1408	65.2	2.9	410	9	ACH48825	Ach48825 Human leu	1481	65.2	2.9	1734	8	ACA70739	Human sec
1409	c1409	65.2	2.9	552	13	ACN45312	Adn45312 Cotton pr	1482	65.2	2.9	1734	8	ACA95249	Novel hum
1410	c1410	65.2	2.9	566	5	ADL43620	Adl43620 Human ova	1483	65.2	2.9	1734	8	ACC86192	Human sec
1411	c1411	65.2	2.9	643	4	AAH70618	Aah70618 Human cer	1484	65.2	2.9	1734	8	ACD45174	Human sec
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1413	c1413	65.2	2.9	773	2	AAx37388	Aax37388 Human sec	1486	65.2	2.9	1734	8	ACD12672	Human sec
1414	c1414	65.2	2.9	931	12	ADM333388	Adm33388 Human PRO	1487	65.2	2.9	1734	8	ACF19902	Human sec
1415	c1415	65.2	2.9	969	11	ACN46632	Adn46632 Breast ca	1488	65.2	2.9	1734	8	ABX76846	Human PRO
1416	c1416	65.2	2.9	1493	3	AAZ43802	Aaz43802 Human adu	1489	65.2	2.9	1734	8	ACA60527	Novel hum
1417	c1417	65.2	2.9	1513	5	AAD20261	Aad20261 Rat integ	1490	65.2	2.9	1734	8	ACA73178	Novel hum
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1419	c1419	65.2	2.9	1734	4	AAF54238	Aaf54238 DNA enco	1492	65.2	2.9	1734	8	ACA74565	CDNA enco
1420	c1420	65.2	2.9	1734	4	AAC87038	Aac87038 Nucleotid	1493	65.2	2.9	1734	8	ACA04517	Novel hum
1421	c1421	65.2	2.9	1734	4	RAA546025	Raa546025 Human DNA	1494	65.2	2.9	1734	8	ACA70432	Human sec
1422	c1422	65.2	2.9	1734	4	AAF92083	Aaf92083 Human PRO	1495	65.2	2.9	1734	8	ACD14618	Human PRO
1423	c1423	65.2	2.9	1734	6	ABK33613	Abk33613 CDNA enco	1496	65.2	2.9	1734	8	ACA93722	Human CDN
1424	c1424	65.2	2.9	1734	6	ABS74403	Abt74403 Human sec	1497	65.2	2.9	1734	8	ACA68290	Novel hum
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1426	c1426	65.2	2.9	1734	8	ACA89475	Aca89475 CDNA enco	1499	65.2	2.9	1734	8	ACA67296	CDNA enco
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1471	c1471	65.2	2.9	1734	8	ACA91275	Aca91275 CDNA enco							
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1474	c1474	65.2	2.9	1734	8	ACC89757	Acc89757 Human sec							
1475	c1475	65.2	2.9	1734	8	ACC92936	Acc92936 Human sec							
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1478	c1478	65.2	2.9	1734	8	ACA69818	Aca69818 Human sec							
1479	c1479	65.2	2.9	1734	8	ACA96961	Aca96961 Novel hum							
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ALIGNMENTS

RESULT 1

ID AAA96348 standard; CDNA; 2242 BP.

XX AAA96348;

08-FEB-2001 (first entry)

DE cDNA encoding a novel polypeptide designated PRO4380.

Secreted protein; transmembrane protein; PRO1484; PRO4334; PRO1122;
PRO1889; PRO1890; PRO1887; PRO1785; PRO4353; PRO4357; PRO4405; PRO4356;
PRO4352; PRO4380; PRO4354; PRO4408; PRO5737; PRO4425; PRO5990; PRO6030;
PRO4424; PRO4422; PRO4430; PRO4499; tumour; obesity; diabetes;
insulinemia; kidney disorder; Bergers disease; nephropathy;
Schonlein-Henoch purpura; celiac disease; dermatitis herpeticiformis;
Crohn's disease; ss.

OS Homo sapiens.

Key Location/Qualifiers
CDS 201..1724

FT /*tag= a

FT /*trans_except= (pos: 888..890, aa: Ile)

FT sig_peptide 201..278

FT /*tag= b

XX WO200056889-A2.

XX 28-SEP-2000.

XX 01-MAR-2000; 2000MO-US005601.

XX 23-MAR-1999; 99US-0125774P.

XX 23-MAR-1999; 99US-0125778P.

XX 24-MAR-1999; 99US-0125826P.

XX 31-MAR-1999; 99US-0127035P.

XX 05-APR-1999; 99US-0127706P.

XX 21-APR-1999; 99US-0130359P.

XX 27-APR-1999; 99US-0131270P.

XX 27-APR-1999; 99US-0131272P.

XX 27-APR-1999; 99US-0132371P.

XX 04-MAY-1999; 99US-0132379P.

XX 04-MAY-1999; 99US-0132383P.

XX 25-MAY-1999; 99US-0135750P.

XX 08-JUN-1999; 99US-0138166P.

XX 20-JUL-1999; 99US-0144791P.

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PR 03-AUG-1999; 99US-0146970P.
PR 09-DEC-1999; 99US-0170262P.
XX
PA (GETH ) GENENTECH INC.
XX
PI Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;
PI Stewart TA, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI; 2000-628263/60.
DR P-PSDB; AAB18921.
XX
XX Novel secreted and transmembrane polypeptides useful for diagnosing tumor
PT in a mammal, for identifying agonists and antagonists of the polypeptide
PT and for therapeutic use.
XX
XX Claim 2; Fig 25; 222pp; English.
XX
XX The present sequence encodes a secreted or transmembrane polypeptide. The
CC specification describes polypeptides designated PRO1484, PRO4334,
CC PRO1122, PRO1889, PRO1890, PRO1887, PRO1785, PRO4353, PRO4357, PRO4405,
CC PRO4356, PRO4352, PRO4380, PRO4354, PRO4408, PRO5737, PRO4425, PRO5990,
CC PRO6030, PRO4424, PRO4430 and PRO4499. PRO1889 polypeptide is
CC useful for diagnosing tumour in a mammal. The polypeptides, their
CC agonists and antagonists are useful treating a condition associated with
CC expression or activity of the polypeptide. Conditions treated include
CC obesity, diabetes or hyper- or hypo-insulinemia. The polypeptides are
CC capable of inducing proliferation of mammalian kidney mesangial cells and
CC are therefore useful for treating kidney disorders associated with
CC decreased mesangial cell function such as Bergers disease or other
CC nephropathies associated with Schonlein-Henoch purpura, celiac disease,
CC dermatitis herpetiformis or Crohns disease. The nucleic acids may be used
CC to generate transgenic animals for use in development and screening of
CC therapeutically useful reagents and also for chromosome identification
CC and tissue typing
XX
SQ Sequence 2242 BP; 606 A; 540 C; 536 G; 559 T; 0 U; 1 Other;

Query Match 100.0%; Score 2241; DB 3; Length 2242;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATGAATACCTCCGAAGCGCTTTGTTCTCCAGATGTGAATAGCTCCATATACAGCC 60
DB 1 GAATGAATACCTCCGAAGCGCTTTGTTCTCCAGATGTGAATAGCTCCATATACAGCC 60

QY 61 TCGTCTTCTTCGGGGGCAACGTTGGTTCAGGCGCAGAGAGATATTTAATGTCAACCT 120
DB 61 TCGTCTTCTTCGGGGGCAACGTTGGTTCAGGCGCAGAGAGATATTTAATGTCAACCT 120

QY 121 CTGGGGCTTTTCATGGGACTCCCTCTGCCACATTTTTCGAGGTGGGAAAGTTGCTAGA 180
DB 121 CTGGGGCTTTTCATGGGACTCCCTCTGCCACATTTTTCGAGGTGGGAAAGTTGCTAGA 180

QY 181 GGCTTCAGAACTCCAGCCTAATGGATCCCAAATCCGGGAGAAATGGTGTGCTGCTGG 240
DB 181 GGCTTCAGAACTCCAGCCTAATGGATCCCAAATCCGGGAGAAATGGTGTGCTGCTGG 240

QY 241 CTGTGCTGCTGCTGCTGGAGCGGGGATGTTCTCTCACCTCCCGCCCCCGCGCG 300
DB 241 CTGTGCTGCTGCTGCTGGAGCGGGGATGTTCTCTCACCTCCCGCCCCCGCGCG 300

QY 301 TGTTAGAAGAAGTCTTCCAGTACATTCACCTCCATCAGGATGAATTTGTGCAGACGCTGA 360
DB 301 TGTTAGAAGAAGTCTTCCAGTACATTCACCTCCATCAGGATGAATTTGTGCAGACGCTGA 360

QY 361 AGAGTGGGTGGGCATCGAGAGCGACTCTGTTCAGCCTGTGCTCGTTCAGACAGAGC 420
DB 361 AGAGTGGGTGGGCATCGAGAGCGACTCTGTTCAGCCTGTGCTCGTTCAGACAGAGC 420

QY 421 TCTTCAGAAATGATGGCGTGGTGGGACACGCTGTCAGCGCTTGGGGGCGCGTGTGSCCT 480
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QY 481 CGGTGACATGGGTCTCTCAGCAGCTGCCCGATGGTTCAGAGTCTTCAATACCTCCCGTCA 540
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QY 601 AGTTCAGCCTGCTGACCGGGCGATGGTGGCTCACGGACCCCTATGTGCTGACGGAGG 660
DB 601 AGTTCAGCCTGCTGACCGGGCGATGGTGGCTCACGGACCCCTATGTGCTGACGGAGG 660

QY 661 TAGACGGGAACTTTATGACGAGGAGCGACCGACAAACAAAGGCCCTGTCTGGCTTGA 720
DB 661 TAGACGGGAACTTTATGACGAGGAGCGACCGACAAACAAAGGCCCTGTCTGGCTTGA 720

QY 721 TCAATGCTGTGAGCGCCTTCAGAGCCCTGGAGCAAGATCTTCTGTGAATATCAAAATCA 780
DB 721 TCAATGCTGTGAGCGCCTTCAGAGCCCTGGAGCAAGATCTTCTGTGAATATCAAAATCA 780

QY 781 TCAATTGAGGGGATGAAGAGGCTGCTCTGTTGCCCTCGAGGAACTTGTGGAAAGAA 840
DB 781 TCAATTGAGGGGATGAAGAGGCTGCTCTGTTGCCCTCGAGGAACTTGTGGAAAGAA 840

QY 841 AGGACCGATTTCTTCTCTGTGTGACTACATTTGTAATTTTCAGATAACCTGTGATCAGCC 900
DB 841 AGGACCGATTTCTTCTCTGTGTGACTACATTTGTAATTTTCAGATAACCTGTGATCAGCC 900

QY 901 AAAGGAGCCAGCAATCACTTATGAAACCGGGGGAACAGCTACTTCTATGTTGGAGTGA 960
DB 901 AAAGGAGCCAGCAATCACTTATGAAACCGGGGGAACAGCTACTTCTATGTTGGAGTGA 960

QY 961 AATGACAGACAGAGATTTTCACTCAGGAACCTTTGTTGGCATCTTTCATGAACCAATGG 1020
DB 961 AATGACAGACAGAGATTTTCACTCAGGAACCTTTGTTGGCATCTTTCATGAACCAATGG 1020

QY 1021 CTGATCTGTTGCTCTTCTCGGTAGCTGGTACATCTGCTGCTATATCTTGTGCTCCCTG 1080
DB 1021 CTGATCTGTTGCTCTTCTCGGTAGCTGGTACATCTGCTGCTATATCTTGTGCTCCCTG 1080

QY 1081 GAATCTATGATCAAGTGGTTCCTCTTACAGAGAGGAAATAATACATAACAAGCCATCC 1140
DB 1081 GAATCTATGATCAAGTGGTTCCTCTTACAGAGAGGAAATAATACATAACAAGCCATCC 1140

QY 1141 ATCTAGACCTAGAAATAACCGGAATAGCAGCGGGTTGAGAAATTTCTGTTCTGATACTA 1200
DB 1141 ATCTAGACCTAGAAATAACCGGAATAGCAGCGGGTTGAGAAATTTCTGTTCTGATACTA 1200

QY 1201 AGGAGAGATTTCTAATGACCTCTGAGGTACCCATCTCTTTCTATTCTATGAGATCGAG 1260
DB 1201 AGGAGAGATTTCTAATGACCTCTGAGGTACCCATCTCTTTCTATTCTATGAGATCGAG 1260

QY 1261 GCGCGTTTCATGAGCTGGAACTTAAACAGTATACCTGCGCGAGTTATAGGAAATTTT 1320
DB 1261 GCGCGTTTCATGAGCTGGAACTTAAACAGTATACCTGCGCGAGTTATAGGAAATTTT 1320

QY 1321 CAATCCGCTAGTCCCTCAATGAATGTGTCTGCGGTGGAAACACAGGTGACACGATC 1380
DB 1321 CAATCCGCTAGTCCCTCAATGAATGTGTCTGCGGTGGAAACACAGGTGACACGATC 1380

QY 1381 TTGAAGATGTTCTCTCAAAAGAAATAGTTTCAACAAAGATGGTGTGTTTCCATGACTTAG 1440
DB 1381 TTGAAGATGTTCTCTCAAAAGAAATAGTTTCAACAAAGATGGTGTGTTTCCATGACTTAG 1440

QY 1441 GACTACACCGCTGGATTTGCAAAATATTGATGACACCCAGTATCTCGCAGCAAAAGAGCGA 1500
DB 1441 GACTACACCGCTGGATTTGCAAAATATTGATGACACCCAGTATCTCGCAGCAAAAGAGCGA 1500

QY 1501 TCAGAAACAGTGTGTTGAAACAGAACCAAGATATGATCCGGGATGGATCCACATTTCCAATTG 1560
DB 1501 TCAGAAACAGTGTGTTGAAACAGAACCAAGATATGATCCGGGATGGATCCACATTTCCAATTG 1560

QY 1561 CCNAAATGTTCCAGGAGATCGTCCACAGAGCGTGGTGTAAATTCCTCGGTGGGAGCTGTTG 1620
```

Db 1561 CCAAAATGTTCCAGGAGATCTCCACAAGAGCGTGGTCTAATTCGCGTGGAGCTGTTG 1620
Qy 1621 ATGATGGAGACATTCGACAGATCAGAAAATCAACAGTGAATACATAGAGGGAACCA 1680
Db 1621 ATGATGGAGACATTCGACAGATCAGAAAATCAACAGTGAATACATAGAGGGAACCA 1680
Qy 1681 AATTATTGTCGCTCTTTCTTAGAGATGGCCAGCTCCATTATATCAAGAACTTTCTA 1740
Db 1681 AATTATTGTCGCTCTTTCTTAGAGATGGCCAGCTCCATTATATCAAGAACTTTCTA 1740
Qy 1741 GTCTGATCTGATCAGTACAGATTCACCTCCCCACATCCCTAGACAGGATGGAATGT 1800
Db 1741 GTCTGATCTGATCAGTACAGATTCACCTCCCCACATCCCTAGACAGGATGGAATGT 1800
Qy 1801 AATATATCAGAGAAATTTGGGCTAGTAGTACATTTTCCCTCCATTTAAATGTCCTTG 1860
Db 1801 AATATATCAGAGAAATTTGGGCTAGTAGTACATTTTCCCTCCATTTAAATGTCCTTG 1860
Qy 1861 GGATATCTGGATCAGTAAATAAATATTTCAAGGCACAGATGTTGGAATGGTTTAAAGGT 1920
Db 1861 GGATATCTGGATCAGTAAATAAATATTTCAAGGCACAGATGTTGGAATGGTTTAAAGGT 1920
Qy 1921 CCCCACATGACACCTTCCTCAAGTCAATAGTCTGCTGAGCAACTTGATTTCCCAAGTC 1980
Db 1921 CCCCACATGACACCTTCCTCAAGTCAATAGTCTGCTGAGCAACTTGATTTCCCAAGTC 1980
Qy 1981 CTGTGCAATAGCCACAGATTTGGATTCCTTCCACCTTTAGCATATCTCCAACTTGCA 2040
Db 1981 CTGTGCAATAGCCACAGATTTGGATTCCTTCCACCTTTAGCATATCTCCAACTTGCA 2040
Qy 2041 ATTTGATGGCATATCACTCCGCTTTGCTTTCTAGTCTCCTCAAGTCTCGTGACACATA 2100
Db 2041 ATTTGATGGCATATCACTCCGCTTTGCTTTCTAGTCTCCTCAAGTCTCGTGACACATA 2100
Qy 2101 ATCATTCATCAAGATCGCTTTGCTTTACCACTCTTTTATCTTTATTAATAA 2160
Db 2101 ATCATTCATCAAGATCGCTTTGCTTTACCACTCTTTTATCTTTATTAATAA 2160
Qy 2161 AATGTTGCTCCACCACTGCTCCCAAAAAA 2242
Db 2161 AATGTTGCTCCACCACTGCTCCCAAAAAA 2242
Qy 2221 AAAAAAAAAAAAAAAAAAAAAA 2242
Db 2221 AAAAAAAAAAAAAAAAAAAAAA 2242

RESULT 2

ACD28837
ID ACD28837 standard; cDNA; 2242 BP.
XX AC ACD28837;
XX DT 27-AUG-2003 (first entry)
XX DE Human secreted / transmembrane polypeptide PRO4380 cDNA.
XX KW Human; ss; gene; gene therapy; diabetes; obesity; hypoinsulinaemia.
XX OS Homo sapiens.
XX PN US2003027249-A1.
XX PD 06-FEB-2003.
XX PF 16-AUG-2001; 2001US-00931836.
XX PR 15-MAY-1998; 98US-0085579P.
PR 15-DEC-1998; 98US-0112514P.
PR 22-DEC-1998; 98US-0113300P.
PR 23-DEC-1998; 98US-0113430P.
PR 23-DEC-1998; 98US-0113605P.

PR 23-DEC-1998; 98US-0113621P.
PR 23-DEC-1998; 98US-0114140P.
PR 12-JAN-1999; 99US-0115552P.
PR 22-JAN-1999; 99US-0116843P.
PR 23-MAR-1999; 99US-0125774P.
PR 24-MAR-1999; 99US-0125778P.
PR 31-MAR-1999; 99US-0125826P.
PR 05-APR-1999; 99US-0127035P.
PR 13-APR-1999; 99US-0129122P.
PR 21-APR-1999; 99US-0130359P.
PR 27-APR-1999; 99US-0131270P.
PR 27-APR-1999; 99US-0131272P.
PR 04-MAY-1999; 99US-0132371P.
PR 04-MAY-1999; 99US-0132379P.
PR 04-MAY-1999; 99US-0132383P.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99US-00310733.
PR 25-MAY-1999; 99US-0135750P.
PR 08-JUN-1999; 99US-0138166P.
PR 20-JUL-1999; 99US-0144791P.
PR 03-AUG-1999; 99US-0146970P.
PR 25-AUG-1999; 99US-00380142.
PR 29-OCT-1999; 99US-0162506P.
PR 02-DEC-1999; 99US-0028551.
PR 22-DEC-1999; 99US-0030720.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 22-AUG-2000; 2000US-00644848.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001US-00869599.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.

(GETH) GENENTECH INC.

Deenoyers L, Baton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;
Stewart TA, Watanabe CK, Wood WI, Zhang Z;

WPI; 2003-492030/46.
P-PSDB; ABO19431.

New isolated, secreted and transmembrane PRO polypeptides and encoding
nucleic acids, useful for the diagnosis and treatment of disorders such
as diabetes, obesity and/or hypoinsulinaemia.

Claim 1; Fig 25; 196pp; English.

The invention relates to a new isolated nucleic acid which encodes a PRO
polypeptide. The methods and compositions of the present invention are
useful for the diagnosis and treatment of disorders associated with the
PRO polypeptides, such as diabetes, obesity and hypoinsulinaemia. The
present sequence represents cDNA encoding a human secreted and
transmembrane PRO polypeptide

Sequence 2242 BP; 606 A; 540 C; 536 G; 559 T; 0 U; 1 Other;

Query Match

100.0%; Score 2241; DB 8; Length 2242;

Best Local Similarity 100.0%; Pred. No. 0;				Matches 2242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	GAATGAATACCTCCGAAGCGCTTTGTTCTCCAGATGTGAATAGTCCACTATACAGCC	60				
Db	1	GAATGAATACCTCCGAAGCGCTTTGTTCTCCAGATGTGAATAGTCCACTATACAGCC	60				
QY	61	TCGCTCTTCTTCCGGGGGACACGCTGGGTGAGGCGACAGAGAGATATTAATGTCAACCT	120				
Db	61	TCGCTCTTCTTCCGGGGGACACGCTGGGTGAGGCGACAGAGAGATATTAATGTCAACCT	120				
QY	121	CTTGGGGCTTTATGAGACTCCCTCTGCGACATTTTTCGAGGTTGGGAAGTTGCTAGA	180				
Db	121	CTTGGGGCTTTATGAGACTCCCTCTGCGACATTTTTCGAGGTTGGGAAGTTGCTAGA	180				
QY	181	GGCTTCAGAACTCCAGCCTAATGGATCCCAAACTCGGAGAAATGGCTGCTGCCCTGG	240				
Db	181	GGCTTCAGAACTCCAGCCTAATGGATCCCAAACTCGGAGAAATGGCTGCTGCCCTGG	240				
QY	241	CTGTGCTGTGCTGCTGCTGAGCGCGGCAATGTTCTCACCTCCCGCGCCCGCGCGC	300				
Db	241	CTGTGCTGTGCTGCTGCTGAGCGCGGCAATGTTCTCACCTCCCGCGCCCGCGCGC	300				
QY	301	TGTTAGAAAGTCTTCCAGTACATTTGATCCCTCAGGATGAATTTGTGACAGCTGA	360				
Db	301	TGTTAGAAAGTCTTCCAGTACATTTGATCCCTCAGGATGAATTTGTGACAGCTGA	360				
QY	361	AGGATGGGTGGCAATCGAGCGCACTCTGTCAGGCTGTGCTCGCTTCAGAACAGAGC	420				
Db	361	AGGATGGGTGGCAATCGAGCGCACTCTGTCAGGCTGTGCTCGCTTCAGAACAGAGC	420				
QY	421	TCCTTCAGAAATGATGGCGTGGCTGCGGACACGCTGACGCGCTTGGGGCGCGTGGCCT	480				
Db	421	TCCTTCAGAAATGATGGCGTGGCTGCGGACACGCTGACGCGCTTGGGGCGCGTGGCCT	480				
QY	481	CGGTGGACATGGTCTCAGACGTGCGGATGCTCAGAGTCTTCAATACCTCCCGTCA	540				
Db	481	CGGTGGACATGGTCTCAGACGTGCGGATGCTCAGAGTCTTCAATACCTCCCGTCA	540				
QY	541	TCCTGGCGAACTTGGGAGCGATCCACGAAAGCACCGTGTGCTTCTACGGCCACTGG	600				
Db	541	TCCTGGCGAACTTGGGAGCGATCCACGAAAGCACCGTGTGCTTCTACGGCCACTGG	600				
QY	601	ACGTGACGCTGTGACCGGGCGATGGTGGCTCAGGACCCCTATGCTCAGCGAGG	660				
Db	601	ACGTGACGCTGTGACCGGGCGATGGTGGCTCAGGACCCCTATGCTCAGCGAGG	660				
QY	661	TAGACGGAACTTTATGGACGAGGCGACCGACAAAGGCGCTGTCTTGGCTTGA	720				
Db	661	TAGACGGAACTTTATGGACGAGGCGACCGACAAAGGCGCTGTCTTGGCTTGA	720				
QY	721	TCAATGCTGTGAGCGCTTCAGAGCCTTGAGCGAAGATCTTCTGTGAATATCAAAATCA	780				
Db	721	TCAATGCTGTGAGCGCTTCAGAGCCTTGAGCGAAGATCTTCTGTGAATATCAAAATCA	780				
QY	781	TCATTGAGGGATGGAGGCTGGCTGTGCTGCTGGAGGAACTTGTGAAAGAA	840				
Db	781	TCATTGAGGGATGGAGGCTGGCTGTGCTGCTGGAGGAACTTGTGAAAGAA	840				
QY	841	AGGACCGATCTTCTCTGCTGTGAGTACATTTGATTTTTCAGATAACCTGTGGATCAGCC	900				
Db	841	AGGACCGATCTTCTCTGCTGTGAGTACATTTGATTTTTCAGATAACCTGTGGATCAGCC	900				
QY	901	AAAGAGCCAGCAATCACTTATGAAACCGGGGGAACAGTACTTTCATGTTGAGGTGA	960				
Db	901	AAAGAGCCAGCAATCACTTATGAAACCGGGGGAACAGTACTTTCATGTTGAGGTGA	960				
QY	961	AATCAGAGACAGGATTTTCACTCAGGAACCTTTGGTGGCATCTTTCATGAACCAATGG	1020				
Db	961	AATCAGAGACAGGATTTTCACTCAGGAACCTTTGGTGGCATCTTTCATGAACCAATGG	1020				
QY	1021	CTGATCTGGTGTCTTCTCGGTAGCCTGGTGTGCTGCTGATTCATATCTGCTGCCCTG	1080				

1021	CTGATCTGGTGTCTTCTCGGTAGCCTGGTAGACTCGTGTGTCATATCTCGTGCCTG	1080
1081	GAATCTATGATGAAGTGGTTCCTCTTACAGAAAGGAAATAAATACATACAAAGCCATCC	1140
1081	GAATCTATGATGAAGTGGTTCCTCTTACAGAAAGGAAATAAATACATACAAAGCCATCC	1140
1141	ATCTAGACCTAGAAATACCGGAATAGCAGCGGGTTGAGAAATTTCTGTTCGATACTA	1200
1141	ATCTAGACCTAGAAATACCGGAATAGCAGCGGGTTGAGAAATTTCTGTTCGATACTA	1200
1201	AGGAGGATTTCTAATGCACTCTGGAGGTACCCATCTCTTTTATTCATGGGATCGAGG	1260
1201	AGGAGGATTTCTAATGCACTCTGGAGGTACCCATCTCTTTTATTCATGGGATCGAGG	1260
1261	GGCGTTTGTAGCTGGAATCAAAAGTATACATCTCGCGGAGTTATAGGAAATTTT	1320
1261	GGCGTTTGTAGCTGGAATCAAAAGTATACATCTCGCGGAGTTATAGGAAATTTT	1320
1321	CAATCCGCTAGTCCCTCACATGATGTGTCTGGGTGGAATAACAGGTGACAGCATC	1380
1321	CAATCCGCTAGTCCCTCACATGATGTGTCTGGGTGGAATAACAGGTGACAGCATC	1380
1381	TTGAAAGTGTGTCTCCAAAGAAATAGTTCACAAAGATGGTGTTCATGACTCTAG	1440
1381	TTGAAAGTGTGTCTCCAAAGAAATAGTTCACAAAGATGGTGTTCATGACTCTAG	1440
1441	GACTACACCGTGGATTCGCAATATTTGATGACACCCAGTATCTCGCAGCAAAAGAGGA	1500
1441	GACTACACCGTGGATTCGCAATATTTGATGACACCCAGTATCTCGCAGCAAAAGAGGA	1500
1501	TCAGAACAGTGTTCGAAACAGAACAGATATGATCCGGGATGGATCCCAATTC	1560
1501	TCAGAACAGTGTTCGAAACAGAACAGATATGATCCGGGATGGATCCCAATTC	1560
1561	CCAAATGTTCAGGAGATCGTCCAAAGAGCGTGTCTAAATCCGCTGGGAGTGTG	1620
1561	CCAAATGTTCAGGAGATCGTCCAAAGAGCGTGTCTAAATCCGCTGGGAGTGTG	1620
1621	ATGATGGAGAACATTCGAGATGAGAAATCAACAGGTGGAACTACATAGAGGAAACCA	1680
1621	ATGATGGAGAACATTCGAGATGAGAAATCAACAGGTGGAACTACATAGAGGAAACCA	1680
1681	AAATATTTGCTGCTCTTTTCTTAGAGATGGCCAGCTCCATTAATACAAAGAACCTTCTA	1740
1681	AAATATTTGCTGCTCTTTTCTTAGAGATGGCCAGCTCCATTAATACAAAGAACCTTCTA	1740
1741	GTCTGATCTGATCCATGACAGATTCACCTCCACATCCCTAGACAGGATGGAATGT	1800
1741	GTCTGATCTGATCCATGACAGATTCACCTCCACATCCCTAGACAGGATGGAATGT	1800
1801	AAATATCCAGAGAAATTTGGGTCTAGTATAGTACATTTTCCCTTCCATTTAAATGTCTTG	1860
1801	AAATATCCAGAGAAATTTGGGTCTAGTATAGTACATTTTCCCTTCCATTTAAATGTCTTG	1860
1861	GGATATCTGGATCAGTAATAAATATTTCAAAGGCAAGATGTTGAAATGTTTAAAGGT	1920
1861	GGATATCTGGATCAGTAATAAATATTTCAAAGGCAAGATGTTGAAATGTTTAAAGGT	1920
1921	CCCCACTGCACACCTTCTCAAGTCATAGCTGTTGAGCAACTTGAATTTCCCAAGTC	1980
1921	CCCCACTGCACACCTTCTCAAGTCATAGCTGTTGAGCAACTTGAATTTCCCAAGTC	1980
1981	CTGTGCAATAGCCCCAGGATTTGGATTTCCATCCCTTTTAGCATATCTCCAACTTGCA	2040
1981	CTGTGCAATAGCCCCAGGATTTGGATTTCCATCCCTTTTAGCATATCTCCAACTTGCA	2040
2041	ATTTGATGTCATTAATCACTCCGGTTGCTTTCTAGGTCCTCAAGTCTCGTACACATA	2100
2041	ATTTGATGTCATTAATCACTCCGGTTGCTTTCTAGGTCCTCAAGTCTCGTACACATA	2100
2101	ATCATTTCCATCCAAATGATCGCCTTTTACCACTCTTTTCTTTTATCTTATTAATAA	2160
2101	ATCATTTCCATCCAAATGATCGCCTTTTACCACTCTTTTCTTTTATCTTATTAATAA	2160

QY 2161 AATGTTGCTCCACCACTGCTCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2220
|||||
Db 2161 AATGTTGCTCCACCACTGCTCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2220
|||||
QY 2221 AAAAAAAAAAAAAAAAAAAAAA 2242
|||||
Db 2221 AAAAAAAAAAAAAAAAAAAAAA 2242
|||||

RESULT 3

ACA06111

ID ACA06111 standard; cDNA; 2242 BP.

XX AC ACA06111;

XX XX

XX DT 02-JUN-2003 (first entry)

XX XX

XX cDNA encoding human PRO polypeptide #13.

XX XX

Human; PRO polypeptide; secreted and transmembrane protein; cancer;
non-insulin dependent diabetes mellitus; septic shock; stroke;
rheumatoid arthritis; graft-versus-host disease; cardiac ischaemia;
psoriasis; inflammatory bowel disease; asthma; antidiabetic; cytostatic;
immunosuppressive; antirheumatic; antiarthritic; cerebroprotective;
vasotropic; antipsoriatic; antiinflammatory; antiasthmatic; gene therapy;
gene; ss.

XX OS Homo sapiens.

XX XX

XX FN US2003008348-A1.

XX XX

XX PD 09-JAN-2003.

XX XX

XX PF 26-DEC-2001; 2001US-00035855.

XX XX

PR 15-MAY-1998; 98US-0085579P.

PR 15-DEC-1998; 98US-0112514P.

PR 22-DEC-1998; 98US-0113300P.

PR 23-DEC-1998; 98US-0113430P.

PR 23-DEC-1998; 98US-0113605P.

PR 23-DEC-1998; 98US-0113621P.

PR 23-DEC-1998; 98US-0114140P.

PR 12-JAN-1999; 99US-0115552P.

PR 22-JAN-1999; 99US-0116843P.

PR 23-MAR-1999; 99US-0125774P.

PR 23-MAR-1999; 99US-0125778P.

PR 24-MAR-1999; 99US-0125846P.

PR 31-MAR-1999; 99US-0127035P.

PR 05-APR-1999; 99US-0127706P.

PR 13-APR-1999; 99US-0129122P.

PR 21-APR-1999; 99US-0130359P.

PR 27-APR-1999; 99US-0131270P.

PR 27-APR-1999; 99US-0131272P.

PR 27-APR-1999; 99US-0131291P.

PR 04-MAY-1999; 99US-0132371P.

PR 04-MAY-1999; 99US-0132379P.

PR 04-MAY-1999; 99US-0132383P.

PR 14-MAY-1999; 99US-0132383P.

PR 14-MAY-1999; 99US-0132383P.

PR 25-MAY-1999; 99US-0135750P.

PR 08-JUN-1999; 99US-0138166P.

PR 20-JUL-1999; 99US-0144791P.

PR 03-AUG-1999; 99US-0146970P.

PR 29-OCT-1999; 99US-0162506P.

PR 02-DEC-1999; 99US-0162506P.

PR 22-DEC-1999; 99US-0162506P.

PR 01-MAR-2000; 2000US-0005601.

PR 02-MAR-2000; 2000US-0005841.

PR 22-MAY-2000; 2000US-0014042.

PR 02-JUN-2000; 2000US-0015264.

PR 23-AUG-2000; 2000US-0023522.

PR 24-AUG-2000; 2000US-0023328.

PR 01-DEC-2000; 2000US-0032678.

PR 20-DEC-2000; 2000US-0034956.
PR 28-FEB-2001; 2001US-0006520.
PR 01-JUN-2001; 2001US-0017800.
PR 20-JUN-2001; 2001US-0019892.
PR 29-JUN-2001; 2001US-0021066.
PR 09-JUL-2001; 2001US-0021735.
PR 16-AUG-2001; 2001US-00931836.
XX (GETH) GENENTECH INC.

XX Deenoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;
XX Stewart TA, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2003-341326/32.
XX P-PSDB; ABU69092.

XX New PRO polypeptides and nucleic acid molecules, useful for diagnosing or
XX treating diabetes mellitus, cancers, septic shock, inflammatory bowel
XX disease or asthma, or in gene therapy, chromosome identification or
XX tissue typing.

XX Claim 2; Fig 25; 196pp; English.

XX The present invention relates to the isolation of novel human PRO
XX polypeptides, and the polynucleotide sequences encoding them. The PRO
XX polypeptides are secreted and transmembrane proteins. The PRO
XX polypeptides and polynucleotides are useful in diagnosing or treating non
XX -insulin dependent diabetes mellitus, cancers, septic shock, rheumatoid
XX arthritis, graft-versus-host disease, stroke, cardiac ischaemia,
XX psoriasis, inflammatory bowel disease or asthma. The PRO polynucleotide
XX sequences may be used as hybridisation probes in chromosome and gene
XX mapping, or in generating antisense RNA and DNA. They are also useful in
XX preparing PRO polypeptides, in assays to identify other proteins or
XX molecules involved in binding reaction, to generate transgenic animals or
XX knockout animals, which in turn are useful in the development and
XX screening of therapeutically useful reagents, for chromosome
XX identification, and tissue typing. The PRO polypeptides and nucleic acid
XX molecules are also useful in gene therapy, and as molecular weight
XX markers for protein electrophoresis purposes. Anti-PRO antibodies may be
XX used in diagnostic assays for PRO polypeptides, or for the affinity
XX purification of the polypeptides from recombinant cell culture or natural
XX sources. The present sequence represents a cDNA encoding a human PRO
XX polypeptide of the invention

XX SQ Sequence 2242 BP; 606 A; 540 C; 536 G; 559 T; 0 U; 1 Other;

Query Match 100.0%; Score 2241; DB 8; Length 2242;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATGAATACCTCCGAAGCCGCTTTGTTCTCCAGATGTGAATAGCTCCACTATACCGCC 60

Db 1 GAATGAATACCTCCGAAGCCGCTTTGTTCTCCAGATGTGAATAGCTCCACTATACCGCC 60

QY 61 TCGTCTTCTTCCGGGGGACACGTTGGGTCCAGGCACAGAGAGATATTTAATGTCAACCT 120

Db 61 TCGTCTTCTTCCGGGGGACACGTTGGGTCCAGGCACAGAGAGATATTTAATGTCAACCT 120

QY 121 CTTGGGGCTTTTCATGGGACTCCCTCTGCCACATTTTTTGGAGGTTGGGAAAGTTGCTAGA 180

Db 121 CTTGGGGCTTTTCATGGGACTCCCTCTGCCACATTTTTTGGAGGTTGGGAAAGTTGCTAGA 180

QY 181 GGCTTCAGAACTCCAGCCTAATGGATCCCAAACTCGGGAGAAATGGCTCCCTGCTGG 240

Db 181 GGCTTCAGAACTCCAGCCTAATGGATCCCAAACTCGGGAGAAATGGCTCCCTGCTGG 240

QY 241 CTGTGCTGTGCTGTCTGGAGCGGGCATGTTCTCCTCACCTCCCGCCCGCCGCGC 300

Db 241 CTGTGCTGTGCTGTCTGGAGCGGGCATGTTCTCCTCACCTCCCGCCCGCCGCGC 300

QY 301 TGTAGAGAAAGTCTTCCAGTACATTTGACCTCCATCAGGATGAATTTGTGACAGCGCTGA 360

Db 301 TGTAGAGAAAGTCTTCCAGTACATTTGACCTCCATCAGGATGAATTTGTGACAGCGCTGA 360

```
QY 361 AGAGTGGGTGGCCATCGAGAGCGACTCTGTCCAGCCTGTGCTCGCTTCAGACAGAGC 420
Db 361 AGAGTGGGTGGCCATCGAGAGCGACTCTGTCCAGCCTGTGCTCGCTTCAGACAGAGC 420
QY 421 TCTTCAGAAATGATGGCCGTGGCTGCGGACACGCTGACGCGCTGCGGGGCCGTGGCT 480
Db 421 TCTTCAGAAATGATGGCCGTGGCTGCGGACACGCTGACGCGCTGCGGGGCCGTGGCT 480
QY 481 CGGTGACATGGTCTCTCAGCAGCTGCCCGATGGTCAGAGTCTTCCAAATACCTCCGCTCA 540
Db 481 CGGTGACATGGTCTCTCAGCAGCTGCCCGATGGTCAGAGTCTTCCAAATACCTCCGCTCA 540
QY 541 TCCTGCCCGAATGCGGGAGGATCCACGAAAGGCAACGCTGTGCTTCTAGGCGCACTTGG 600
Db 541 TCCTGCCCGAATGCGGGAGGATCCACGAAAGGCAACGCTGTGCTTCTAGGCGCACTTGG 600
QY 601 ACCTGACGCTCTGACCGGGGCGATGGGTGGCTCACGACCCCTATGTGCTGACGAGG 660
Db 601 ACCTGACGCTCTGACCGGGGCGATGGGTGGCTCACGACCCCTATGTGCTGACGAGG 660
QY 661 TAGACGGGAACTTTATGACGAGGAGCGACCGACAAAGGCCCTGTCTTGGCTTGA 720
Db 661 TAGACGGGAACTTTATGACGAGGAGCGACCGACAAAGGCCCTGTCTTGGCTTGA 720
QY 721 TCAATCTGTGAGCGCTTCAGAGCCTCGGAGCAAGATCTTCTGTGAATATCAAAATTC 780
Db 721 TCAATCTGTGAGCGCTTCAGAGCCTCGGAGCAAGATCTTCTGTGAATATCAAAATTC 780
QY 781 TCATTGAGGGGATGGAAGAGCTGGCTGTGTGCTCGGAGCAACTTGTGGAAAAAGAA 840
Db 781 TCATTGAGGGGATGGAAGAGCTGGCTGTGTGCTCGGAGCAACTTGTGGAAAAAGAA 840
QY 841 AGACCCGATCTTCTGTGTGCGACTACATTTGATTAATTTTCAGATAACCTGTGGATCAGCC 900
Db 841 AGACCCGATCTTCTGTGTGCGACTACATTTGATTAATTTTCAGATAACCTGTGGATCAGCC 900
QY 901 AAAGGAGCCAGCAATCACTTATGGAACCGGGGACAGCTACTTCAATGGTGGAGTGA 960
Db 901 AAAGGAGCCAGCAATCACTTATGGAACCGGGGACAGCTACTTCAATGGTGGAGTGA 960
QY 961 AATGCAGAGACAGGATTTTCACTCAGGAACCTTTGTGGCATCTTTCATGAACCAATGG 1020
Db 961 AATGCAGAGACAGGATTTTCACTCAGGAACCTTTGTGGCATCTTTCATGAACCAATGG 1020
QY 1021 CTGATCTGGTGTCTTCTCGGTAGCTGTGATGACTCGCTGTGTGTATATCTTGGTCCCTG 1080
Db 1021 CTGATCTGGTGTCTTCTCGGTAGCTGTGATGACTCGCTGTGTGTATATCTTGGTCCCTG 1080
QY 1081 GAATCTATGATGAAGTGTCTTCTTACAGAAGGAAATAATACATACAAAGCCATCC 1140
Db 1081 GAATCTATGATGAAGTGTCTTCTTACAGAAGGAAATAATACATACAAAGCCATCC 1140
QY 1141 ATCTAGACCTAGAAATACCGGAATAGCAGCGGGTTGAGAAATTTCTGTTCGATACTA 1200
Db 1141 ATCTAGACCTAGAAATACCGGAATAGCAGCGGGTTGAGAAATTTCTGTTCGATACTA 1200
QY 1201 AGAGGAGATCTTAATGCACTCTGAGAGTACCCTCTTTCTTCTATTTCAATGGATCGAG 1260
Db 1201 AGAGGAGATCTTAATGCACTCTGAGAGTACCCTCTTTCTTCTATTTCAATGGATCGAG 1260
QY 1261 GCGGTTTGTATGAGCCTGGAACCTTAACAGCTCATACCTGCCGAGTTATAGGAAATTTT 1320
Db 1261 GCGGTTTGTATGAGCCTGGAACCTTAACAGCTCATACCTGCCGAGTTATAGGAAATTTT 1320
QY 1321 CAATCCGCTAGTCCCTCACAATGATGTCTCGGTGGAAAAACAGGTGACACGATC 1380
Db 1321 CAATCCGCTAGTCCCTCACAATGATGTCTCGGTGGAAAAACAGGTGACACGATC 1380
QY 1381 TTGAAGTGTCTTCTCAAAAGAAATAGTTCGAACAGATGGTGTTCATCACTCTAG 1440
Db 1381 TTGAAGTGTCTTCTCAAAAGAAATAGTTCGAACAGATGGTGTTCATCACTCTAG 1440
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QY 1441 GACTACACCGTGGATTCGAAATATTGATGACACCCAGTATCTCGCAGCAAAAAAGAGCGA 1500
Db 1441 GACTACACCGTGGATTCGAAATATTGATGACACCCAGTATCTCGCAGCAAAAAAGAGCGA 1500
QY 1501 TCAGAACAGTGTTCGGAACAGAACAGATATGATCCGGGATGGATCCACCATTCCAATTTG 1560
Db 1501 TCAGAACAGTGTTCGGAACAGAACAGATATGATCCGGGATGGATCCACCATTCCAATTTG 1560
QY 1561 CAAAATGTTTCAGAGATCGTCCACAGAGCGTGGTGTAAATTCGGCTGGGAGCTGTG 1620
Db 1561 CAAAATGTTTCAGAGATCGTCCACAGAGCGTGGTGTAAATTCGGCTGGGAGCTGTG 1620
QY 1621 ATGATGGAGAACATTCGCGAGATGAGAAATCAAAGGTGGAACTACATAGAGGAAACCA 1680
Db 1621 ATGATGGAGAACATTCGCGAGATGAGAAATCAAAGGTGGAACTACATAGAGGAAACCA 1680
QY 1681 AATTATTTGCTGCTTTTCTTAGAGATGGCCAGCTCCATTAATCAACAAGAACCTTCTA 1740
Db 1681 AATTATTTGCTGCTTTTCTTAGAGATGGCCAGCTCCATTAATCAACAAGAACCTTCTA 1740
QY 1741 GTCTGATCTGATCCACTGACAGATTCACCTCCGCCACATCCCTAGACAGGATGGAATGT 1800
Db 1741 GTCTGATCTGATCCACTGACAGATTCACCTCCGCCACATCCCTAGACAGGATGGAATGT 1800
QY 1801 AAATATCCAGAGAAATTTGGGTCTAGTATAGTACATTTTCCCTTCCATTTAAATGTCTTG 1860
Db 1801 AAATATCCAGAGAAATTTGGGTCTAGTATAGTACATTTTCCCTTCCATTTAAATGTCTTG 1860
QY 1861 GGATATCTGGATCAGTAAATAAATATTTCAAAGGACAGATGTTGGAATGTTTAAAGT 1920
Db 1861 GGATATCTGGATCAGTAAATAAATATTTCAAAGGACAGATGTTGGAATGTTTAAAGT 1920
QY 1921 CCCCCACTGCACACCTTCTCAAGTCATAGCTGTTGACAGCAACTTGTATTTCCCAAGTC 1980
Db 1921 CCCCCACTGCACACCTTCTCAAGTCATAGCTGTTGACAGCAACTTGTATTTCCCAAGTC 1980
QY 1981 CTGTGCAATAGCCCCAGGATTTGGATTCCTTCCAAACCTTTTAGCATATCTCCAACTTGCA 2040
Db 1981 CTGTGCAATAGCCCCAGGATTTGGATTCCTTCCAAACCTTTTAGCATATCTCCAACTTGCA 2040
QY 2041 ATTGATTTGGCATATACCTCCGGTTGCTTCTAGTCTCTCAAGTCTCTGAGTCTCGTGACATA 2100
Db 2041 ATTGATTTGGCATATACCTCCGGTTGCTTCTAGTCTCTCAAGTCTCTGAGTCTCGTGACATA 2100
QY 2101 ATCATTTCCATCCAAATGATCGCTTTGCTTTACCATCTTTTCTTTTATTTAATAA 2160
Db 2101 ATCATTTCCATCCAAATGATCGCTTTGCTTTACCATCTTTTCTTTTATTTAATAA 2160
QY 2161 AATGTTGGTCTCCACCACCTGCTCCCAAAAAAATAAAAAAATAAAAAAATAAAAAA 2220
Db 2161 AATGTTGGTCTCCACCACCTGCTCCCAAAAAAATAAAAAAATAAAAAAATAAAAAA 2220
QY 2221 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 2242
Db 2221 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 2242

RESULT 4
ACA67734
ID ACA67734 standard; cDNA; 2242 BP.
XX
AC ACA67734;
XX
DT 24-JUN-2003 (first entry)
XX
cDNA encoding human secreted polypeptide PRO4380.
Human; gene; ss; inflammatory disease; organ failure; atherosclerosis;
cardiac injury; infertility; birth defect; premature aging; AIDS; cancer;
differentiation disorder; cell adhesion disorder; skin disorder;
neural receptor disorder; diabetic complication; tissue typing.
XX
OS Homo sapiens.
```

XX US2002192751-A1.
XX 19-DEC-2002.
XX 26-DEC-2001; 2001US-00036041.
XX 15-MAY-1998; 98US-0085579P.
XX 15-DEC-1998; 98US-0112514P.
XX 22-DEC-1998; 98US-0113300P.
XX 23-DEC-1998; 98US-0113430P.
XX 23-DEC-1998; 98US-0113605P.
XX 23-DEC-1998; 98US-0113621P.
XX 23-DEC-1998; 98US-0114140P.
XX 12-JAN-1999; 99US-0115552P.
XX 22-JAN-1999; 99US-0116843P.
XX 23-MAR-1999; 99US-0125774P.
XX 23-MAR-1999; 99US-0125778P.
XX 24-MAR-1999; 99US-0125826P.
XX 31-MAR-1999; 99US-0127035P.
XX 05-APR-1999; 99US-012706P.
XX 13-APR-1999; 99US-0129122P.
XX 21-APR-1999; 99US-0130359P.
XX 27-APR-1999; 99US-0131270P.
XX 27-APR-1999; 99US-0131272P.
XX 27-APR-1999; 99US-0131291P.
XX 04-MAY-1999; 99US-0132371P.
XX 04-MAY-1999; 99US-0132379P.
XX 04-MAY-1999; 99US-0132383P.
XX 14-MAY-1999; 99WO-US010733.
XX 25-MAY-1999; 99US-0135750P.
XX 08-JUN-1999; 99US-0138166P.
XX 20-JUL-1999; 99US-0144791P.
XX 03-AUG-1999; 99US-0146970P.
XX 29-OCT-1999; 99US-0162506P.
XX 02-DEC-1999; 99WO-US028551.
XX 22-DEC-1999; 99WO-US030720.
XX 01-MAR-2000; 2000WO-US005601.
XX 02-MAR-2000; 2000WO-US005841.
XX 22-MAY-2000; 2000WO-US014042.
XX 02-JUN-2000; 2000WO-US015264.
XX 23-AUG-2000; 2000WO-US023522.
XX 24-AUG-2000; 2000WO-US023328.
XX 01-DEC-2000; 2000WO-US032678.
XX 20-DEC-2000; 2000WO-US034956.
XX 28-FEB-2001; 2001WO-US006520.
XX 01-JUN-2001; 2001WO-US017800.
XX 20-JUN-2001; 2001WO-US019692.
XX 29-JUN-2001; 2001WO-US021066.
XX 09-JUL-2001; 2001WO-US021735.
XX 16-AUG-2001; 2001US-00931836.
XX (GETH) GENENTECH INC.
XX Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;
PI Stewart TA, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2003-341079/32.
XX P-PSDB; ABU81556.
XX New secreted and transmembrane nucleic acids and polypeptides, designated
PT as PRO, useful for treating inflammation, organ failure, atherosclerosis,
PT cardiac injury, infertility, birth defects, premature aging, AIDS, or
PT cancer.
XX Claim 2; Fig 25; 195pp; English.
XX The invention relates to an isolated nucleic acid that encodes a PRO
XX polypeptide. The nucleic acids and polypeptides are useful for treating
XX inflammatory diseases, organ failure, atherosclerosis, cardiac injury,
XX infertility, birth defects, premature aging, acquired immunodeficiency
XX syndrome (AIDS), cancer, differentiation disorders, cell adhesion
XX disorders, neural receptor disorders, skin disorders or diabetic
XX

CC complications. The nucleic acids are useful as hybridisation probes, in
CC chromosome and gene mapping and in generating antisense RNA or DNA. The
CC polypeptides are useful as pharmaceuticals, diagnostics, biosensors or
CC bioreactors. Both are useful in tissue typing. The present sequence
CC represents a cDNA encoding a PRO polypeptide of the invention
XX
SQ Sequence 2242 BP; 606 A; 540 C; 536 G; 559 T; 0 U; 1 Other;
Query Match 100.0%; Score 2241; DB 9; Length 2242;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAATGAATACCTCCGAAGCGCTTTGTTCTCCAGATGTGAATAGCTCCACTATACAGCC 60
Db 1 GAATGAATACCTCCGAAGCGCTTTGTTCTCCAGATGTGAATAGCTCCACTATACAGCC 60
Qy 61 TCGTCTTCTTCGCGGGGACAAAGTGGGTGAGGCGACAGAGAGATATTTAATGTACCCCT 120
Db 61 TCGTCTTCTTCGCGGGGACAAAGTGGGTGAGGCGACAGAGAGATATTTAATGTACCCCT 120
Qy 121 CTTGGGGCTTTTCATGGGACTCCCTCTGCCACATTTTTTGGAGTTGGGAAAGTTGCTAGA 180
Db 121 CTTGGGGCTTTTCATGGGACTCCCTCTGCCACATTTTTTGGAGTTGGGAAAGTTGCTAGA 180
Qy 181 GGCTTCAGAACTCCAGCTTAATGGATCCCAAACTCGGAGAAATGGCTCCCTGCTGG 240
Db 181 GGCTTCAGAACTCCAGCTTAATGGATCCCAAACTCGGAGAAATGGCTCCCTGCTGG 240
Qy 241 CTGTGCTGTGCTGTGCTGGAGCGGCGATGTTCTCTCACCTCCCGCCCGCGGCGC 300
Db 241 CTGTGCTGTGCTGTGCTGGAGCGGCGATGTTCTCTCACCTCCCGCCCGCGGCGC 300
Qy 301 TGTTAGAGAAAGTCTTCCAGTACATTCAGCTCCATCAGGATGAATTTGTGCAGACGCTGA 360
Db 301 TGTTAGAGAAAGTCTTCCAGTACATTCAGCTCCATCAGGATGAATTTGTGCAGACGCTGA 360
Qy 361 AGGAGTGGTGGCCATCGAGAGCGACTCTGTCCAGCCTGTGCTCTTCCAGCAAGAGC 420
Db 361 AGGAGTGGTGGCCATCGAGAGCGACTCTGTCCAGCCTGTGCTCTTCCAGCAAGAGC 420
Qy 421 TCTTCAGATGATGGCGTGGCTGCGGACAGCGCTGACGCCCTGGGGGCGCGTGGGCT 480
Db 421 TCTTCAGATGATGGCGTGGCTGCGGACAGCGCTGACGCCCTGGGGGCGCGTGGGCT 480
Qy 481 CGGTGGACATGGTCTCTCAGCAGCTGCCCGATGCTCAGAGTCTTCCAATACCTCCCGTCA 540
Db 481 CGGTGGACATGGTCTCTCAGCAGCTGCCCGATGCTCAGAGTCTTCCAATACCTCCCGTCA 540
Qy 541 TCCTGGCCGAACTCTTATGGACGAGGAGCGACCCACGAAAGGCGACCGTGTGCTTCTACGGCCACTGG 600
Db 541 TCCTGGCCGAACTCTTATGGACGAGGAGCGATCCACGAAAGGCGACCGTGTGCTTCTACGGCCACTGG 600
Qy 601 ACGTGACGCTGTGACCGGGGCGATGGGTGGCTCAGGACCCCTATGTGCTGACGAGG 660
Db 601 ACGTGACGCTGTGACCGGGGCGATGGGTGGCTCAGGACCCCTATGTGCTGACGAGG 660
Qy 661 TAGACGGGAACTTTATGGACGAGGAGCGACCCACGAAAGGCGACCGTGTGCTTCTGCTTGGGA 720
Db 661 TAGACGGGAACTTTATGGACGAGGAGCGACCCACGAAAGGCGACCGTGTGCTTCTGCTTGGGA 720
Qy 721 TCAATGCTGTGAGCGCTTCAGAGCCCTCGAGAGATCTTCTCTGTAATATCAAAATCA 780
Db 721 TCAATGCTGTGAGCGCTTCAGAGCCCTCGAGAGATCTTCTCTGTAATATCAAAATCA 780
Qy 781 TCAATGAGGGGATGGAAGAGGCTGGCTCTGTTGCCCTGGAGGAACTTGTGGAAAAAGAAA 840
Db 781 TCAATGAGGGGATGGAAGAGGCTGGCTCTGTTGCCCTGGAGGAACTTGTGGAAAAAGAAA 840
Qy 841 AGGACCGATTTCTCTCTGGTGTGAGTACATTCGATTAATTTTCAGATAACCTCTGGATCAGCC 900
Db 841 AGGACCGATTTCTCTCTGGTGTGAGTACATTCGATTAATTTTCAGATAACCTCTGGATCAGCC 900
Qy 901 AAAGGAAGCCAGCAATCACTTATGGAAACCCGGGGGAAACAGCTACTTTCATGTTGGAGGTGA 960

PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 16-AUG-2001; 2001US-00931836.
XX (GETH) GENENTECH INC.
PA
XX
XX Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;
PI Stewart TA, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI; 2003-615764/58.
DR P-PSDB; ADA76582.
XX
XX Novel isolated secreted and transmembrane polypeptides, designated as PRO
PT polypeptides e.g. PRO1484, PRO4334 and PRO1122, useful for inhibiting
PT tumor cell growth, and for preparing medicaments for therapeutic use.
XX
XX Claim 2; Fig 25; 201pp; English.
XX
XX The invention describes an isolated secreted and transmembrane PRO
CC polypeptide (I), having at least 80% identity to or scoring at least 80%
CC positives when compared to, a sequence (S1) comprising 246, 440, 197, 97,
CC 273, 571, 209, 888, 502, 310, 251, 800, 507, 248, 223, 134, 136, 468,
CC 328, 221, 194, 899, or 339 amino acids fully defined in the
CC specification. An anti-(I)-antibody is useful for determining the
CC presence of (I) in a cell. (I) is useful for identifying a compound
CC capable of inhibiting the expression and/or activity of (I). (I) and the
CC antibody are useful for inhibiting the growth of tumour cells, and for
CC the preparation of a medicament useful in the treatment of a condition
CC which is responsive to (I) or the antibody. A polynucleotide (II)
CC encoding (I) is also useful for isolating full-length PRO cDNA for
CC generating transgenic animals or knock-out animals, which are, in turn,
CC are useful in the development in the screening of therapeutically useful
CC reagents, and in gene therapy. PRO is useful in assays to identify other
CC proteins or molecules involved in binding interactions, for screening
CC inhibitors or agonists of binding interactions and for screening chemical
CC libraries. (II) is useful as molecular weight marker for protein
CC electrophoresis, and as therapeutic agents. (I) or (II) is useful for
CC tissue typing and for chromosome identification. Ab is useful in
CC diagnostic assays for PRO, in affinity purification of PRO, and for
CC detection of PRO in biological samples. This sequence encodes a novel
CC human secreted and transmembrane PRO polypeptide.
XX
SQ Sequence 2242 BP; 606 A; 540 C; 536 G; 559 T; 0 U; 1 Other;

Query Match 100.0%; Score 2241; DB 9; Length 2242;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATGAATACCTCGAAGCGCTTGTCTCCAGATGTGAATAGCTCCATATACAGCC 60
DB 1 GAATGAATACCTCGAAGCGCTTGTCTCCAGATGTGAATAGCTCCATATACAGCC 60
QY 61 TCGTCTTCTCCGGGGGCAACAGTGGGTGAGGCAAGAGATATTTAATGTCAACCT 120
DB 61 TCGTCTTCTTCCGGGGGCAACAGTGGGTGAGGCAAGAGATATTTAATGTCAACCT 120
QY 121 CTTGGGGCTTTCATGGGACTCCCTCTGCCACATTTTGGAGGTGGGAAAGTGTCTAGA 180
DB 121 CTTGGGGCTTTCATGGGACTCCCTCTGCCACATTTTGGAGGTGGGAAAGTGTCTAGA 180
QY 181 GGCTTCAGAACTCCAGGCTTAATGATCCCAAACTCGGGGAAATGGCTGCCCTGCTGG 240
DB 181 GGCTTCAGAACTCCAGGCTTAATGATCCCAAACTCGGGGAAATGGCTGCCCTGCTGG 240
QY 241 CTGTGCTGTGCTGCTGTGGAGCGGCGATGTTCTCTCACCTCCCGCCCGCGCGC 300

DB 241 CTGTGCTGTGCTGCTGTGGAGCGGCGATGTTCTCTCACCTCCCGCCCGCGCGC 300
QY 301 TGTTAGAGAAAGTCTTCCAGTACATTTGACCTCCATCAGGATGAATTTGTCCAGACGCTGA 360
DB 301 TGTTAGAGAAAGTCTTCCAGTACATTTGACCTCCATCAGGATGAATTTGTCCAGACGCTGA 360
QY 361 AGGAGTGGGTGGCCATCGAGAGCGACTCTGTCCAGCGCTGTGCCTTCGCTTCAGACAAAGC 420
DB 361 AGGAGTGGGTGGCCATCGAGAGCGACTCTGTCCAGCGCTGTGCCTTCGCTTCAGACAAAGC 420
QY 421 TCTTCAGATGATGGCCGTGGCTGCGGACACCGCTGCAGCGCTGGGGGCGCGTGTGGCCT 480
DB 421 TCTTCAGATGATGGCCGTGGCTGCGGACACCGCTGCAGCGCTGGGGGCGCGTGTGGCCT 480
QY 481 CGGTGACATGGTCTCTCAGCAGCTGCCCGATGGTCTCAGAGTCTTCCAAATACCTCCCGTCA 540
DB 481 CGGTGACATGGTCTCTCAGCAGCTGCCCGATGGTCTCAGAGTCTTCCAAATACCTCCCGTCA 540
QY 541 TCCTGGCCGAACCTGGGGAGCGATCCCAAGAAAGCGACCGTGTGCTTCTACGGCCACTTGG 600
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QY 601 ACCTGAGCGCTGTGACCGGGGCGATGGGTGGCTCAGGACCCCTATGTCTCAGCGAGG 660
DB 601 ACCTGAGCGCTGTGACCGGGGCGATGGGTGGCTCAGGACCCCTATGTCTCAGCGAGG 660
QY 661 TAGACGGGAACTTTATGACGAGGAGCGACCCACAAAGCGCCCTGTCTGGCTTGGGA 720
DB 661 TAGACGGGAACTTTATGACGAGGAGCGACCCACAAAGCGCCCTGTCTGGCTTGGGA 720
QY 721 TCAATGCTGTGAGCGCTTTCAGAGCCCTGGAGCAAGATCTTCTGTGAATATCAAAATCA 780
DB 721 TCAATGCTGTGAGCGCTTTCAGAGCCCTGGAGCAAGATCTTCTGTGAATATCAAAATCA 780
QY 781 TCATTGAGGGATGGAAGAGCTGGCTGTGTCCTGGAGGAACTTGTGGAAGAAAGAA 840
DB 781 TCATTGAGGGATGGAAGAGCTGGCTGTGTCCTGGAGGAACTTGTGGAAGAAAGAA 840
QY 841 AGGACCGATTTCTCTCTGCTGTGAGTACATCTTAAATTCAGATAAATCTGTGATCAGCC 900
DB 841 AGGACCGATTTCTCTCTGCTGTGAGTACATCTTAAATTCAGATAAATCTGTGATCAGCC 900
QY 901 AAAGGAAGCCAGCAATCACTTATGGAACCGCGGGGAAACAGTACTTTCATGTTGAGGTGA 960
DB 901 AAAGGAAGCCAGCAATCACTTATGGAACCGCGGGGAAACAGTACTTTCATGTTGAGGTGA 960
QY 961 AATGAGAGACAGGATTTTCACTCAGGAACTTTGTTGGCATCTTTCATGAACCAATGG 1020
DB 961 AATGAGAGACAGGATTTTCACTCAGGAACTTTGTTGGCATCTTTCATGAACCAATGG 1020
QY 1021 CTGATCTGGTTGCTTCTTCGGGTAGCTGTGAGTCTGCTGTGCTCATATCTTGTGCTCTG 1080
DB 1021 CTGATCTGGTTGCTTCTTCGGGTAGCTGTGAGTCTGCTGTGCTCATATCTTGTGCTCTG 1080
QY 1081 GAATCTATGATGAAGTGGTTTCTCTTACAGAGAGGAAATAAATACATACAAAGCCATCC 1140
DB 1081 GAATCTATGATGAAGTGGTTTCTCTTACAGAGAGGAAATAAATACATACAAAGCCATCC 1140
QY 1141 ATCTAGACCTAGAAAGATACCGGAATAGCAGCGGGTTGAGAAATTTCTGTTCGATCTA 1200
DB 1141 ATCTAGACCTAGAAAGATACCGGAATAGCAGCGGGTTGAGAAATTTCTGTTCGATCTA 1200
QY 1201 AGGAGAGATTTCTAATGCACTCTGAGGATPACCATCTCTTTCTATTTCATGGGATCAGG 1260
DB 1201 AGGAGAGATTTCTAATGCACTCTGAGGATPACCATCTCTTTCTATTTCATGGGATCAGG 1260
QY 1261 GCCTGTTTATGATGAGCTTGAACCTAAACAGTCTATCTGCGCGAGTTATAGGAAATTTT 1320
DB 1261 GCCTGTTTATGATGAGCTTGAACCTAAACAGTCTATCTGCGCGAGTTATAGGAAATTTT 1320
QY 1321 CAATCGCTGTAGTCCCTCAGATGAATGTGTCTGGGTGGAAGAAACAGGTGACAGCATC 1380

D5 1321 CAATCCGCTAGTCCCTCACAATGATGCTGCGGTGGAAGAAACAGGTGACACGACATC 1380
QY 1381 TTGAAGATGTTCTCCAAAGAAATAGTTTCCAAAGATGTTGTTTCCATGACTCTAG 1440
D5 1381 TTGAAGATGTTCTCCAAAGAAATAGTTTCCAAAGATGTTGTTTCCATGACTCTAG 1440
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D5 1441 GACTACACCCGTGGATGCAATATATGATGACACCCAGTATCTCGAGCAAAAAGCGA 1500
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D5 1501 TCAGAACAGTGTGGAACAGAACAGATATGATCCGGATCGATCCACATTCCAATTG 1560
QY 1561 CCAAAATGTTCCAGGAGATCGTCCAAAGAGCGTGTGTAATTCGGCTGGAGCTGTG 1620
D5 1561 CCAAAATGTTCCAGGAGATCGTCCAAAGAGCGTGTGTAATTCGGCTGGAGCTGTG 1620
QY 1621 ATGATGGAGAACATTCGCAAGATGAGAAATCAACAGGTGGAACACTACATAGAGGGAACCA 1680
D5 1621 ATGATGGAGAACATTCGCAAGATGAGAAATCAACAGGTGGAACACTACATAGAGGGAACCA 1680
QY 1681 AATTATTTCTGCTTTTCTTAGAGATGCGCCAGCTCCATTAATCACAAAGAACCTTCTA 1740
D5 1681 AATTATTTCTGCTTTTCTTAGAGATGCGCCAGCTCCATTAATCACAAAGAACCTTCTA 1740
QY 1741 GTCTGATCTGATCCACTGACAGATTCACCTGCCCAATCCCTAGACAGGATGGAATGT 1800
D5 1741 GTCTGATCTGATCCACTGACAGATTCACCTGCCCAATCCCTAGACAGGATGGAATGT 1800
QY 1801 AATATCCAGAGATTTGGTCTAGTATAGTATCATTTTCCCTTCCATTTAAATGCTTG 1860
D5 1801 AATATCCAGAGATTTGGTCTAGTATAGTATCATTTTCCCTTCCATTTAAATGCTTG 1860
QY 1861 GGATATCTGATCAGTAATAAATAATTTCAAAGGCACAGATGTTGAAATGTTTAAAGT 1920
D5 1861 GGATATCTGATCAGTAATAAATAATTTCAAAGGCACAGATGTTGAAATGTTTAAAGT 1920
QY 1921 CCCCCTGACACCTTCTCAAGTATAGTCTGCTTCCAGCACTGATTTCCCAAGTC 1980
D5 1921 CCCCCTGACACCTTCTCAAGTATAGTCTGCTTCCAGCACTGATTTCCCAAGTC 1980
QY 1981 CTGTGCAATAGCCCAAGATGATTCCTTCAACCTTTTAGCATATCTCCAACTTGCA 2040
D5 1981 CTGTGCAATAGCCCAAGATGATTCCTTCAACCTTTTAGCATATCTCCAACTTGCA 2040
QY 2041 ATTTGATGTCATAATCACTCCCGTTGCTTTCTAGTCTCAAGTCTGTCGACACATA 2100
D5 2041 ATTTGATGTCATAATCACTCCCGTTGCTTTCTAGTCTCAAGTCTGTCGACACATA 2100
QY 2101 ATCATTCCTCAATGATGCTGCTTTTACCACTCTTCTTATCTTATTAATAA 2160
D5 2101 ATCATTCCTCAATGATGCTGCTTTTACCACTCTTCTTATCTTATTAATAA 2160
QY 2161 AATGTTGCTTCCACCACTGCTTCCCAAAAAAATAAAAAAATAAAAAAATAAAAAA 2220
D5 2161 AATGTTGCTTCCACCACTGCTTCCCAAAAAAATAAAAAAATAAAAAAATAAAAAA 2220
QY 2221 AAAAAAAAAAAAAAAAAAAAAA 2242
D5 2221 AAAAAAAAAAAAAAAAAAAAAA 2242

RESULT 6
ACD42296
ID ACD42296 standard; cDNA; 2242 BP.

XX ACD42296;

XX 05-SEP-2003 (first entry)

XX Human cDNA encoding secreted/transmembrane protein PRO4380.

KW Human; ss; gene; PRO; secreted protein; transmembrane protein;
KW septic shock; gene therapy.

XX Homo sapiens.

XX US2003044842-A1.

XX 06-MAR-2003.

XX 26-DEC-2001; 2001US-00036160.

XX 15-MAY-1998; 98US-0085579P.

XX 15-DEC-1998; 98US-0112514P.

XX 22-DEC-1998; 98US-0113300P.

XX 23-DEC-1998; 98US-0113430P.

XX 23-DEC-1998; 98US-0113605P.

XX 23-DEC-1998; 98US-0113621P.

XX 23-DEC-1998; 98US-0114140P.

XX 12-JAN-1999; 99US-0115552P.

XX 22-JAN-1999; 99US-0116843P.

XX 23-MAR-1999; 99US-0125774P.

XX 23-MAR-1999; 99US-0125778P.

XX 24-MAR-1999; 99US-0125826P.

XX 31-MAR-1999; 99US-0127035P.

XX 05-APR-1999; 99US-0127706P.

XX 13-APR-1999; 99US-0129122P.

XX 21-APR-1999; 99US-0130359P.

XX 27-APR-1999; 99US-0131270P.

XX 27-APR-1999; 99US-0131272P.

XX 27-APR-1999; 99US-0131291P.

XX 04-MAY-1999; 99US-0132371P.

XX 04-MAY-1999; 99US-0132379P.

XX 04-MAY-1999; 99US-0132383P.

XX 14-MAY-1999; 99US-0132703P.

XX 25-MAY-1999; 99US-0132750P.

XX 08-JUN-1999; 99US-0138166P.

XX 20-JUL-1999; 99US-0144791P.

XX 03-AUG-1999; 99US-0146970P.

XX 29-OCT-1999; 99US-0162506P.

XX 02-DEC-1999; 99US-028551.

XX 22-DEC-1999; 99US-030720.

XX 01-MAR-2000; 2000US-005601.

XX 02-MAR-2000; 2000US-005841.

XX 22-MAY-2000; 2000US-0014042.

XX 02-JUN-2000; 2000US-0015264.

XX 23-AUG-2000; 2000US-0023522.

XX 24-AUG-2000; 2000US-0023328.

XX 01-DEC-2000; 2000US-0032678.

XX 20-DEC-2000; 2000US-0034956.

XX 28-FEB-2001; 2001US-0006520.

XX 01-JUN-2001; 2001US-0017800.

XX 20-JUN-2001; 2001US-0019692.

XX 29-JUN-2001; 2001US-0021066.

XX 09-JUL-2001; 2001US-0021735.

XX 16-AUG-2001; 2001US-00931836.

(GETH) GENENTECH INC.

Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;

Stewart TA, Watanabe CK, Wood WI, Zhang Z;

WPI; 2003-492260/46.

P-PSDB; ABO25139.

Novel secreted and transmembrane polypeptide for identifying agonists or antagonists of polypeptide, and as molecular weight markers.

Claim 2; Fig 25; 195pp; English.

The invention relates to an isolated, secreted and transmembrane polypeptide, termed PRO polypeptide, PRO having at least 80 % sequence identity to any one of the 23 100-900 residue amino acid sequences, given in the specification or to a sequence encoded by a nucleic acid molecule

CC deposited under any one of the ATCC accession numbers given in the
 CC specification. Also included are an isolated nucleic acid molecule having
 CC at least 80 % sequence identity to any one of 23 400-3500 nucleotide
 CC sequences given in the specification, (or a nucleotide sequence encoding
 CC PRO, a full-length PRO coding sequence, a full-length coding sequence of
 CC DNA deposited under any ATCC accession number given in the specification)
 CC or at least 80 % identity to a nucleotide sequence encoding PRO, lacking
 CC its associated signal peptide, a sequence encoding extracellular domain
 CC of PRO with or without its associated signal peptide, a vector comprising
 CC the PRO nucleic acid, a host cell comprising the vector, preparation of
 CC PRO, a chimeric molecule comprising PRO fused to a heterologous amino
 CC acid sequence and an anti-PRO antibody. PRO is useful for identifying
 CC ant/agonists or antagonists of PRO, preparing a variant of PRO, as
 CC molecular weight markers and PRO nucleic acid is useful for recombinantly
 CC expressing those markers. PRO is also useful as therapeutic agent. PRO is
 CC useful in assays to identify molecules or proteins which bind to PRO and
 CC for identifying inhibitors of PRO. PRO nucleic acid is useful as a
 CC hybridisation probe, in chromosome and gene mapping, in generation of
 CC antisense RNA and DNA, for generating transgenic animals or knockout
 CC animals which in turn are useful in the development and screening of
 CC therapeutically useful reagents. PRO nucleic acid is also useful in
 CC mapping the gene which encodes the PRO and for the genetic analysis of
 CC individuals with genetic disorders, in gene therapy, for chromosome
 CC identification, as chromosome marker, and for generating probes for PCR,
 CC Northern analysis, Southern analysis and Western analysis. The antibody
 CC useful in diagnostic assays for PRO, for affinity purification of PRO,
 CC and for treating septic shock. PRO or the antibody is useful for the
 CC preparation of medicament for treating conditions which is responsive to
 CC the PRO polypeptide or anti-PRO antibody. PRO and PRO nucleic acid are
 CC useful for tissue typing. The present sequence encodes a PRO protein
 XX
 SQ Sequence 2242 BP; 606 A; 540 C; 536 G; 559 T; 0 U; 1 Other;

Query March 100.0%; Score 2241; DB 9; Length 2242;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATGAATACCTCCGAGCGCTTTGTTCTCCAGATGTGAATAGCTCCACTATACCAGCC 60
 DB 1 GAATGAATACCTCCGAGCGCTTTGTTCTCCAGATGTGAATAGCTCCACTATACCAGCC 60

QY 61 TCGTCTTCTCCGGGGGCAACGTTGGGTGAGGCAAGAGATATTAATGTCAACCT 120
 DB 61 TCGTCTTCTTCCGGGGGCAACGTTGGGTGAGGCAAGAGATATTAATGTCAACCT 120

QY 121 CTTGGGGCTTTCATGGGACTCCCTCTGCCACATTTTTTGGAGGTTGGGAAAGTTGTCTAGA 180
 DB 121 CTTGGGGCTTTCATGGGACTCCCTCTGCCACATTTTTTGGAGGTTGGGAAAGTTGTCTAGA 180

QY 181 GGCTTCAGAACTCCAGGCTTAATGGATCCCAAACTCCGGGAAATGGCTCGCTCCCTGTGG 240
 DB 181 GGCTTCAGAACTCCAGGCTTAATGGATCCCAAACTCCGGGAAATGGCTCGCTCCCTGTGG 240

QY 241 CTGTGCTGTGCTGTCTGGAGCGGGAATGTTCTCTCACTCCCGCGCCCGCGCGC 300
 DB 241 CTGTGCTGTGCTGTCTGGAGCGGGAATGTTCTCTCACTCCCGCGCCCGCGCGC 300

QY 301 TGTTAGAGAAAGTCTCCAGTACATTCACCTCCATCAGGATGAATTTGTGCAGACGCTGA 360
 DB 301 TGTTAGAGAAAGTCTCCAGTACATTCACCTCCATCAGGATGAATTTGTGCAGACGCTGA 360

QY 361 AGAGTGGGTGGCCATCGAGAGGACTCTGTCTCCAGCCTGTGCGCTTCAGACAAGAGC 420
 DB 361 AGAGTGGGTGGCCATCGAGAGGACTCTGTCTCCAGCCTGTGCGCTTCAGACAAGAGC 420

QY 421 TCTTCAGAAATGATGGCGTGGTGGGACACGCTGACGCGCTGGGGGCGCGTGTGSCCT 480
 DB 421 TCTTCAGAAATGATGGCGTGGTGGGACACGCTGACGCGCTGGGGGCGCGTGTGSCCT 480

QY 481 CGGTGGACATGGGTTCCTCAGCAGTCCCGATGGTGTGAGCTTCCAAATACCTCCCGTCA 540
 DB 481 CGGTGGACATGGGTTCCTCAGCAGTCCCGATGGTGTGAGCTTCCAAATACCTCCCGTCA 540

QY 541 TCCTGGCCGAACCTGGGGAGCGATCCACGAAAGCACCCTGTGTCTTCTACGGCCACTTGG 600
 DB 541 TCCTGGCCGAACCTGGGGAGCGATCCACGAAAGCACCCTGTGTCTTCTACGGCCACTTGG 600

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 DB 661 TAGACGGGAACCTTTATGGACGAGGAGCGACCGACCAACAAAGGCCCTGTCTTGGCTTGA 720

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 DB 721 TCAATGCTGTGAGCGCTTCAGAGCCCTGGAGCAAGATCTTCTGTGAATATCAAAATCA 780

QY 781 TCATTTAGGGGATGGAAGAGCGCTCTGTTGCCCTGGAGGAACTTGTGTGAAAGAAA 840
 DB 781 TCATTTAGGGGATGGAAGAGCGCTCTGTTGCCCTGGAGGAACTTGTGTGAAAGAAA 840

QY 841 AGGACCGATTTCTCTCTGGTGTGAGCTACATTTGTAATTTTCAGATAAACCCTGTGGATCAGCC 900
 DB 841 AGGACCGATTTCTCTCTGGTGTGAGCTACATTTGTAATTTTCAGATAAACCCTGTGGATCAGCC 900

QY 901 AAAGGAAGCCAGCAATCACTTTATGGAAACCCGGGGGAAACAGCTACTTTCATGTGGAGTGA 960
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QY 961 AATGCAAGACCAAGATTTTCACTCAGGAAACCTTTGGTGGCATCTTTCATGAACCAATGG 1020
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 DB 1201 AGGAGAGATTTCTAATGCACTCTGGAGTACCCTCTCTTTCTATTTCATGGGATCCAGG 1260

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 DB 1381 TTCAAGATGTGTCTCCAAAGAAATAGTTCCCAACAGATGGTTGTTTCCATGACTCTAG 1440

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 DB 1441 GACTACACCGGTGGATTTGCAATATTTGATGACACCCAGTATCTCGCAGCAAAAAGACGA 1500

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 DB 1501 TCAGAACAGTGTGGAACAGAACCCAGATATGATCCGGGATGGATCCACCATTTCCAATTTG 1560

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Db 1621 ATGATGGAGAACATTGCGAGAAATGAGAAATCAACAGGTGGAACTACATAGAGGAAACA 1680
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Db 1681 AATTATTTGCTGCTTTTCTTTAGAGATGGCCAGCTCCATTAAATCAACAAGAACCTTCTA 1740
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Db 1741 GTCTGATCTGATCCATGACAGATTCACTCCCTCCCAACATCCCTAGACAGGGATGGAATG 1800
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Db 1801 AAATATCCAGAGAAATTTGGGTCTAGTATAGTACATTTTCCCTTCCATTTAAATGCTCTG 1860
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Db 1861 GGATATCTGGATCAGTAATAATAATATTTCAAAAGGCACAGATGTTGAAATGGTTAAAGT 1920
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Db 1921 CCCCCACTGCACACTTCTCAAGTCATAGCTGCTTGCAGCAACTTGATTTCCCAAGTC 1980
QY 1981 CTGTGCAATGAGCCCAAGGATGGATTCCTTCCAAACCTTTTAGCATATCTCCAACCTTGCA 2040
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Db 2101 ATCATTTCCATCCATGATGCTTGTGCTTACACCTTTTACACCTTTTCTTATTAATAA 2160
QY 2161 AATGTTGTTGCTCCACCACTGCTCCCAAAAAAATAAAAAAAAAAAAAAAAAAAAAA 2220
Db 2161 AATGTTGTTGCTCCACCACTGCTCCCAAAAAAATAAAAAAAAAAAAAAAAAAAAAA 2220
QY 2221 AAAAAAAAAAAAAAAAAAAAAA 2242
Db 2221 AAAAAAAAAAAAAAAAAAAAAA 2242

RESULT 7
AAD59362
ID AAD59362 standard; cdna; 2242 BP.

AC AAD59362;
DT 18-DEC-2003 (first entry)
XX Human PRO4380 cdna.
DE Human; PRO protein; inflammation; nephropathy; bone disorder; arthritis;
KW cartilage disorder; diabetes; gene therapy; antisense therapy; gene; ds.
XX Homo sapiens.
XX Key Location/Qualifiers
FH CDS 201..1724
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FT /product= "Human PRO protein"
FT sig_peptide 201..278
FT /*tag= b
FT mat_peptide 279..1721
FT /*tag= c
FT /product= "Mature human PRO protein"
XX US2003049733-A1.
XX 13-MAR-2003.
XX

PF 26-DEC-2001; 2001US-00035958.
XX 15-MAY-1998; 98US-0085579P.
PR 15-DEC-1998; 98US-0112514P.
PR 22-DEC-1998; 98US-0113300P.
PR 23-DEC-1998; 98US-0113430P.
PR 23-DEC-1998; 98US-0113605P.
PR 23-DEC-1998; 98US-0113621P.
PR 23-DEC-1998; 98US-0114140P.
PR 12-JAN-1999; 99US-0115552P.
PR 22-JAN-1999; 99US-0116843P.
PR 23-MAR-1999; 99US-0125774P.
PR 23-MAR-1999; 99US-0125778P.
PR 24-MAR-1999; 99US-0125828P.
PR 31-MAR-1999; 99US-0127035P.
PR 05-APR-1999; 99US-0127066P.
PR 13-APR-1999; 99US-0129122P.
PR 21-APR-1999; 99US-0130359P.
PR 27-APR-1999; 99US-0131270P.
PR 27-APR-1999; 99US-0131272P.
PR 27-APR-1999; 99US-0131291P.
PR 04-MAY-1999; 99US-0132371P.
PR 04-MAY-1999; 99US-0132379P.
PR 04-MAY-1999; 99US-0132383P.
PR 14-MAY-1999; 99US-0135750P.
PR 25-MAY-1999; 99US-0135750P.
PR 08-JUN-1999; 99US-0138166P.
PR 20-JUL-1999; 99US-0144791P.
PR 03-AUG-1999; 99US-0146970P.
PR 29-OCT-1999; 99US-0162506P.
PR 02-DEC-1999; 99US-02028551.
PR 22-DEC-1999; 99US-02030720.
PR 01-MAR-2000; 2000US-0005601.
PR 02-MAR-2000; 2000US-0005841.
PR 22-MAY-2000; 2000US-0014042.
PR 02-JUN-2000; 2000US-0015264.
PR 23-AUG-2000; 2000US-0023222.
PR 24-AUG-2000; 2000US-0023328.
PR 01-DEC-2000; 2000US-0032678.
PR 20-DEC-2000; 2000US-0034956.
PR 28-FEB-2001; 2001US-0006520.
PR 01-JUN-2001; 2001US-0017800.
PR 20-JUN-2001; 2001US-0019692.
PR 29-JUN-2001; 2001US-0021066.
PR 09-JUL-2001; 2001US-0021735.
PR 16-AUG-2001; 2001US-00931836.
XX (GETH) GENENTECH INC.
XX Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;
PI Stewart TA, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2003-585109/55.
DR P-PSDB; AAE39109.
XX New isolated, secreted and transmembrane PRO polypeptides and nucleic
PT acids, useful for diagnosing, preventing and/or treating inflammation,
PT nephropathies, bone and cartilage disorders, and diabetes.
XX Claim 2; Fig 25; 203pp; English.
PS The invention relates to an isolated nucleic acid that encodes a PRO
CC polypeptide. The methods and compositions of the present invention are
CC useful for the diagnosis, prevention and/or treatment of inflammation,
CC nephropathies, bone and cartilage disorders, such as arthritis and
CC disorders that affect glucose or free fatty acid (FFA) uptake, such as
CC diabetes, hypoinulinaemia or hyperinsulinaemia. The PRO polypeptides are
CC also useful as molecular weight markers or for chromosome identification.
CC The PRO genes are useful as hybridisation probes or for screening
CC libraries of human cdna, genomic DNA or mRNA. The PRO genes may also be
CC used in gene therapy and antisense therapy. The present sequence is human
CC PRO cdna

SQ	Sequence	2242 BP; 606 A; 540 C; 536 G; 559 T; 0 U; 1 Other;
	Query Match	100.0%; Score 2241; DB 10; Length 2242;
	Best Local Similarity	100.0%; Pred. No. 0;
	Matches 2242; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Qy	1	GAATGAATACCTCCGAAGCGCTTTGTTCTCCAGATGTGAATAGCTCCACTATACACGACC 60
Db	1	GAATGAATACCTCCGAAGCGCTTTGTTCTCCAGATGTGAATAGCTCCACTATACACGACC 60
Qy	61	TCGTCTTCCTCCGGGGGACAACTGGGTGAGGACAGAGAGATATTTAATGTCACCT 120
Db	61	TCGTCTTCCTCCGGGGGACAACTGGGTGAGGACAGAGAGATATTTAATGTCACCT 120
Qy	121	CTTGGGCTTTCATGGGACTCCCTCTGCCACATTTTGGAGGTTGGAAAGTTGCTAGA 180
Db	121	CTTGGGCTTTCATGGGACTCCCTCTGCCACATTTTGGAGGTTGGAAAGTTGCTAGA 180
Qy	181	GGCTTCAGAACTCCAGGCTTAATGGATCCAAACTCGGGAGAAATGGCTGCCCTGCTGG 240
Db	181	GGCTTCAGAACTCCAGGCTTAATGGATCCAAACTCGGGAGAAATGGCTGCCCTGCTGG 240
Qy	241	CTGTGCTGCTGCTGCTGAGCGCGGATGTTCTCTCAGCTCCCTCCCGCCCGCGGC 300
Db	241	CTGTGCTGCTGCTGCTGAGCGCGGATGTTCTCTCAGCTCCCTCCCGCCCGCGGC 300
Qy	301	TGTTAGAGAAAGTCTCCAGTACATTCAGCTCCATCAGGATGAATTTGTGAGACGCTGA 360
Db	301	TGTTAGAGAAAGTCTCCAGTACATTCAGCTCCATCAGGATGAATTTGTGAGACGCTGA 360
Qy	361	AGGAGTGGGTGGCCATCGAGACGACTCTGTCCAGCCTGTGCCCTCGCTTCAGACAGAGC 420
Db	361	AGGAGTGGGTGGCCATCGAGACGACTCTGTCCAGCCTGTGCCCTCGCTTCAGACAGAGC 420
Qy	421	TCCTCAGAAATGATGGCGTGGCTGCGGACAGCTGAGCGCTGGGGGCGCGTGTGCCT 480
Db	421	TCCTCAGAAATGATGGCGTGGCTGCGGACAGCTGAGCGCTGGGGGCGCGTGTGCCT 480
Qy	481	CGGTGGACATGGGTCTCAGCAGCTGCCGATGTCAGAGTCTTCCAAATACCTCCCGTCA 540
Db	481	CGGTGGACATGGGTCTCAGCAGCTGCCGATGTCAGAGTCTTCCAAATACCTCCCGTCA 540
Qy	541	TCCTGGCCGAATCGGGAGCGATCCCAAGAGCACCGTGTGCTTCTACGGCCACTTGG 600
Db	541	TCCTGGCCGAATCGGGAGCGATCCCAAGAGCACCGTGTGCTTCTACGGCCACTTGG 600
Qy	601	ACGTGAGCTGCTGACCGGGGCGATGGGTGCTCAGGACCCCTATGTGCTGACGGAG 660
Db	601	ACGTGAGCTGCTGACCGGGGCGATGGGTGCTCAGGACCCCTATGTGCTGACGGAG 660
Qy	661	TAGACGGGAACTTTATGGACGAGGAGCGACCGACAAAGCCCTGTCTTGGCTTGA 720
Db	661	TAGACGGGAACTTTATGGACGAGGAGCGACCGACAAAGCCCTGTCTTGGCTTGA 720
Qy	721	TCAATGCTGTGAGCGCTTCAGAGCCTCGGACGAAGATCTTCTGTGAATATCAAAATCA 780
Db	721	TCAATGCTGTGAGCGCTTCAGAGCCTCGGACGAAGATCTTCTGTGAATATCAAAATCA 780
Qy	781	TCATTGAGGGGATGGAAGAGCTGGCTCTGTGGCTCGGAGGAACTTGTGGAAAGAAA 840
Db	781	TCATTGAGGGGATGGAAGAGCTGGCTCTGTGGCTCGGAGGAACTTGTGGAAAGAAA 840
Qy	841	AGGACCGATTTCTCTGTGTGTGACTACATTTGTAATTTCCAGATAACCTGTGATCAGCC 900
Db	841	AGGACCGATTTCTCTGTGTGTGACTACATTTGTAATTTCCAGATAACCTGTGATCAGCC 900
Qy	901	AAAGGAAGCCAGCAATCACTTATGGAACCCGGGGGAAACAGTACTTTCATGGTGGAGTGA 960
Db	901	AAAGGAAGCCAGCAATCACTTATGGAACCCGGGGGAAACAGTACTTTCATGGTGGAGTGA 960
Qy	961	AATGCAGAGACCAAGATTTTCACTCAGGAACCTTTGGTGGCATCTTTCATGAACCAATGG 1020
Db	961	AATGCAGAGACCAAGATTTTCACTCAGGAACCTTTGGTGGCATCTTTCATGAACCAATGG 1020

Qy	1021	CTGATCTGGTTGCTCTTCTCGGTAGCCTGGTAGCTCGTCTGTGTCATATCTCGTGTCCCTG 1080
Db	1021	CTGATCTGGTTGCTCTTCTCGGTAGCCTGGTAGCTCGTCTGTGTCATATCTCGTGTCCCTG 1080
Qy	1081	GAATCTATGATGAAGTGGTTCCCTCTTACAGAAGAGGAAATAAATACATACAAAGCCATCC 1140
Db	1081	GAATCTATGATGAAGTGGTTCCCTCTTACAGAAGAGGAAATAAATACATACAAAGCCATCC 1140
Qy	1141	ATCTAGACCTAGAGAATAACCGGAATAGCAGCGGGTTGAGAAATTTCTGTTCGATACTA 1200
Db	1141	ATCTAGACCTAGAGAATAACCGGAATAGCAGCGGGTTGAGAAATTTCTGTTCGATACTA 1200
Qy	1201	AGGAGGAGATTTCTAATGCACTCTGAGAGGTACCCATCTCTTTCTATTTCATGGGATCCAGG 1260
Db	1201	AGGAGGAGATTTCTAATGCACTCTGAGAGGTACCCATCTCTTTCTATTTCATGGGATCCAGG 1260
Qy	1261	GCAGCTTTGATGAGCCTGGAACTAAACACGTCTATACCTGGCCGAGTTATAGGAAAATTTT 1320
Db	1261	GCAGCTTTGATGAGCCTGGAACTAAACACGTCTATACCTGGCCGAGTTATAGGAAAATTTT 1320
Qy	1321	CAATCCGTCTAGTCCCTCAGATGAAATGTGTCTGGGTGGAAAAACAGGTGACAGCATC 1380
Db	1321	CAATCCGTCTAGTCCCTCAGATGAAATGTGTCTGGGTGGAAAAACAGGTGACAGCATC 1380
Qy	1381	TTCAAGATGTGTCTCCAAAGAAATAGTTTCCAAAGATGTTTCCAAAGATGTTTCCATGACTCTAG 1440
Db	1381	TTCAAGATGTGTCTCCAAAGAAATAGTTTCCAAAGATGTTTCCAAAGATGTTTCCATGACTCTAG 1440
Qy	1441	GACTACACCGGTGGATTTGCAAAATATTGATGACACCCAGTATCTCGCAGCAAAAAAGAGCGA 1500
Db	1441	GACTACACCGGTGGATTTGCAAAATATTGATGACACCCAGTATCTCGCAGCAAAAAAGAGCGA 1500
Qy	1501	TCAGAACAGTGTGGAAACAGAACAGATATGATCCGGATGATCCACCATTTCCAAATTTG 1560
Db	1501	TCAGAACAGTGTGGAAACAGAACAGATATGATCCGGATGATCCACCATTTCCAAATTTG 1560
Qy	1561	CCAAATGTTCCAGGAGATCGTCCAAAGAGCGTGTGCTAAATTTCCGCTGGGAGCTGTG 1620
Db	1561	CCAAATGTTCCAGGAGATCGTCCAAAGAGCGTGTGCTAAATTTCCGCTGGGAGCTGTG 1620
Qy	1621	ATGATGGAGAACATTCGAGAATGAGAAAAACAACAGGTGGAACTACATAGAGGAAACCA 1680
Db	1621	ATGATGGAGAACATTCGAGAATGAGAAAAACAACAGGTGGAACTACATAGAGGAAACCA 1680
Qy	1681	AATTATTTGCTGCTTTTCTTAGAGATGSCCAGCTCCATTAATTCACAAAGACCTTCTA 1740
Db	1681	AATTATTTGCTGCTTTTCTTAGAGATGSCCAGCTCCATTAATTCACAAAGACCTTCTA 1740
Qy	1741	GTCTGATCTGATCCACTGCAGATTCACCTTCCCTCCCATCCCTAGACAGGATGGAATGT 1800
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Qy	1801	AAATATCCAGAGAAATTTGGGTCTAGTATAGTACATTTTCCCTTCCATTTAAATGTCTTG 1860
Db	1801	AAATATCCAGAGAAATTTGGGTCTAGTATAGTACATTTTCCCTTCCATTTAAATGTCTTG 1860
Qy	1861	GGATATCTGGATCAGTAAATAAATAATTTCAAAGGACAGATGTTGAAATGTTTAAGGT 1920
Db	1861	GGATATCTGGATCAGTAAATAAATAATTTCAAAGGACAGATGTTGAAATGTTTAAGGT 1920
Qy	1921	CCCCCACTGCACACCTTCTCCTCAAGTCATAGCTGCTTGCAGCACTTCTGATTTCCCAAGTC 1980
Db	1921	CCCCCACTGCACACCTTCTCCTCAAGTCATAGCTGCTTGCAGCACTTCTGATTTCCCAAGTC 1980
Qy	1981	CTGTGCAATAGCCCCAGGATTTGATTTCTTCCAACTTTTTCAGATATCTCCAACTTTGCA 2040
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Qy	2041	ATTTGATTTGGCATAAATCACTCCCGTTTGTCTTCTAGGTCTCAAGTCTCTGTCACACATA 2100
Db	2041	ATTTGATTTGGCATAAATCACTCCCGTTTGTCTTCTAGGTCTCTCAAGTCTCTGTCACACATA 2100

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2101	ATCATTCATCAATGATCGCCTTGGCTTTACCACTCTTTCTCTTTATCTTATTATAAA	2160
2161	AATGTTGGTCTCCACCACTGCTCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2220
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2221	AAAAAAAAAAAAAAAAAAAAA 2242	
2221	AAAAAAAAAAAAAAAAAAAAA 2242	
RESULT 8		
AAD59237		
ID	AAD59237 standard; cDNA; 2242 BP.	
XX	AC AAD59237;	
AC	AC AAD59237;	
DT	18-DEC-2003 (first entry)	
DT	Human PRO4380 cDNA.	
DE	Human; diagnosis; inflammation; nephropathy; bone disorder; arthritis;	
KW	cartilage disorder; hypoinulinaemia; hyperinsulinaemia; gene therapy;	
KW	antisease therapy; diabetes; PRO; gene; ss.	
XX	Homo sapiens.	
OS	Homo sapiens.	
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FT	mat_peptide	279..1721
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XX	US2003049734-A1.	
PN	13-MAR-2003.	
XX	26-DEC-2001; 2001US-00036150.	
XX	15-MAY-1998; 98US-0085579P.	
PR	15-DEC-1998; 98US-0112514P.	
PR	22-DEC-1998; 98US-0113300P.	
PR	23-DEC-1998; 98US-0113430P.	
PR	23-DEC-1998; 98US-0113605P.	
PR	23-DEC-1998; 98US-0113621P.	
PR	23-DEC-1998; 98US-0114140P.	
PR	12-JAN-1999; 99US-0115552P.	
PR	22-JAN-1999; 99US-0116843P.	
PR	23-MAR-1999; 99US-0125774P.	
PR	23-MAR-1999; 99US-0125778P.	
PR	24-MAR-1999; 99US-0125826P.	
PR	31-MAR-1999; 99US-0127035P.	
PR	05-APR-1999; 99US-0127706P.	
PR	13-APR-1999; 99US-0129122P.	
PR	21-APR-1999; 99US-0130359P.	
PR	27-APR-1999; 99US-0131270P.	
PR	27-APR-1999; 99US-0131272P.	
PR	27-APR-1999; 99US-0131291P.	
PR	04-MAY-1999; 99US-0132371P.	
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PR	04-MAY-1999; 99US-0132383P.	
PR	14-MAY-1999; 99WO-US010733.	
PR	25-MAY-1999; 99US-0135750P.	
PR	08-JUN-1999; 99US-0138166P.	
PR	20-JUL-1999; 99US-0144791P.	
PR	03-AUG-1999; 99US-0146970P.	
PR	29-OCT-1999; 99US-0162506P.	

Db 361 AGGAGTGGGTGGCCATCGAGCGGACTCTGTCCAGCCCTGTGCTCCGCTTCAGACAAGAGC 420
Qy 421 TCTTCAGAAATGATCGCGTGGCTGCGGACACGCTGCGAGCGCTGGGGGCCCGTGTGSCCT 480
Db 421 TCTTCAGAAATGATCGCGTGGCTGCGGACACGCTGCGAGCGCTGGGGGCCCGTGTGSCCT 480
Qy 481 CGGTGGACATGGGTCTCTCAGCAGCTGCCCGATGGTCCAGAGTCTTCCAATACCTCCCGTCA 540
Db 481 CGGTGGACATGGGTCTCTCAGCAGCTGCCCGATGGTCCAGAGTCTTCCAATACCTCCCGTCA 540
Qy 541 TCCCTGGCCGAACTGGGGAGGATCCACGAAAGCAGCGTGTGCTTACGGCCACTTGG 600
Db 541 TCCCTGGCCGAACTGGGGAGGATCCACGAAAGCAGCGTGTGCTTACGGCCACTTGG 600
Qy 601 ACCTGCACTGCTGACCGGGGCGATGGGTGGCTCACGGACCCCTATGTGCTGACGGAGG 660
Db 601 ACCTGCACTGCTGACCGGGGCGATGGGTGGCTCACGGACCCCTATGTGCTGACGGAGG 660
Qy 661 TAGACGGGAACTTTATGGACGAGGCGACCGCAACAAAGGCCCTGTCTTGGCTTGGGA 720
Db 661 TAGACGGGAACTTTATGGACGAGGCGACCGCAACAAAGGCCCTGTCTTGGCTTGGGA 720
Qy 721 TCAATGCTGTGAGCGCCTTCAGAGCCCTGAGCAGAGATCTTCTGTGAATATCAAAATTC 780
Db 721 TCAATGCTGTGAGCGCCTTCAGAGCCCTGAGCAGAGATCTTCTGTGAATATCAAAATTC 780
Qy 781 TCATTGAGGGGATGGAAAGAGCTGGCTCTGTGCTGGAGGAACTTGTGGAAGAAAGAA 840
Db 781 TCATTGAGGGGATGGAAAGAGCTGGCTCTGTGCTGGAGGAACTTGTGGAAGAAAGAA 840
Qy 841 AGGACCGAATCTTCTCTGCTGTGAGCTACATTTGTAATTTTTCAGATAACCTGTGGATCAGCC 900
Db 841 AGGACCGAATCTTCTCTGCTGTGAGCTACATTTGTAATTTTTCAGATAACCTGTGGATCAGCC 900
Qy 901 AAAGGAAGCCAGCAATCACTATTGGAACCCGGGGGAAACAGCTACTTCATGGTGAGGTGA 960
Db 901 AAAGGAAGCCAGCAATCACTATTGGAACCCGGGGGAAACAGCTACTTCATGGTGAGGTGA 960
Qy 961 AATGCAAGACACAGGATTTTCACTCAGGAACCTTTGGTGGCACTCTTCATGAACCAATGG 1020
Db 961 AATGCAAGACACAGGATTTTCACTCAGGAACCTTTGGTGGCACTCTTCATGAACCAATGG 1020
Qy 1021 CTGATCTGGTGTCTTCTCGGTAGCCTGGTAGACTCGTCTGGTCAATCTCGTCCCTG 1080
Db 1021 CTGATCTGGTGTCTTCTCGGTAGCCTGGTAGACTCGTCTGGTCAATCTCGTCCCTG 1080
Qy 1081 GAATCTATGATGAAGTGGTTCCTCTTACAGAGAGGAAATATAACATACAAAGCCATCC 1140
Db 1081 GAATCTATGATGAAGTGGTTCCTCTTACAGAGAGGAAATATAACATACAAAGCCATCC 1140
Qy 1141 ATCTAGACCTAGAAATACCGGAATAGCAGCGGGTTGAGAAATTTCTGTTGATACTA 1200
Db 1141 ATCTAGACCTAGAAATACCGGAATAGCAGCGGGTTGAGAAATTTCTGTTGATACTA 1200
Qy 1201 AGGAGGAGATTTCTAATGACCTCTGGAGGTACCCATCTCTTTCTATTTCATGGGATCGAGG 1260
Db 1201 AGGAGGAGATTTCTAATGACCTCTGGAGGTACCCATCTCTTTCTATTTCATGGGATCGAGG 1260
Qy 1261 GCGGTTTGTATGAGCTGGAACTAAACAGTCACTACCTGGCCGAGTTATAGGAAATTTT 1320
Db 1261 GCGGTTTGTATGAGCTGGAACTAAACAGTCACTACCTGGCCGAGTTATAGGAAATTTT 1320
Qy 1321 CAATCGTCTAGTCCCTCACATGAATGTCTGCGGTGGAAACACAGGTGACACGACATC 1380
Db 1321 CAATCGTCTAGTCCCTCACATGAATGTCTGCGGTGGAAACACAGGTGACACGACATC 1380
Qy 1381 TTGAAGATGTGTTCTCCAAAGAAATAGTTCACACAGATGGTGTGTTTCCATGACTCTAG 1440
Db 1381 TTGAAGATGTGTTCTCCAAAGAAATAGTTCACACAGATGGTGTGTTTCCATGACTCTAG 1440
Qy 1441 GACTACACCGGTGATTTGGAATATTTGATGACACCCAGTATCTCGAGCAAAAGAGCGGA 1500
Db 1441 GACTACACCGGTGATTTGGAATATTTGATGACACCCAGTATCTCGAGCAAAAGAGCGGA 1500

Qy 1501 TCAGAACAGTGTGTTGGAAACAGAACCCAGATATGATCCGGGATGGATCCACCATTTCCAATTG 1560
Db 1501 TCAGAACAGTGTGTTGGAAACAGAACCCAGATATGATCCGGGATGGATCCACCATTTCCAATTG 1560
Qy 1561 CCAAAATGTTCCAGGAGATCGTCCACAAGAGCGTGTGCTAAATTCCTCGGAGCTGTG 1620
Db 1561 CCAAAATGTTCCAGGAGATCGTCCACAAGAGCGTGTGCTAAATTCCTCGGAGCTGTG 1620
Qy 1621 ATGATGGAGAACATTCGACAGAAATGAGAAATCAACAGGTGGAACCTACATAGAGGGAACCA 1680
Db 1621 ATGATGGAGAACATTCGACAGAAATGAGAAATCAACAGGTGGAACCTACATAGAGGGAACCA 1680
Qy 1681 AATTATTTGCTGCTTTTCTTAGAGATGGCCAGCTCCATTAAATCAACAAGAACCTTCTA 1740
Db 1681 AATTATTTGCTGCTTTTCTTAGAGATGGCCAGCTCCATTAAATCAACAAGAACCTTCTA 1740
Qy 1741 GTCTGATCTGATCCACTGACAGATTCACCTCCCCACATCCCTAGACAGGATGGAATGT 1800
Db 1741 GTCTGATCTGATCCACTGACAGATTCACCTCCCCACATCCCTAGACAGGATGGAATGT 1800
Qy 1801 AAATATCCAGAGAAATTTGGGTCTAGTATAGTACATTTTCCCTTCCATTTAAATGTCTTG 1860
Db 1801 AAATATCCAGAGAAATTTGGGTCTAGTATAGTACATTTTCCCTTCCATTTAAATGTCTTG 1860
Qy 1861 GGATATCTGGATCAGTAATAAATAATTTCAAAGGCACAGATGTTGGAAATGGTTTAAAGGT 1920
Db 1861 GGATATCTGGATCAGTAATAAATAATTTCAAAGGCACAGATGTTGGAAATGGTTTAAAGGT 1920
Qy 1921 CCCCCACTGCACACCTTCTCCTCAAGTCAATAGCTGCTTGCAGCAACTTGATTTCCCAAGTC 1980
Db 1921 CCCCCACTGCACACCTTCTCCTCAAGTCAATAGCTGCTTGCAGCAACTTGATTTCCCAAGTC 1980
Qy 1981 CTGTGCAATAGCCCGCAGGATGGATTCCTTCCAACTTTTAGCATATCTCAACCTTTGCA 2040
Db 1981 CTGTGCAATAGCCCGCAGGATGGATTCCTTCCAACTTTTAGCATATCTCAACCTTTGCA 2040
Qy 2041 AATTGATTTGGCATAAATCACTCCGCTTGTCTTAGTCTCTCAAGTCTCTGAGACATA 2100
Db 2041 AATTGATTTGGCATAAATCACTCCGCTTGTCTTAGTCTCTCAAGTCTCTGAGACATA 2100
Qy 2101 ATCATTTCCATCCAAATGATCGCTTTGCTTTACCACTCTTTCTTTTATCTTATTAATAA 2160
Db 2101 ATCATTTCCATCCAAATGATCGCTTTGCTTTACCACTCTTTCTTTTATCTTATTAATAA 2160
Qy 2161 AATGTTGGTCTCCACCACTGCTCCCAAAAAAAGGAAAAAAAAAAAAAAAAAAAAA 2220
Db 2161 AATGTTGGTCTCCACCACTGCTCCCAAAAAAAGGAAAAAAAAAAAAAAAAAAAAA 2220
Qy 2221 AAAAAAAAAAAAAAAAAAAAAA 2242
Db 2221 AAAAAAAAAAAAAAAAAAAAAA 2242

RESULT 9

ADC29812

ID ADC29812 standard; cDNA; 2242 BP.

XX ADC29812;

XX 18-DEC-2003 (first entry)

DT

XX

XX

DE Novel human secreted and transmembrane protein PRO4380 cDNA.

XX

KW human; secreted and transmembrane protein; P80; vulnery; antiarthritic;

KW antidiabetic; anorectic; antianemic; dermatological; antiinflammatory;

KW antiallergic; immunosuppressive; gastrointestinal;

KW chondrocyte cell differentiation; glucose uptake stimulator;

KW pancreatic beta cell differentiation; mesangial cell proliferation;

KW tissue typing; chromosome identification; gene therapy;

KW chromosome mapping; gene mapping; sports injury; arthritis; diabetes;

KW obesity; hyper-insulinaemia; hypo-insulinaemia; thalassaemia;

KW Berger disease; Schonlein-Henoch purpura; celiac disease;

PR	27-APR-1999;	99US-0131291P.	Db	1	GAATGAATACCTCCGAGCGCTTTGTTCCAGATGTGAATAGTCCACTATACAGCC	60
PR	04-MAY-1999;	99US-0132371P.	Qy	61	TCGTCCTTCCTCCGGGGGACAAACGTGGGTAGGGGACAGAGAGATATTTAATGTACACCT	120
PR	04-MAY-1999;	99US-0132379P.	Db	61	TCGTCTTCCTTCCTCCGGGGGACAAACGTGGGTAGGGGACAGAGAGATATTTAATGTACACCT	120
PR	14-MAY-1999;	99WO-US010733.	Qy	121	CTTGGGGCTTTTCATGGGACTCCCTCTGCCACATTTTTTGGAGGTGGGAAAGTGTCTAGA	180
PR	08-JUN-1999;	99US-0135750P.	Db	121	CTTGGGGCTTTTCATGGGACTCCCTCTGCCACATTTTTTGGAGGTGGGAAAGTGTCTAGA	180
PR	20-JUL-1999;	99US-0144791P.	Qy	181	GGCTTCAGAACTCCAGCCCTAATGATCCAAACTCGGAGAAATGGCTCGTCCCTGCTGG	240
PR	03-AUG-1999;	99US-0146970P.	Db	181	GGCTTCAGAACTCCAGCCCTAATGATCCAAACTCGGAGAAATGGCTCGTCCCTGCTGG	240
PR	29-OCT-1999;	99US-0162506P.	Qy	241	CTGTGCTGCTGCTGTGAGCGCGCATGTTCTCTCACCTCCCGCGCGCGCGCGC	300
PR	02-DEC-1999;	99WO-US028551.	Db	241	CTGTGCTGCTGCTGTGAGCGCGCATGTTCTCTCACCTCCCGCGCGCGCGCGC	300
PR	22-DEC-1999;	99WO-US030720.	Qy	301	TGTTAGAGAAAGTCTTCCAGTACATTGACCTCCATCAGGATGAATTTGTGCAGACGCTGA	360
PR	01-MAR-2000;	2000WO-US005841.	Db	301	TGTTAGAGAAAGTCTTCCAGTACATTGACCTCCATCAGGATGAATTTGTGCAGACGCTGA	360
PR	02-MAR-2000;	2000WO-US014042.	Qy	361	AGGAGTGGGTGCCATCGAGAGCGACTCTGTCCAGCTGTGCCTCGCTTCAGACAAGAGC	420
PR	22-MAY-2000;	2000WO-US015264.	Db	361	AGGAGTGGGTGCCATCGAGAGCGACTCTGTCCAGCTGTGCCTCGCTTCAGACAAGAGC	420
PR	23-AUG-2000;	2000WO-US023522.	Qy	421	TCCTTCAGATGATGCGCTGCTGGGACAGCTGCAGCGCTGGGGCGCGCTGTGGGCT	480
PR	24-AUG-2000;	2000WO-US023328.	Db	421	TCCTTCAGATGATGCGCTGCTGGGACAGCTGCAGCGCTGGGGCGCGCTGTGGGCT	480
PR	01-DEC-2000;	2000WO-US032678.	Qy	481	CGGTGGACATGGGTCTCTCAGCAGCTGCCCGATGGTTCAGAGTCTTCAATACCTCCGCTCA	540
PR	20-DEC-2000;	2000WO-US034956.	Db	481	CGGTGGACATGGGTCTCTCAGCAGCTGCCCGATGGTTCAGAGTCTTCAATACCTCCGCTCA	540
PR	28-FEB-2001;	2001WO-US006520.	Qy	541	TCCTGCCGAACTGGGGAGCGATCCACGAAAGGACCGTGTGCTTCTACGGCCACTTGG	600
PR	01-JUN-2001;	2001WO-US017800.	Db	541	TCCTGCCGAACTGGGGAGCGATCCACGAAAGGACCGTGTGCTTCTACGGCCACTTGG	600
PR	20-JUN-2001;	2001WO-US019692.	Qy	601	ACGTGCAGCTCTGACCGGGCGGATGGGTGCTCAGCGACCCCTATGTGCTGACGGAGG	660
PR	29-JUN-2001;	2001WO-US021066.	Db	601	ACGTGCAGCTCTGACCGGGCGGATGGGTGCTCAGCGACCCCTATGTGCTGACGGAGG	660
PR	09-JUL-2001;	2001WO-US021735.	Qy	661	TAGACGGGAACTTTATGGAACGAGGAGCGACGACAAAGAGCCCTGTCTGGCTTGA	720
PR	16-AUG-2001;	2001US-00931836.	Db	661	TAGACGGGAACTTTATGGAACGAGGAGCGACGACAAAGAGCCCTGTCTGGCTTGA	720
XX	(GETH) GENENTECH INC.		Qy	721	TCATGCTGTGAGCGCTTCAGAGCCCTGGAGCAAGATCTTCTGTGAATATCAAAATCA	780
XX	Deenoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;		Db	721	TCATGCTGTGAGCGCTTCAGAGCCCTGGAGCAAGATCTTCTGTGAATATCAAAATCA	780
XX	Stewart TA, Watanabe CK, Wood WI, Zhang Z;		Qy	781	TCATTCAGGGGATGGAAGAGGCTGGCTCTGTTGCCCTGGAGGAACCTTGTGAAAAAGAAA	840
XX	WPI; 2003-341962/32.		Db	781	TCATTCAGGGGATGGAAGAGGCTGGCTCTGTTGCCCTGGAGGAACCTTGTGAAAAAGAAA	840
XX	P-PSDB; ABU69115.		Qy	841	AGGACCGATCTTCTCTGCTGTGGACTACATTTGTAATTTTCAGATAACCTGTGGATCAGCC	900
XX	Novel isolated PRO polypeptides e.g., PRO4334, PRO1122, PRO1889, PRO1890,		Db	841	AGGACCGATCTTCTCTGCTGTGGACTACATTTGTAATTTTCAGATAACCTGTGGATCAGCC	900
XX	PRO1887, PRO1785, PRO4353, useful for treating sports injuries,		Qy	901	AAAGGAAGCCAGCAATCACTTATGGAACCCGGGGAAACAGTACTTCTATGTTGGAGGTGA	960
XX	arthritis, diabetes, obesity, hyper- or hypo-insulinemia.		Db	901	AAAGGAAGCCAGCAATCACTTATGGAACCCGGGGAAACAGTACTTCTATGTTGGAGGTGA	960
XX	Claim 2; Fig 25; 194pp; English.		Qy	961	AATGCAGAGACCAAGGATTTTCACTCAGGAACCTTTGGTGGCATCTTTCATGAACCAATGG	1020
XX	The present invention relates to the isolation of novel human PRO		Db	961	AATGCAGAGACCAAGGATTTTCACTCAGGAACCTTTGGTGGCATCTTTCATGAACCAATGG	1020
XX	polypeptides, and the polynucleotide sequences encoding them. The PRO		Qy	1021	CTGATCTGTTGCTCTTCTCGGTAGCTGCTGAGACTCGTCTGCTGATATCTCTGCTCCCTG	1080
XX	polypeptides are secreted and transmembrane proteins. The PRO		Db	1021	CTGATCTGTTGCTCTTCTCGGTAGCTGCTGAGACTCGTCTGCTGATATCTCTGCTCCCTG	1080
XX	polypeptides and polynucleotides are useful in diagnosing or treating		Qy	1081	GAATCTATGATGAAGTGGTTCCTCTTACAGAGAGGAAATAAATACATACAAAGCATCC	1140
XX	various bone and/or cartilage disorders (e.g. sports injuries,					
XX	arthritis), various insulin deficient states (e.g. diabetes mellitus,					
XX	hypo-insulinaemia), obesity, hyper-insulinaemia, haemoglobin-associated					
XX	disorders (e.g. thalassaemias), kidney disorders associated with					
XX	decreased mesangial cell function (e.g. Berger disease), or other					
XX	nephropathies associated with Schönlein-Henoch purpura, celiac disease,					
XX	dermatitis herpetiformis or Crohn's disease. The PRO polynucleotide					
XX	sequences may be used as hybridisation probes in chromosome and gene					
XX	mapping, or in generating antisense RNA and DNA. They are also useful in					
XX	preparing PRO polypeptides, in assays to identify other proteins or					
XX	molecules involved in binding reaction, to generate transgenic animals or					
XX	knockout animals, which in turn are useful in the development and					
XX	screening of therapeutically useful reagents, for chromosome					
XX	identification, and tissue typing. The PRO polypeptides and nucleic acid					
XX	molecules are also useful in gene therapy, and as molecular weight					
XX	markers for protein electrophoresis purposes. Anti-PRO antibodies may be					
XX	used in diagnostic assays for PRO polypeptides, or for the affinity					
XX	purification of the polypeptides from recombinant cell culture or natural					
XX	sources. The present sequence represents a cDNA encoding a human PRO					
XX	polypeptide of the invention					
XX	Sequence 2242 BP; 606 A; 540 C; 536 G; 559 T; 0 U; 1 Other;					
XX	Query Match 100.0%; Score 2241; DB 10; Length 2242;					
XX	Best Local Similarity 100.0%; Pred. No. 0;					
XX	Matches 2242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy	1	GAATGAATACCTCCGAGCGCTTTGTTCTCCAGATGTGAATAGTCCACTATACAGCC				

Db 1081 GAATCTATGATCAAGTGGTCTCTCTTACAGAGAGAAATAAATACATACAAAGCCATCC 1140
Qy 1141 ATCTAGACCTAGAGAAATACCGGATAGCAGCGGTTGAGAAATTTCTGTTGCATACTA 1200
Db 1141 ATCTAGACCTAGAGAAATACCGGATAGCAGCGGTTGAGAAATTTCTGTTGCATACTA 1200
Qy 1201 AGGAGGAGATCTTAATGCACTCTCTGGAGTACCCATCTCTTTCTATTATCGGATCGAGG 1260
Db 1201 AGGAGGAGATCTTAATGCACTCTCTGGAGTACCCATCTCTTTCTATTATCGGATCGAGG 1260
Qy 1261 GCGGTTTGTAGAGCTGGAACCTAAACAGTACATACCTGGCGGATTAAGGAAAAATTTT 1320
Db 1261 GCGGTTTGTAGAGCTGGAACCTAAACAGTACATACCTGGCGGATTAAGGAAAAATTTT 1320
Qy 1321 CAATCCGCTAGTCCCTCACATGAATGCTCGGTTGGAAGAAACAGTGACAGCATC 1380
Db 1321 CAATCCGCTAGTCCCTCACATGAATGCTCGGTTGGAAGAAACAGTGACAGCATC 1380
Qy 1381 TTGAAGATGTGTTCTCCAAAAAGAAATAGTTCACCAAGATGTTGTTTCCATGACTCTAG 1440
Db 1381 TTGAAGATGTGTTCTCCAAAAAGAAATAGTTCACCAAGATGTTGTTTCCATGACTCTAG 1440
Qy 1441 GACTACACCCGTGATTCGAAATATGATGACACCCAGTATCTCGAGCAAAAAAGAGCGA 1500
Db 1441 GACTACACCCGTGATTCGAAATATGATGACACCCAGTATCTCGAGCAAAAAAGAGCGA 1500
Qy 1501 TCAGAACAGTGTGTTGGACAGAACAGATATGATCCGGATGGATCCACCATTCCTCAATTG 1560
Db 1501 TCAGAACAGTGTGTTGGACAGAACAGATATGATCCGGATGGATCCACCATTCCTCAATTG 1560
Qy 1561 CCAAAATGTTCCAGGAGATCGTCCACAGAGCGTGTGTTAAATTCGCGTGGAGCTGTG 1620
Db 1561 CCAAAATGTTCCAGGAGATCGTCCACAGAGCGTGTGTTAAATTCGCGTGGAGCTGTG 1620
Qy 1621 ATGATGAGAACATTCGAGAAATGAGAAATCAACAGGTGAACTACATAGAGGGAACCA 1680
Db 1621 ATGATGAGAACATTCGAGAAATGAGAAATCAACAGGTGAACTACATAGAGGGAACCA 1680
Qy 1681 AATTATTGCTGCTTTTCTAGAGATGGCCAGCTCCATTATCAAGAACTTCTA 1740
Db 1681 AATTATTGCTGCTTTTCTAGAGATGGCCAGCTCCATTATCAAGAACTTCTA 1740
Qy 1741 GTCTGATCTGATCCACTGACAGATTCACCTCCCTCCACATCCCTAGACAGGATGGAATGT 1800
Db 1741 GTCTGATCTGATCCACTGACAGATTCACCTCCCTCCACATCCCTAGACAGGATGGAATGT 1800
Qy 1801 AAATATCCAGAGAAATTTGGGCTAGTATAGTACATTTTCCCTCCATTTAAATGCTTTG 1860
Db 1801 AAATATCCAGAGAAATTTGGGCTAGTATAGTACATTTTCCCTCCATTTAAATGCTTTG 1860
Qy 1861 GGATATCTGGATCAGTAATAAATATTTCAAGGCACAGATGTTGGAATGCTTTAAGGT 1920
Db 1861 GGATATCTGGATCAGTAATAAATATTTCAAGGCACAGATGTTGGAATGCTTTAAGGT 1920
Qy 1921 CCCCACCTGACACCTTCTCAAGTCATAGTGTGTCAGCAAACTTGATTTCCCAAGTC 1980
Db 1921 CCCCACCTGACACCTTCTCAAGTCATAGTGTGTCAGCAAACTTGATTTCCCAAGTC 1980
Qy 1981 CTGTGCAATAGCCCCAGATTTGGATTCCTCCAACTTTTAGCATATCTCCAACTTTGCA 2040
Db 1981 CTGTGCAATAGCCCCAGATTTGGATTCCTCCAACTTTTAGCATATCTCCAACTTTGCA 2040
Qy 2041 ATTTGATTTGGCATATCACTCCGTTTCTCTAGTCTCTCAAGTCTCGTGACACATA 2100
Db 2041 ATTTGATTTGGCATATCACTCCGTTTCTCTAGTCTCTCAAGTCTCGTGACACATA 2100
Qy 2101 ATCATTCATCCAAATGATCGCTTTGCTTTTACCACTCTTCTCTTTTATTAATAAAA 2160
Db 2101 ATCATTCATCCAAATGATCGCTTTGCTTTTACCACTCTTCTCTTTTATTAATAAAA 2160
Qy 2161 AATGTTGCTCTCCACCACTGCTCCCAAAAAAATAAAAAAATAAAAAAATAAAAAA 2220
Db 2161 AATGTTGCTCTCCACCACTGCTCCCAAAAAAATAAAAAAATAAAAAAATAAAAAA 2220

Qy 2221 AAAAAAAAAAAAAAAAAAAAAA 2242
Db 2221 AAAAAAAAAAAAAAAAAAAAAA 2242

RESULT 11

ADF09255
ID ADF09255 standard; cDNA; 2242 BP.

XX ADF09255;

XX 12-FEB-2004 (first entry)

XX Human secreted and transmembrane protein PRO4380 cDNA.

XX cytosolic; gene therapy; human; secreted and transmembrane; PRO; cancer;
KW tumour; chromosome mapping; gene mapping; therapeutic reagent; gene; ss.

XX Homo sapiens.

XX US2003134327-A1.

XX 17-JUL-2003.

XX 26-DEC-2001; 2001US-00035977.

XX 15-MAY-1998; 98US-0085579P.

XX 15-DEC-1998; 98US-0112514P.

XX 22-DEC-1998; 98US-0113300P.

XX 23-DEC-1998; 98US-0113430P.

XX 23-DEC-1998; 98US-0113605P.

XX 23-DEC-1998; 98US-0113621P.

XX 23-DEC-1998; 98US-011440P.

XX 12-JAN-1999; 99US-0115552P.

XX 22-JAN-1999; 99US-0116843P.

XX 23-MAR-1999; 99US-0125774P.

XX 23-MAR-1999; 99US-0125778P.

XX 24-MAR-1999; 99US-0125826P.

XX 31-MAR-1999; 99US-0127035P.

XX 05-APR-1999; 99US-0127706P.

XX 13-APR-1999; 99US-0129122P.

XX 21-APR-1999; 99US-0130359P.

XX 27-APR-1999; 99US-0131270P.

XX 27-APR-1999; 99US-0131272P.

XX 27-APR-1999; 99US-0131291P.

XX 04-MAY-1999; 99US-0132371P.

XX 04-MAY-1999; 99US-0132379P.

XX 04-MAY-1999; 99US-0132383P.

XX 14-MAY-1999; 99US-0132383P.

XX 25-MAY-1999; 99US-0135750P.

XX 08-JUN-1999; 99US-0138166P.

XX 20-JUL-1999; 99US-0144791P.

XX 03-AUG-1999; 99US-0162506P.

XX 02-DEC-1999; 99US-0162506P.

XX 22-DEC-1999; 99US-0162506P.

XX 01-MAR-2000; 2000US-0005601.

XX 02-MAR-2000; 2000US-0005601.

XX 22-MAY-2000; 2000US-0014042.

XX 02-JUN-2000; 2000US-0015264.

XX 23-AUG-2000; 2000US-0023522.

XX 24-AUG-2000; 2000US-0023522.

XX 01-DEC-2000; 2000US-0032678.

XX 20-DEC-2000; 2000US-0034956.

XX 28-FEB-2001; 2001US-0006520.

XX 01-JUN-2001; 2001US-0017800.

XX 20-JUN-2001; 2001US-0019692.

XX 29-JUN-2001; 2001US-0021066.

XX 09-JUL-2001; 2001US-0021735.

XX 16-AUG-2001; 2001US-00231836.

(GETH) GENENTECH INC.

PA

XX Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Fan J;
PI Stewart TA, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2004-031325/03.
DR P-PSDB; ADF09256.
XX Twenty three nucleic acids encoding PRO polypeptides, useful in
PT chromosome and gene mapping, in generating antisense RNA and DNA and in
PT gene therapy.
XX Claim 2; SEQ ID NO 56; 261pp; English.
XX The invention describes 23 nucleic acids encoding human secreted and
CC transmembrane PRO polypeptides. The PRO polypeptides and nucleic acids
CC are useful for the therapeutic treatment of cancerous tumours. The PRO
CC polynucleotide is useful in molecular biology, including uses as
CC hybridisation probes, in chromosome and gene mapping, in generating
CC antisense RNA and DNA, and in gene therapy. The polynucleotide may also
CC be used in preparing PRO polypeptides by recombinant techniques, and in
CC generating either transgenic animals or knock-out animals which, in turn,
CC are useful in the development and screening of therapeutically useful
CC reagents. This sequence encodes novel human secreted and transmembrane
CC protein PRO1484.
XX SQ Sequence 2242 BP; 606 A; 540 C; 536 G; 559 T; 0 U; 1 Other;
Query Match 100.0%; Score 2241; DB 12; Length 2242;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAATGAATACCTCGAAGCGCTTTGTTCTCCAGATGTGAATAGCTCCACTATACCAGCC 60
DB 1 GAATGAATACCTCGAAGCGCTTTGTTCTCCAGATGTGAATAGCTCCACTATACCAGCC 60
QY 61 TCGTCTTCCTTCGGGGGCAACAGTGGTCCAGGCAAGAGAGATATTTAATGTCAACCT 120
DB 61 TCGTCTTCCTTCGGGGGCAACAGTGGTCCAGGCAAGAGAGATATTTAATGTCAACCT 120
QY 121 CTTGGGGCTTTTCATGGAGCTCCCTCTGCCACATTTTTCGAGGTTGGGAAAGTTGTGAGA 180
DB 121 CTTGGGGCTTTTCATGGAGCTCCCTCTGCCACATTTTTCGAGGTTGGGAAAGTTGTGAGA 180
QY 181 GGCTTCAGAACTCAGACCTAATGATCCAAACTCGGGAGATGGCTGCTCCCTGCTGG 240
DB 181 GGCTTCAGAACTCAGACCTAATGATCCAAACTCGGGAGATGGCTGCTCCCTGCTGG 240
QY 241 CTGTGCTGCTGCTGCTGGAGCGCGCATGTTCTCTCACCCCTCCCGCCCGCCCGCGC 300
DB 241 CTGTGCTGCTGCTGCTGGAGCGCGCATGTTCTCTCACCCCTCCCGCCCGCCCGCGC 300
QY 301 TGTTCAGAAAGTCTTCCAGTACATTGACCTCCATCAGGATGAATTTGTGACAGCGCTGA 360
DB 301 TGTTCAGAAAGTCTTCCAGTACATTGACCTCCATCAGGATGAATTTGTGACAGCGCTGA 360
QY 361 AGGAGTGGTGGCCATCCAGAGCGACTGTGTCAGGCTGCTCCCTGCTTCAGACAAAGC 420
DB 361 AGGAGTGGTGGCCATCCAGAGCGACTGTGTCAGGCTGCTCCCTGCTTCAGACAAAGC 420
QY 421 TCTTCAGAAATGATGGCCGCTGGCTGGGACACGCTGCAGCGCTCGGGGCGCCGCTGTGSCCT 480
DB 421 TCTTCAGAAATGATGGCCGCTGGCTGGGACACGCTGCAGCGCTCGGGGCGCCGCTGTGSCCT 480
QY 481 CGGTGGACATGGGTCTCAGACGCTGCGGATGCTCAGAGTCTTCATACCTCCCGTCA 540
DB 481 CGGTGGACATGGGTCTCAGACGCTGCGGATGCTCAGAGTCTTCATACCTCCCGTCA 540
QY 541 TCCTGGCGCACTGGGGAGCGATCCAGAAAGGCAACGCTGTGCTTCTACGGCCACTTGG 600
DB 541 TCCTGGCGCACTGGGGAGCGATCCAGAAAGGCAACGCTGTGCTTCTACGGCCACTTGG 600
QY 601 AGTGCAGCTGCTCAGCGGGCGAGTGGTGCTCAGCGACCCCTATGTGTGAGCGAGG 660
DB 601 AGTGCAGCTGCTCAGCGGGCGAGTGGTGCTCAGCGACCCCTATGTGTGAGCGAGG 660

DB 601 ACGTGCAGCTGCTGACCGGGCGAGTGGTGGTCTCAGGACCCCTATGTGTGTCGACGGAGG 660
QY 661 TAGACGGGAAACTTTATGGACGAGGACCGACCGACCAACAAGGCGCTGTCTTGGCTTGA 720
DB 661 TAGACGGGAAACTTTATGGACGAGGACCGACCGACCAACAAGGCGCTGTCTTGGCTTGA 720
QY 721 TCAATGTCTGACGCGCTTTCAGAGCCCTGGAGCAAGATCTTCTGTGTAATCAAAATCA 780
DB 721 TCAATGTCTGACGCGCTTTCAGAGCCCTGGAGCAAGATCTTCTGTGTAATCAAAATCA 780
QY 781 TCATTGAGGGGATGGAAGAGGCTGGCTCTGTGGCCCTGGAGAACTTGTGGAAGAAAGAA 840
DB 781 TCATTGAGGGGATGGAAGAGGCTGGCTCTGTGGCCCTGGAGAACTTGTGGAAGAAAGAA 840
QY 841 AGGACCGATTTCTCTCGTGGTGGACTACATTTGAATTTTCAGATAACCTGTGGATCAGCC 900
DB 841 AGGACCGATTTCTCTCGTGGTGGACTACATTTGAATTTTCAGATAACCTGTGGATCAGCC 900
QY 901 AAAGGAAGCCAGCAATCACTTATGGAAACCGGGGGAACAGCTACTTCAATGGTGGAGTGA 960
DB 901 AAAGGAAGCCAGCAATCACTTATGGAAACCGGGGGAACAGCTACTTCAATGGTGGAGTGA 960
QY 961 AATGACAGACAGAGATTTTCACTCAGGAACTTTTGGTGGCATCTTTCATGACCAATGG 1020
DB 961 AATGACAGACAGAGATTTTCACTCAGGAACTTTTGGTGGCATCTTTCATGACCAATGG 1020
QY 1021 CTGATCTGGTGTCTCTCTCGTAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
DB 1021 CTGATCTGGTGTCTCTCTCGTAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
QY 1081 GAATCTATGATGAAGTGGTTCCTTTACAGAGAGGAAATAAATACATACAAAGCATCC 1140
DB 1081 GAATCTATGATGAAGTGGTTCCTTTACAGAGAGGAAATAAATACATACAAAGCATCC 1140
QY 1141 ATCTAGACCTGAGAAATACCGGAATAGCAGCGGGTTGAGAAATTTCTGTTCCGATCTA 1200
DB 1141 ATCTAGACCTGAGAAATACCGGAATAGCAGCGGGTTGAGAAATTTCTGTTCCGATCTA 1200
QY 1201 AGGAGGAGATTTCTAATGACCTCTGGAGTACCCATCTCTTCTATTTTCATGGGATCGAGG 1260
DB 1201 AGGAGGAGATTTCTAATGACCTCTGGAGTACCCATCTCTTCTATTTTCATGGGATCGAGG 1260
QY 1261 GCGCGTTTTCATGAGCTGGAACTAAACAGTCAATACCTGCGCGGAGTTATAGGAAATTTT 1320
DB 1261 GCGCGTTTTCATGAGCTGGAACTAAACAGTCAATACCTGCGCGGAGTTATAGGAAATTTT 1320
QY 1321 CAATCGCTAGTCTGCTCAGATGATGTCTGCGGTGGAATAACAGGTGACACGATC 1380
DB 1321 CAATCGCTAGTCTGCTCAGATGATGTCTGCGGTGGAATAACAGGTGACACGATC 1380
QY 1381 TTGAAGATGTGTTCTCCAAAGAAATAGTTTCCAAAGAAATAGTTTCCATGACTCTAG 1440
DB 1381 TTGAAGATGTGTTCTCCAAAGAAATAGTTTCCAAAGAAATAGTTTCCATGACTCTAG 1440
QY 1441 GACTACACCGGTGGATTTGAAATATTTGATGACACCCAGTATCTCCGAGCAAAAGAGCGA 1500
DB 1441 GACTACACCGGTGGATTTGAAATATTTGATGACACCCAGTATCTCCGAGCAAAAGAGCGA 1500
QY 1501 TCAGAACAGTGTGTTGGAACAGAACAGATGATGATCCGGATGGATCCACATTTCCAATTG 1560
DB 1501 TCAGAACAGTGTGTTGGAACAGAACAGATGATGATCCGGATGGATCCACATTTCCAATTG 1560
QY 1561 CCAAAATGTTTCCAGGAGATCGTCCAAGAGCGTGTGTGTAATTCGCTGGGAGCTGTG 1620
DB 1561 CCAAAATGTTTCCAGGAGATCGTCCAAGAGCGTGTGTGTAATTCGCTGGGAGCTGTG 1620
QY 1621 ATGATGAGAACATTCGAGAAATGAGAAATCAACAGGTGGAACTACATAGAGGAAACCA 1680
DB 1621 ATGATGAGAACATTCGAGAAATGAGAAATCAACAGGTGGAACTACATAGAGGAAACCA 1680
QY 1681 AATTATTTGCTGCTTTTCTTAGAGATGGCCAGCTCCATTATTAATCAAGAAACCTTCTA 1740
DB 1681 AATTATTTGCTGCTTTTCTTAGAGATGGCCAGCTCCATTATTAATCAAGAAACCTTCTA 1740

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QY 1741 GTCTGATCTGATCCACTGACAGATTACCTCCCCACATCCCTAGACAGGATGAATGT 1800
Db 1741 GTCTGATCTGATCCACTGACAGATTACCTCCCCACATCCCTAGACAGGATGAATGT 1800
QY 1801 AATATATCAGAGAATTTGGGTCTAGTAGTACATTTTCCCTTCCATTTAAATGTCTTG 1860
Db 1801 AATATATCAGAGAATTTGGGTCTAGTAGTACATTTTCCCTTCCATTTAAATGTCTTG 1860
QY 1861 GGATATCTGGATCACTAATAAATATTTCAAGGCACAGATGTTGGAAATGTTAAGGT 1920
Db 1861 GGATATCTGGATCACTAATAAATATTTCAAGGCACAGATGTTGGAAATGTTAAGGT 1920
QY 1921 CCCCACCTGCACACCTTCTCCTCAAGTCATAGCTGCTTGCAGCAACTTGAATTTCCCAAGTC 1980
Db 1921 CCCCACCTGCACACCTTCTCCTCAAGTCATAGCTGCTTGCAGCAACTTGAATTTCCCAAGTC 1980
QY 1981 CTGTGCAATAGCCCGAGATTGGATTTCTTCCAACTTTTAGCATATCTCCAACTTGCA 2040
Db 1981 CTGTGCAATAGCCCGAGATTGGATTTCTTCCAACTTTTAGCATATCTCCAACTTGCA 2040
QY 2041 ATTTGATGGCATATCACTCCGGTTTCTTCTAGTCTCCTCAAGTCTCGTGACACATA 2100
Db 2041 ATTTGATGGCATATCACTCCGGTTTCTTCTAGTCTCCTCAAGTCTCGTGACACATA 2100
QY 2101 ATCATTCATCAATGATCGCTTTGCTTTTACCACCTCTTCTTCTTTATTTAATAAA 2160
Db 2101 ATCATTCATCAATGATCGCTTTGCTTTTACCACCTCTTCTTCTTTATTTAATAAA 2160
QY 2161 AATGTGGTCTCCACCACTGCTCCCAAAAAAATAAAAAAATAAAAAAATAAAAAA 2220
Db 2161 AATGTGGTCTCCACCACTGCTCCCAAAAAAATAAAAAAATAAAAAAATAAAAAA 2220
QY 2221 AAAAAAAAAAAAAAAAAAAAAA 2242
Db 2221 AAAAAAAAAAAAAAAAAAAAAA 2242

RESULT 12
ABL58476
ID ABL58476 standard; cDNA; 2784 BP.
XX AC ABL58476;
XX AC
DT 30-JUL-2002 (first entry)
XX DE Human metalloprotease, 55054 cDNA sequence.
XX KW 55054; human; metalloprotease; neural cell; cerebral injury; vulnerability;
XX KW gene; ss.
XX OS Homo sapiens.
XX PH Key Location/Qualifiers
XX CDS 602..2125
XX FT /*tag= a
XX FT /product= "metalloprotease 55054"
XX FT /note= "the coding sequence (ABL58477) is specifically
XX FT claimed"
XX PN W0200226948-A2.
XX PD 04-APR-2002.
XX PF 25-SEP-2001; 2001WO-US030016.
XX PR 25-SEP-2000; 2000US-0235055P.
XX PA (MILL-) MILLENNIUM PHARM INC.
XX PI Kapeller-Libermann R;
XX DR WPI; 2002-405051/43.
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DR P-PSDB; ABB07950.

Identifying modulator of neural cell growth or transition metal neurotoxicity, involves contacting test compound with novel human metalloprotease polypeptide and determining if the polypeptide binds the test compound.

Claim 6; Fig 1A-D; 103pp; English.

The invention provides a method for identifying a modulator of neural cell growth, cerebral injury or wound healing, transition metal neurotoxicity, histamine production, neural/hepatic cell proliferation or degradation of extracellular matrix, neurotransmitter or soluble intracellular/extracellular dipeptide. The method involves contacting a test compound and metalloprotease polypeptide, selected from a human metalloprotease polypeptide, termed 55054, and determining if 55054 binds the test compound. The metalloprotease, 55054 is useful for making a pharmaceutical composition for inhibiting the ability of a cell selected from a neural cell such as glial cell or neuron (a sensory neuron or olfactory sensory neuron), astrocyte, oligodendrocyte and ensheathing cell, to cleave a polypeptide. The present sequence represents a cDNA encoding the human metalloprotease, 55054

Sequence 2784 BP; 682 A; 680 C; 666 G; 726 T; 0 U; 30 Other;

Query Match 97.4%; Score 2182.8; DB 6; Length 2784;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2184; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1 GAATGAATACCTCCGAAGCCGCTTTGTTCTCCAGATGTGAATAGCTCCATATACCAAGCC 60
Db 402 GAATGAATACCTCCGAAGCCGCTTTGTTCTCCAGATGTGAATAGCTCCATATACCAAGCC 461
QY 61 TCGTCTTCTTCCGGGGGACAAAGTGGGTGAGGACAGAGAGATATTTAATGCACCT 120
Db 462 TCGTCTTCTTCCGGGGGACAAAGTGGGTGAGGACAGAGAGATATTTAATGCACCT 521
QY 121 CTTGGGGCTTTTCATGGGACTCCCTTCGCCACATTTTTTGGAGGTTGGGAAAGTTGCTAGA 180
Db 522 CTTGGGGCTTTTCATGGGACTCCCTTCGCCACATTTTTTGGAGGTTGGGAAAGTTGCTAGA 581
QY 181 GGCTTCAGAACTCCAGCTTAATGAATCCCAAACTCGGAGAAAGTGGTCCGCTGCTGG 240
Db 582 GGCTTCAGAACTCCAGCTTAATGAATCCCAAACTCGGAGAAAGTGGTCCGCTGCTGG 641
QY 241 CTGTGCTGCTGCTGCTGAGGGGGGAGTGTCTCTCACCTCCCGCCCGCCGGGCGC 300
Db 642 CTGTGCTGCTGCTGCTGAGGGGGGAGTGTCTCTCACCTCCCGCCCGCCGGGCGC 701
QY 301 TGTTAGAGAAAGTCTTCCAGTACATTCAGCTCCATCAGGATGAATTTGTGCAGACGCTGA 360
Db 702 TGTTAGAGAAAGTCTTCCAGTACATTCAGCTCCATCAGGATGAATTTGTGCAGACGCTGA 761
QY 361 AGGAGTGGTGGCCATCGAGAGCACTCTGTCCAGCTGTGCTCTGCTTCCAGCAAGAGC 420
Db 762 AGGAGTGGTGGCCATCGAGAGCACTCTGTCCAGCTGTGCTCTGCTTCCAGCAAGAGC 821
QY 421 TCTTCAGAAATGATGGCGTGGCTGCGGACACGCTGAGCCCTGGGGGGCGGTGGGCT 480
Db 822 TCTTCAGAAATGATGGCGTGGCTGCGGACACGCTGAGCCCTGGGGGGCGGTGGGCT 881
QY 481 CGGTGGACATGGGTCTTCCAGCTGCTCCGATGCTCAGAGTCTTCCAAATACCTCCCGTCA 540
Db 882 CGGTGGACATGGGTCTTCCAGCTGCTCCGATGCTCAGAGTCTTCCAAATACCTCCCGTCA 941
QY 541 TCCTGGCCGAACCTGGGAGCGATCCCAAGAAAGGCAACCGTGTGCTTCTACGGCCACTTGG 600
Db 942 TCCTGGCCGAACCTGGGAGCGATCCCAAGAAAGGCAACCGTGTGCTTCTACGGCCACTTGG 1001
QY 601 ACCTGACGCTGCTGACCGGGGGGATGGGTGGCTCAGGACCCCTATGTCTGACGAGG 660
Db 1002 ACCTGACGCTGCTGACCGGGGGGATGGGTGGCTCAGGACCCCTATGTCTGACGAGG 1061
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QY 2101 ATCATTCATCCATGATCGCTTCTGCTTTACCACTCTTCTCTTTATCTTATTAATAAA 2160
DB |||||
DB 2259 ATCATTCATCCATGATCGCTTCTGCTTTACCACTCTTCTCTTTATCTTATTAATAAA 2318
QY 2161 AATGTTGGTCTCCACCACTGCTCCCA 2187
DB |||||
DB 2319 AATGTTGGTCTCCACCACTGACTACAA 2345
|||
RESULT 14
AAH64725
ID AAH64725 standard; cDNA; 2201 BP.
XX
AC AAH64725;
XX
DT 11-SEP-2001 (first entry)
XX
DE Human secreted protein cDNA, SEQ ID NO: 1.
XX
KW Human; secreted protein; gene therapy; vaccine; treatment; diagnosis;
KW GENSET; 88.
XX
OS Homo sapiens.
XX
PN WO200142451-A2.
XX
XX 14-JUN-2001.
XX
PF 07-DEC-2000; 2000MO-IB001938.
XX
XX 08-DEC-1999; 99US-0169629P.
PR 06-MAR-2000; 2000US-0187470P.
XX
XX
PA (GEST) GENSET.
XX
XX Dumas Milne Edwards J, Bougueleret L, Jobert S;
XX WPI; 2001-367870/38.
XX P-PSDB; AAG89122.
XX
PT Full length GENSET human nucleic acids encoding potentially secreted
PT proteins, useful in gene therapy and vaccination against a variety of
PT diseases, and for diagnosis of those diseases.
XX
PS Claim 7; Page 556-558; 921pp; English.
XX
CC The invention relates to full length GENSET human nucleic acids encoding
CC potentially secreted proteins. The nucleic acids and the polypeptides
CC they encode may be used in the prevention, treatment and diagnosis of
CC diseases associated with inappropriate GENSET gene expression. For
CC example, they be used to treat disorders associated with decreased GENSET
CC gene expression by rectifying mutations or deletions in a patient's
CC genome that affect the activity of GENSET or by supplementing the
CC patients own production of GENSET polypeptides. Conversely, antisense
CC nucleic acid molecules may be administered to down regulate GENSET
CC expression by binding with the cells' own genes and preventing their
CC expression. The sense and antisense nucleic acids may also be used as DNA
CC probes in diagnostic assays to detect and quantitate the presence of
CC similar nucleic acid sequences in samples, and hence to determine which
CC patients may be in need of restorative therapy. The GENSET polypeptides
CC may be used as antigens in the production of antibodies and in assays to
CC identify modulators (agonists and antagonists) of GENSET polypeptide
CC expression and activity. The present sequence is a GENSET nucleic acid of
CC the invention
XX
SQ Sequence 2201 BP; 593 A; 527 C; 531 G; 550 T; 0 U; 0 Other;
Query Match 96.9%; Score 2172.8; DB 5; Length 2201;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 2190; Conservative
1;
Gaps 3; Indels 8; Mismatches 0;
33 AGATGTGAATAGTCCACTATACCAAGCCCTCGTCTTCTCCGGGGGACAACTGGGTGAC 92
|||||

DB 1 AGATGTGAATAGTCCACTATACCAAGCCCTCGTCTTCTTCCGGGGGACAACTGGGTGAC 60
QY 93 GGCACAGAGAGATATTTAATGTCAACCTCTTGGGGCTTTTCATGGACTCCCTCTGCCACA 152
DB |||||
DB 61 GGCACAGAGAGATATTTAATGTCAACCTCTTGGGGCTTTTCATGGACTCCCTCTGCCACA 120
QY 153 TTTTGTGGAGGTTGGGAAAGTTGCTAGAGGCTTCAGAACTCCAGGCTTAATGATCCCAA 212
DB |||||
DB 121 TTTTGTGGAGGTTGGGAAAGTTGCTAGAGGCTTCAGAACTCCAGGCTTAATGATCCCAA 180
QY 213 CTCGGGAGAGTGGCTGCGTCCCTGCTGGCTG---TGCTGCTGCTGCTGCTGAGCGCGC 269
DB |||||
DB 181 CTCGGGAGAGTGGCTGCGTCCCTGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
QY 270 ATGTTCTCTCCTCACCTCCCGCCCGCGCTGTTAGAGAAAGTCTTCAGTACATTGAC 329
DB |||||
DB 241 ATGTTCTCTCCTCACCTCCCGCCCGCGCTGTTAGAGAAAGTCTTCAGTACATTGAC 300
QY 330 CTCATCAGGATGAATTTGTGCAGACGCTGAGAGGAGTGGTGGCCATCGAGAGCACTCT 389
DB |||||
DB 301 CTCATCAGGATGAATTTGTGCAGACGCTGAGAGGAGTGGTGGCCATCGAGAGCACTCT 360
QY 390 GTCCAGCCTGCTGCTGCTTCAGACAGAGCTCTTCAGAAATGATGGCGTGGCTGGGAC 449
DB |||||
DB 361 GTCCAGCCTGCTGCTTTCAGACAGAGCTCTTCAGAAATGATGGCGTGGCTGGGAC 420
QY 450 ACGCTGCAGCGCTGGGGCGCGTGTGGCTCGGTGGACATGGGTCTTCAGAGCTGCC 509
DB |||||
DB 421 ACGCTGCAGCGCTGGGGCGCGTGTGGCTCGGTGGACATGGGTCTTCAGAGCTGCC 480
QY 510 GATGCTCAGAGTCTTCCAATACCTCCCGTCACTTGGCGGAACTGGGGAGCGATCCCACG 569
DB |||||
DB 481 GATGCTCAGAGTCTTCCAATACCTCCCGTCACTTGGCGGAACTGGGGAGCGATCCCACG 540
QY 570 AAAGCACCGTGTCTTCAAGGCACTTGGAGCTGCGAGCTGCTGACCGGGCGGATGGG 529
DB |||||
DB 541 AAAGCACCGTGTCTTCAAGGCACTTGGAGCTGCGAGCTGCTGACCGGGCGGATGGG 600
QY 630 TGGCTCAGCGACCCCTATGTGCTGAGCGAGGTAGACGGGAACTTTATGACGAGAGCG 689
DB |||||
DB 601 TGGCTCAGCGACCCCTATGTGCTGAGCGAGGTAGACGGGAACTTTATGACGAGAGCG 660
QY 690 ACCGACAAAGGCGCTGTCTTGGCTTGGATCAATGTGTGAGCGCTTCAGAGCCCTG 749
DB |||||
DB 661 ACCGACAAAGGCGCTGTCTTGGCTTGGATCAATGTGTGAGCGCTTCAGAGCCCTG 720
QY 750 GAGCAAGATCTTCTGTGAATATCAATTCATCATGAGGGATGGAAGAGCTGCTCT 809
DB |||||
DB 721 GAGCAAGATCTTCTGTGAATATCAATTCATCATGAGGGATGGAAGAGCTGCTCT 780
QY 810 GTTGGCTGGAGAACTTGTGGAAAAAGAAAGGACCGATTCTTCTCTGTTGGACTAC 869
DB |||||
DB 781 GTTGGCTGGAGAACTTGTGGAAAAAGAAAGGACCGATTCTTCTCTGTTGGACTAC 840
QY 870 ATTGTAATTTAGATAAACCCTGTGGATCAGCCAAAGAAAGGACCGATCACTTATGAACC 929
DB |||||
DB 841 ATTGTAATTTAGATAAACCCTGTGGATCAGCCAAAGAAAGGACCGATCACTTATGAACC 900
QY 930 CCGGGGACAGTACTTCACTGTTGGAGTGAATTCAGAGACCGAGATTTTCACTCAGGA 989
DB |||||
DB 901 CCGGGGACAGTACTTCACTGTTGGAGTGAATTCAGAGACCGAGATTTTCACTCAGGA 960
QY 990 ACTTTGGTGGCATCTTTCATGAACCAATGGCTGATCTGTTGCTCTTCTCGGTAGCCTG 1049
DB |||||
DB 961 ACTTTGGTGGCATCTTTCATGAACCAATGGCTGATCTGTTGCTCTTCTCGGTAGCCTG 1020
QY 1050 GTAGACTCGTGTGGTCATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1109
DB |||||
DB 1021 GTAGACTCGTGTGGTCATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
QY 1110 GAAAGGAAATAAATACATACAAAGCCATCCATCTAGACCTAGAGAAATACCGGATAGC 1169
DB |||||
DB 1081 GAAAGGAAATAAATACATACAAAGCCATCCATCTAGACCTAGAGAAATACCGGATAGC 1140

SQ	Sequence	2851 BP; 717 A; 712 C; 659 G; 763 T; 0 U; 0 Other;	
	Query Match	97.4%; Score 2182.8; DB 10; Length 2851;	
	Best Local Similarity	99.9%; Pred. No. 0;	
	Matches 2184; Conservative	0; Mismatches 3; Indels 0; Gaps 0;	
Qy	1	GAATGAATACCTCCGAAGCCGCTTTGTTCTCCAGATGTGAATAGCTCCACATATACCAAGCC	60
Db	159	GAATGAATACCTCCGAAGCCGCTTTGTTCTCCAGATGTGAATAGCTCCACATATACCAAGCC	218
Qy	61	TCGTCTTCCTTCCGGGGGACAACTGGGTCAAGGCACAGAGAGATATTTAATGTCACCCCT	120
Db	219	TCGTCTTCCTTCCGGGGGACAACTGGGTCAAGGCACAGAGAGATATTTAATGTCACCCCT	278
Qy	121	CTTGGGGCTTCATGGGACTCCCTCTGCCACATTTTTTTGGAGTTGGAAAGTTGCTAGA	180
Db	279	CTTGGGGCTTCATGGGACTCCCTCTGCCACATTTTTTTGGAGTTGGAAAGTTGCTAGA	338
Qy	181	GGCTTCAGAACTCCAGCCTAATGGATCCAAACTCGGAGAAATGGCTGCGTCCCTGCTGG	240
Db	339	GGCTTCAGAACTCCAGCCTAATGGATCCAAACTCGGAGAAATGGCTGCGTCCCTGCTGG	398
Qy	241	CTGTGCTGCTGCTGCTGGAGCGGCGCATGTTCTCTCAACCTCCCGGCCCGCGCGC	300
Db	399	CTGTGCTGCTGCTGCTGGAGCGGCGCATGTTCTCTCAACCTCCCGGCCCGCGCGC	458
Qy	301	TGTTAGAGAAAGTCTTCAGTACATTTGACCTCCATCAGGATGAATTTGTGACAGCGTGA	360
Db	459	TGTTAGAGAAAGTCTTCAGTACATTTGACCTCCATCAGGATGAATTTGTGACAGCGTGA	518
Qy	361	AGGAGTGGGTGGCCATCGAGAGCGACTCTGTCCAGCCTGTGCTTCAGACAAAGAGC	420
Db	519	AGGAGTGGGTGGCCATCGAGAGCGACTCTGTCCAGCCTGTGCTTCAGACAAAGAGC	578
Qy	421	TCCTTCAGAAATGATGGCCGTGCTGCGGACACGCTGACAGCGCTGGGGCCCGTGTGSCCT	480
Db	579	TCCTTCAGAAATGATGGCCGTGCTGCGGACACGCTGACAGCGCTGGGGCCCGTGTGSCCT	638
Qy	481	CGGTGGACATGGGTCTCAGCAGCTGCCGATGCTCAGAGTCTCCAAATCCTCCCGTCA	540
Db	639	CGGTGGACATGGGTCTCAGCAGCTGCCGATGCTCAGAGTCTCCAAATCCTCCCGTCA	698
Qy	541	TCCTGGCCGAATCGGGAGCGATCCCAAGAGCACCGTGTGCTTCTACGGCCACTTGG	600
Db	699	TCCTGGCCGAATCGGGAGCGATCCCAAGAGCACCGTGTGCTTCTACGGCCACTTGG	758
Qy	601	ACGTGCAAGCTGTGACCGGGGCGATGGTGGCTCAAGACCCCTATGTGCTGACGAGG	660
Db	759	ACGTGCAAGCTGTGACCGGGGCGATGGTGGCTCAAGACCCCTATGTGCTGACGAGG	818
Qy	661	TAGACGGGAATTTATGGAGGAGCGACCGACAAAGGCCCTGCTCTTGGCTTGA	720
Db	819	TAGACGGGAATTTATGGAGGAGCGACCGACAAAGGCCCTGCTCTTGGCTTGA	878
Qy	721	TCAATGTCTGTGAGCGCCTTCAGAGCCCTGGAGCAAGATCTTCCTGTGAATCAAAATCA	780
Db	879	TCAATGTCTGTGAGCGCCTTCAGAGCCCTGGAGCAAGATCTTCCTGTGAATCAAAATCA	938
Qy	781	TCATTTAGGGATGGAGAGCGCTGGCTGTGTGGCTGGAGGAACCTGTGGAAAGAAA	840
Db	939	TCATTTAGGGATGGAGAGCGCTGGCTGTGTGGCTGGAGGAACCTGTGGAAAGAAA	998
Qy	841	AGGACCGATCTCTCTGCTGTGACTACATTTGTAATTTTCCAGATAAAGCTGTGGATCAGCC	900
Db	999	AGGACCGATCTCTCTGCTGTGACTACATTTGTAATTTTCCAGATAAAGCTGTGGATCAGCC	1058
Qy	901	AAAGGAAGCCAGCAATCACTTATGGAACCCGGGGGAAACAGCTACTTCAATGTTGAGGTGA	960
Db	1059	AAAGGAAGCCAGCAATCACTTATGGAACCCGGGGGAAACAGCTACTTCAATGTTGAGGTGA	1118
Qy	961	AATGCAGAGACAGGATTTTCACTCAGGAACCTTTGGTGGCATCTTTCATGAAACCAATGG	1020
Db	1119	AATGCAGAGACAGGATTTTCACTCAGGAACCTTTGGTGGCATCTTTCATGAAACCAATGG	1178

Qy	1021	CTGATCTGGTTGCTCTTCTCGGTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1080
Db	1179	CTGATCTGGTTGCTCTTCTCGGTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1238
Qy	1081	GAATCTATGATGAAGTGGTTCCCTTACAGAAGAGGAAATAAATACATACATAAAGCCATCC	1140
Db	1239	GAATCTATGATGAAGTGGTTCCCTTACAGAAGAGGAAATAAATACATACATAAAGCCATCC	1298
Qy	1141	ATCTAGACCTTAGAAGAAATACCGGAATAGCAGCGGGTTGAGAAATTTCTGTTCTGATCTA	1200
Db	1299	ATCTAGACCTTAGAAGAAATACCGGAATAGCAGCGGGTTGAGAAATTTCTGTTCTGATCTA	1358
Qy	1201	AGGAGGAGATTTCTAAATGACCTCTGGAGGTACCATCTCTTTCTATTCTATGATGGATCCAGG	1260
Db	1359	AGGAGGAGATTTCTAAATGACCTCTGGAGGTACCATCTCTTTCTATTCTATGATGGATCCAGG	1418
Qy	1261	GCAGCTTTGATGAGCCCTGGAACTAAACAGTCACTACCTGCGCGAGTTATAGGAAAATTTT	1320
Db	1419	GCAGCTTTGATGAGCCCTGGAACTAAACAGTCACTACCTGCGCGAGTTATAGGAAAATTTT	1478
Qy	1321	CAATCCGTCTAGTCCCTCACAATGATGTGTCTGGGTGGAAAAACAGGTGACAGCATC	1380
Db	1479	CAATCCGTCTAGTCCCTCACAATGATGTGTCTGGGTGGAAAAACAGGTGACAGCATC	1538
Qy	1381	TTGAAGATGTGTTCTCCAAAGAAATAGTTCCAAAGATGGTTGTTTCCATGACTCTAG	1440
Db	1539	TTGAAGATGTGTTCTCCAAAGAAATAGTTCCAAAGATGGTTGTTTCCATGACTCTAG	1598
Qy	1441	GACTACACCCGTGGATTTGCAAAATATTTGATGACACCCAGTATCTCGCAGCAAAAAGACGA	1500
Db	1599	GACTACACCCGTGGATTTGCAAAATATTTGATGACACCCAGTATCTCGCAGCAAAAAGACGA	1658
Qy	1501	TCAGAACAGTGTGTTGGAAACAGAACAGATATGATCCGGGATGATCCACCATTTCCAATTTG	1560
Db	1659	TCAGAACAGTGTGTTGGAAACAGAACAGATATGATCCGGGATGATCCACCATTTCCAATTTG	1718
Qy	1561	CCAAAATGTTCCAGGAGATCGTCCACAAGAGCGTGGTGTAAATTCCTGCTGGAGCTGTTG	1620
Db	1719	CCAAAATGTTCCAGGAGATCGTCCACAAGAGCGTGGTGTAAATTCCTGCTGGAGCTGTTG	1778
Qy	1621	ATGATGGAGAACATTCGAGAAATGAGAAATCAACAGGTGGAACTACATAGAGGAAACCA	1680
Db	1779	ATGATGGAGAACATTCGAGAAATGAGAAATCAACAGGTGGAACTACATAGAGGAAACCA	1838
Qy	1681	AAATATTTGCTGCTTTTCTTAGAGATGGCCAGCTCCATTAATCAACAAGACCTTCTA	1740
Db	1839	AAATATTTGCTGCTTTTCTTAGAGATGGCCAGCTCCATTAATCAACAAGACCTTCTA	1898
Qy	1741	GTCTGATCTGATCCACTGACAGATTACCTCCCCCAATCCCTAGACAGGATGGAATGT	1800
Db	1899	GTCTGATCTGATCCACTGACAGATTACCTCCCCCAATCCCTAGACAGGATGGAATGT	1958
Qy	1801	AAATATCCAGAGAAATTTGGGTCTAGTATAGTACATTTTCCCTTCCATTTAAATGTCTTG	1860
Db	1959	AAATATCCAGAGAAATTTGGGTCTAGTATAGTACATTTTCCCTTCCATTTAAATGTCTTG	2018
Qy	1861	GGATATCTGATCAGTAATAAATATTTCAAGCAGAGATGTTGGAAATGTTTAAAGGT	1920
Db	2019	GGATATCTGATCAGTAATAAATATTTCAAGCAGAGATGTTGGAAATGTTTAAAGGT	2078
Qy	1921	CCCCCACTGCACACCTTCTCCTCAAGTCACTAGTCTGCTGACAGCAACTTGATTTCCCAAGTC	1980
Db	2079	CCCCCACTGCACACCTTCTCCTCAAGTCACTAGTCTGCTGACAGCAACTTGATTTCCCAAGTC	2138
Qy	1981	CTGTGCAATAGCCCCAGGATTTGGATTCCTTCCAACTTTTAGCATATCTCCAACTTGCA	2040
Db	2139	CTGTGCAATAGCCCCAGGATTTGGATTCCTTCCAACTTTTAGCATATCTCCAACTTGCA	2198
Qy	2041	ATTTGATTTGCATAAATCACTCCCGTTTGTCTTTCTAGGTCTCTCAAGTCTGCTGACACATA	2100
Db	2199	ATTTGATTTGCATAAATCACTCCCGTTTGTCTTTCTAGGTCTCTCAAGTCTGCTGACACATA	2258

1170 AGCCGGTGTGAGAAATTTCTGTCGATACTAAGGAGGAGATTCTAATGCACTCTGGAGG 1229
1141 AGCCGGTGTGAGAAATTTCTGTCGATACTAAGGAGGAGATTCTAATGCACTCTGGAGG 1200
1230 TACCCTCTCTTTCTATTATGAGATCGAGGCGGCTTTGATGAGCCTGGAACATAAACA 1289
1201 TACCCTCTCTTTCTATTATGAGATCGAGGCGGCTTTGATGAGCCTGGAACATAAACA 1260
1290 GTCACTCTGCGGATATAGGAAATTTTCAATCCGTCCTAGTCCCTCAGTCAATGATG 1349
1261 GTCACTCTGCGGATATAGGAAATTTTCAATCCGTCCTAGTCCCTCAGTCAATGATG 1320
1350 TCTCGGTGGAACAAACAGGTGACACGACATCTTGAAGATGTTTCTCCAAAGAAATAGT 1409
1321 TCTCGGTGGAACAAACAGGTGACACGACATCTTGAAGATGTTTCTCCAAAGAAATAGT 1380
1410 TCCAAAGATGTTGTTTCCATGACTCTAGGACTACACCGGTGGATGCAATATTTGAT 1469
1381 TCCAAAGATGTTGTTTCCATGACTCTAGGACTACACCGGTGGATGCAATATTTGAT 1440
1470 GACACCCAGTATCTCGCAGCAAAAGAGCGATCAGACAGTGTGGAACAGACACAGAT 1529
1441 GACACCCAGTATCTCGCAGCAAAAGAGCGATCAGACAGTGTGGAACAGACACAGAT 1500
1530 ATGATCCGGATGATCCACCATTTCCAATTTGCCAAATGTTTCCAGGAGATCGTCCACAAG 1589
1501 ATGATCCGGATGATCCACCATTTCCAATTTGCCAAATGTTTCCAGGAGATCGTCCACAAG 1560
1590 AGCGTGTGCTAATTCGCTGGGAGCTGTTGATGATGAGGAAACATTCGCAAGATGAGAA 1649
1561 AGCGTGTGCTAATTCGCTGGGAGCTGTTGATGATGAGGAAACATTCGCAAGATGAGAA 1620
1650 ATCAACAGGTGGAACTACATAGAGGGAACCAATTTATTTGCTGCTTTTCTTAGAGATG 1709
1621 ATCAACAGGTGGAACTACATAGAGGGAACCAATTTATTTGCTGCTTTTCTTAGAGATG 1680
1710 GCCAGCTCCATTAATCACAAGAACCTTTCTAGTCTGATCTGATCCACTGACAGATTCAAC 1769
1681 GCCAGCTCCATTAATCACAAGAACCTTTCTAGTCTGATCTGATCCACTGACAGATTCAAC 1740
1770 TCCCCACATCCCTAGACAGGATGGAATGTAATATCCAGAGATTTGGGTCTAGTATA 1829
1741 TCCCCACATCCCTAGACAGGATGGAATGTAATATCCAGAGATTTGGGTCTAGTATA 1800
1830 GTACATTTTCCCTTCCATTTAAATGCTTTGGGATATCTGGATCAGTAATAAATATTTTC 1889
1801 GTACATTTTCCCTTCCATTTAAATGCTTTGGGATATCTGGATCAGTAATAAATATTTTC 1860
1890 AAAGGCACAGATGTTGAAATGTTTAAAGGTCCCCCACTGCACACCTTCTCAAGTCATA 1949
1861 AAAGGCACAGATGTTGAAATGTTTAAAGGTCCCCCACTGCACACCTTCTCAAGTCATA 1920
1950 GCTGCTTGACGAACTATGATTTCCCAAGTCTGTGCAATAGCCGCCAGGATGGATTCCT 2009
1921 GCTGCTTGACGAACTATGATTTCCCAAGTCTGTGCAATAGCCGCCAGGATGGATTCCT 1980
2010 TCCAACTTTTACGATATCTCCAACTTGCATTTGATTTGGATGATTAATCACTCCGTTTGC 2069
1981 TCCAACTTTTACGATATCTCCAACTTGCATTTGATTTGGATGATTAATCACTCCGTTTGC 2040
2070 TTTCTAGGTCCTCAAGTCTCGTGACACATAATCATTTCCATCCAAATGATCGCTTTGCTT 2129
2041 TTTCTAGGTCCTCAAGTCTCGTGACACATAATCATTTCCATCCAAATGATCGCTTTGCTT 2100
2130 TACACCTCTTTTCTTTATTAATAAATAATGTTGGTCTCCACACTGCTGCTCCAAA 2189
2101 TACACCTCTTTTCTTTATTAATAAATAATGTTGGTCTCCACACTGCTGCTGAAAAA 2160
2190 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2230
2161 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2201

RESULT 15

AAC84452
ID AAC84452 standard; cDNA; 2235 BP.

XX AAC84452;

XX 02-APR-2001 (first entry)

XX Nucleotide sequence of mddt cDNA clone ID No: 436857.2.

XX Molecule for disease detection and treatment; mddt; human; cirrhosis;
XX cell proliferative disorder; arteriosclerosis; bursitis; hepatitis;
XX connective tissue disease; myelofibrosis; cancer; leukemia; autoimmune;
XX acquired immunodeficiency syndrome; AIDS; Addison's disease; allergy;
XX anemia; bronchitis; gout; Hashimoto's thyroiditis; multiple sclerosis;
XX cyostatic; immunomodulator; anti-inflammatory; gene therapy; ss.

OS Homo sapiens.

XX WO200075298-A2.

XX 14-DEC-2000.

XX 01-JUN-2000; 2000WO-US015344.

XX 03-JUN-1999; 99US-0137412P.

XX 05-AUG-1999; 99US-0147500P.

XX 05-AUG-1999; 99US-0147501P.

XX 05-AUG-1999; 99US-0147542P.

XX (INCY-) INCYTE GENOMICS INC.

XX Hodgson DM, Lincoln SE, Russo FD, Spiro PA, Banville SC;
XX Bratcher SR, Dufour GE, Cohen HJ, Rosen BH, Chalup MS, Hillman JL;
XX Jones AL, Yu JY, Greenawalt LB, Panzer SR, Roseberry AM, Wright RJ;
XX Daniels SE;

XX WPI; 2001-071068/08.

XX New polypeptide and polynucleotide molecules for disease detection and
XX treatment are useful in diagnosis and gene therapy of proliferative
XX disorders (e.g. breast cancer), autoimmune and inflammatory disorders
XX (e.g. AIDS or allergy).

XX Claim 1; Page 95-96; 99pp; English.

XX Sequences AAC8445-C84458 are new isolated polynucleotide molecules for
XX disease detection and treatment (mddt). The mddt polynucleotides are
XX useful for diagnosing or treating disorders associated with disease
XX detection and treatment molecules. These diseases include cell
XX proliferative disorders (e.g. arteriosclerosis, bursitis, cirrhosis,
XX hepatitis, mixed connective tissue disease, myelofibrosis, or cancers
XX such as leukemia, or breast or brain cancers), autoimmune or inflammatory
XX disorders (e.g. acquired immunodeficiency syndrome (AIDS), Addison's
XX disease, allergies, anemia, autoimmune haemolytic anemia, bronchitis,
XX gout, Hashimoto's thyroiditis, multiple sclerosis or cancers). The mddt
XX are especially useful for somatic or germline gene therapy. The mddt may
XX also be used to detect the presence of, or to quantify the amount of, an
XX isolating full length cDNA sequences utilizing hybridization and/or
XX amplification procedures, for generating hybridization probes useful in
XX chromosomal mapping of naturally occurring genomic sequences, as
XX molecular weight markers, or for monitoring the progress of disorders
XX associated with abnormal levels of mddt expression or evaluating the
XX efficacy of a particular treatment. The recombinant nucleic acids are
XX useful as part of a viral vector (e.g. based on a vaccinia virus) for
XX vaccinating a mammal and inducing a protective immunological response in
XX the mammal. The MDDT polypeptides are useful for screening molecules that
XX bind to or are bound by the polypeptides, i.e. for screening agonists,
XX antagonists or modulators of MDDT

XX Sequence 2235 BP; 557 A; 543 C; 536 G; 568 T; 0 U; 31 Other;

Query Match 95.8%; Score 2147.4; DB 4; Length 2235;									
Best Local Similarity 98.5%; Pred. No. 0;									
Matches 2148; Conservative 0; Mismatches 32; Indels 0; Gaps 0;									
QY	1	GAATGAATACCTCCGAAGCGCTTTGTTCTCCAGATGTGAATAGTCCACTATACCAGCC	60						
DB	56	GAATGAATACCTCCGAAGCGCTTTGTTCTCCAGATGTGAATAGTCCACTATACCAGCC	115						
QY	61	TGCTCTTCCTTCGGGGGCAACAGTGGGTTCAGGGCAACAGAGAGATATTAATGTCAACCT	120						
DB	116	TGCTCTTCCTTCGGGGGCAACAGTGGGTTCAGGGCAACAGAGAGATATTAATGTCAACCT	175						
QY	121	CTTGGGGCTTTATGGGACTCCTCTCTGGCCACATTTTTTGGAGGTTGGGAAAGTTGCTAGA	180						
DB	176	CTTGGGGCTTTATGGGACTCCTCTCTGGCCACATTTTTTGGAGGTTGGGAAAGTTGCTAGA	235						
QY	181	GGCTTCAGAACTCCAGCCTAAATGGATCCCAACTCGGGAGATGGCTGGCTCCCTGCTGG	240						
DB	236	GGCTTCAGAACTCCAGCCTAAATGGATCCCAACTCGGGAGATGGCTGGCTCCNNNNNN	295						
QY	241	CTGTGCTGTGCTGTGGAGCGGCGATGTTCTCTCACCTCCCGCCCCCGGGCGC	300						
DB	296	NNNNNNNNNNNNNNNNNNNGCGCATGTTCTCTCACCTCCCGCCCCCGGGCGC	355						
QY	301	TGTTAGAGAAAGTCTTCCAGTACATTGACTCCATCAGGATGAATTTGTGCAGACGCTGA	360						
DB	356	TGTTAGAGAAAGTCTTCCAGTACATTGACTCCATCAGGATGAATTTGTGCAGACGCTGA	415						
QY	361	AGAGTGGGTGGCCATCGAGAGCGACTCTGTCCAGCCTGTGCTCCCTTCAGACAAGAGC	420						
DB	416	AGAGTGGGTGGCCATCGAGAGCGACTCTGTCCAGCCTGTGCTCCCTTCAGACAAGAGC	475						
QY	421	TCCTCAGAAATGATGGCCGTGTGCGGACACGCTGCAGCGCTGTGGGGCCCGTGTGGCTT	480						
DB	476	TCCTCAGAAATGATGGCCGTGTGCGGACACGCTGCAGCGCTGTGGGGCCCGTGTGGCTT	535						
QY	481	CGGTGACATGGTCTCAGCAGCTCCCGATGGTCAGAGTCTTCCAAATACCTCCCGTCA	540						
DB	536	CGGTGACATGGTCTCAGCAGCTCCCGATGGTCAGAGTCTTCCAAATACCTCCCGTCA	595						
QY	541	TCCTGGCCGAACCTGGGGAGCGATCCCAAGAAAGCCAGCTGTGCTTCTACGGCCACTTGG	600						
DB	596	TCCTGGCCGAACCTGGGGAGCGATCCCAAGAAAGCCAGCTGTGCTTCTACGGCCACTTGG	655						
QY	601	ACGTGACGCTGTGACCGGGGCGATGGTGGCTCAGGACCCCTATGTGCTGACGGAGG	660						
DB	656	ACGTGACGCTGTGACCGGGGCGATGGTGGCTCAGGACCCCTATGTGCTGACGGAGG	715						
QY	661	TAGACGGAAACTTTATGGACGAGGAGCGACCGACAAAGGCCCTGTCTGGCTTGA	720						
DB	716	TAGACGGAAACTTTATGGACGAGGAGCGACCGACAAAGGCCCTGTCTGGCTTGA	775						
QY	721	TCAATGCTGTGAGCGCTTCAGAGCCCTGGAGCAAGATCTTCTGTGAATATCAAAATCA	780						
DB	776	TCAATGCTGTGAGCGCTTCAGAGCCCTGGAGCAAGATCTTCTGTGAATATCAAAATCA	835						
QY	781	TCATTGAGGGGATGGAAGGCTGGCTGTGTTGCCCTGGAGGAACTTGTGGAAAGAA	840						
DB	836	TCATTGAGGGGATGGAAGGCTGGCTGTGTTGCCCTGGAGGAACTTGTGGAAAGAA	895						
QY	841	AGGACCGATTCTTCTCTGGTGTGGACTACATTGTGAATTTTCAGATAACCTGTGGATCAGCC	900						
DB	896	AGGACCGATTCTTCTCTGGTGTGGACTACATTGTGAATTTTCAGATAACCTGTGGATCAGCC	955						
QY	901	AAAGGAAGCCAGCAATCACTTATGGAACCCGGGGGAACAGCTACTTCATGGTGGAGTGA	960						
DB	956	AAAGGAAGCCAGCAATCACTTATGGAACCCGGGGGAACAGCTACTTCATGGTGGAGTGA	1015						
QY	961	AATGCAGAGACGAGATTTTCACTCAGGAACCTTTGGTGCATCCTTTCATGAACCAATGG	1020						
DB	1016	AATGCAGAGACGAGATTTTCACTCAGGAACCTTTGGTGCATCCTTTCATGAACCAATGG	1075						
QY	1021	CTGATCTGTTGCTCTTCTCGGTAGCTGCTGCTGATCATCTCTGGTCCCTG	1080						
DB	1076	CTGATCTGTTGCTCTTCTCGGTAGCTGCTGCTGATCATCTCTGGTCCCTG	1135						
QY	1081	GAATCTATGATGAAGTGGTTCCTCTTACAGAGAGGAATAAATACATCAAAAGCATCC	1140						
DB	1136	GAATCTATGATGAAGTGGTTCCTCTTACAGAGAGGAATAAATACATCAAAAGCATCC	1195						
QY	1141	ATCTAGACTAGAGAATAACCGGAATAGCAGCCGGGTTGAGAAATTTCTGTTCGATACTA	1200						
DB	1196	ATCTAGACTAGAGAATAACCGGAATAGCAGCCGGGTTGAGAAATTTCTGTTCGATACTA	1255						
QY	1201	AGGAGGAGATTCTAATGCACCTCTCGAGTACCCATCTCTTCTATTTATGCGATCGAGG	1260						
DB	1256	AGGAGGAGATTCTAATGCACCTCTCGAGTACCCATCTCTTCTATTTATGCGATCGAGG	1315						
QY	1261	GGCGGTTTGTAGAGCTGGAACTAAACAGTCATACCTGGCCGAGTTATAGGAAATTTT	1320						
DB	1316	GGCGGTTTGTAGAGCTGGAACTAAACAGTCATACCTGGCCGAGTTATAGGAAATTTT	1375						
QY	1321	CAATCGGCTAGTCCCTCACATGAATGTCTCGCGTGGAAAAACAGGTGACACGACATC	1380						
DB	1376	CAATCGGCTAGTCCCTCACATGAATGTCTCGCGTGGAAAAACAGGTGACACGACATC	1435						
QY	1381	TTGAAAGATGTGTTTCCAAAAGAAATAGTTTCCAAAGATGGTTGTTTCCATGACTTAG	1440						
DB	1436	TTGAAAGATGTGTTTCCAAAAGAAATAGTTTCCAAAGATGGTTGTTTCCATGACTTAG	1495						
QY	1441	GACTACACCGTGGATTTGCAAAATATTGATGACACCCAGTATCTCGCAGCAAAAAGCGA	1500						
DB	1496	GACTACACCGTGGATTTGCAAAATATTGATGACACCCAGTATCTCGCAGCAAAAAGCGA	1555						
QY	1501	TCAGAACAGTGTGTTTGGAAACAGAACAGATATGATCCGGATGGATCCACATTTCAAATG	1560						
DB	1556	TCAGAACAGTGTGTTTGGAAACAGAACAGATATGATCCGGATGGATCCACATTTCAAATG	1615						
QY	1561	CCAAAATGTTCCAGGAGATCGTCCAAGAGCGTGGTGTAAATCCGCTGGGAGCTGTG	1620						
DB	1616	CCAAAATGTTCCAGGAGATCGTCCAAGAGCGTGGTGTAAATCCGCTGGGAGCTGTG	1675						
QY	1621	ATGATGGAGAACTTTGCGAGATGAGAAATCAAAGGTGGAACTACATAGAGGGAACCA	1680						
DB	1676	ATGATGGAGAACTTTGCGAGATGAGAAATCAAAGGTGGAACTACATAGAGGGAACCA	1735						
QY	1681	AATTAATTTCTGCTTTTCTTAGAGATGGCCAGCTCCATTAATCACAAGAACCTTCTA	1740						
DB	1736	AATTAATTTCTGCTTTTCTTAGAGATGGCCAGCTCCATTAATCACAAGAACCTTCTA	1795						
QY	1741	GTCTGATCTGATCCACTGACAGATTCACTCCGCCACATCCCTAGACGGGATGGAATGT	1800						
DB	1796	GTCTGATCTGATCCACTGACAGATTCACTCCGCCACATCCCTAGACGGGATGGAATGT	1855						
QY	1801	AAATATCCAGAAATTTGGTCTAGTATAGTACATTTTCCCTTCCATTTAAATGTCCTG	1860						
DB	1856	AAATATCCAGAAATTTGGTCTAGTATAGTACATTTTCCCTTCCATTTAAATGTCCTG	1915						
QY	1861	GGATATCTGATCAGTAATAAATAATTTCAAAGGCAACAGATGTTGAAATGTTTAAAGT	1920						
DB	1916	GGATATCTGATCAGTAATAAATAATTTCAAAGGCAACAGATGTTGAAATGTTTAAAGT	1975						
QY	1921	CCCCCTCGACACCTTCTCAAGTCATAGTCTGTCGACCACTTGATTTCCCCAAGTC	1980						
DB	1976	CCCCCTCGACACCTTCTCAAGTCATAGTCTGTCGACCACTTGATTTCCCCAAGTC	2035						
QY	1981	CTGTGCAATAGCCCCCAGGATTTGATTTCTTCCAACTTTTAGCATATCTCCAACTTTGCA	2040						
DB	2036	CTGTGCAATAGCCCCCAGGATTTGATTTCTTCCAACTTTTAGCATATCTCCAACTTTGCA	2095						
QY	2041	ATTGTAATGGCATAAATCACTCCGGTTTGTCTTAGGTCTCAAGTGTCTGTGACACATA	2100						
DB	2096	ATTGTAATGGCATAAATCACTCCGGTTTGTCTTAGGTCTCAAGTGTCTGTGACACATA	2155						
QY	2101	ATCATTTCCATCCAAATGATCGCCTTTGCTTACCACTCTTCTCTTTTATTAATAA	2160						

Db 2156 ATCATTCATCAATGATGCGCTTTGCTTTACCACTCTTCTTTATCTATTATAAA 2215
Qy 2161 AATGTTGGTCTCCACCACTG 2180
Db 2216 AATGTTGGTCTCCACCACTG 2235
RESULT 16
AAZ65270
ID AAZ65270 standard; DNA; 2152 BP.
XX AAZ65270;
XX DT 23-MAR-2000 (first entry)
XX Human secreted protein gene 21.
XX Human; secreted protein; cancer; tumour; developmental abnormality;
KW foetal deficiency; blood disorder; immune system disorder; inflammation;
KW autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;
KW schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder;
KW atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;
KW digestive disorder; endocrine disorder; infection; AIDS; leukaemia;
KW therapy; chromosome 18q22-23; ds.
XX Homo sapiens.
XX WO9958660-A1.
XX 18-NOV-1999.
XX 06-MAY-1999; 99WO-US009847.
XX 12-MAY-1998; 98US-0085093P.
XX 12-MAY-1998; 98US-0085094P.
XX 12-MAY-1998; 98US-0085105P.
XX 12-MAY-1998; 98US-0085180P.
XX 18-MAY-1998; 98US-0085906P.
XX 18-MAY-1998; 98US-0085920P.
XX 18-MAY-1998; 98US-0085921P.
XX 18-MAY-1998; 98US-0085922P.
XX 18-MAY-1998; 98US-0085923P.
XX 18-MAY-1998; 98US-0085924P.
XX 18-MAY-1998; 98US-0085925P.
XX 18-MAY-1998; 98US-0085927P.
XX 18-MAY-1998; 98US-0085928P.
(HUMA-) HUMAN GENOME SCI INC.
XX Ruben SM, Florence K, Ni J, Rosen CA, Carter KC, Moore PA;
PI Olsen HS, Shi Y, Young PE, Wei F, Brewer LA, Soppet DR, Lafleur DW;
PI Endress GA, Ebner R;
XX WPI; 2000-062296/05.
XX P-PSDB; AAY76144.
XX New isolated human genes and the secreted polypeptides they encode,
PT useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders.
XX Claim 1; Page 309; 475pp; English.
XX AAZ65250 to AAZ65350 represent 97 isolated human secreted protein genes.
CC This sequence was found to be present on human chromosome 18q22-23.
CC AAY76124 to AAY76223 represent the secreted proteins encoded by the 97
CC human genes. The genes and their corresponding secreted polypeptides are
CC useful for preventing, treating or ameliorating medical conditions, e.g.
CC by protein or gene therapy. Also pathological conditions can be diagnosed
CC by determining the amount of the new polypeptides in a sample or by
CC determining the presence of mutations in the new genes. Specific uses are
CC described for each of the 97 genes, based on which tissues they are most
CC highly expressed in, and include developing products for the diagnosis or

CC treatment of cancer, tumours, developmental abnormalities and foetal
CC deficiencies, blood disorders, diseases of the immune system, autoimmune
CC diseases, inflammation, allergies, Alzheimer's and cognitive disorders,
CC schizophrenia, arthritis, asthma, psoriasis, sepsis, skin disorders,
CC atherosclerosis, diabetes, cardiovascular disorders, kidney disorders,
CC digestive disorders, infections and AIDS. The polypeptides are
CC also useful for identifying their binding partners. The sequences shown
CC in AAY76224 to AAY76424 represent fragments of the secreted proteins
XX
XX Sequence 2152 BP; 541 A; 526 C; 531 G; 553 T; 0 U; 1 Other;
Query Match 95.3%; Score 2135.6; DB 3; Length 2152;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2148; Conservative 1; Mismatches 0; Indels 3; Gaps 1;
Qy 19 CCGCTTTGTTCTCCAGATGTAATAGCTCCACTATACCAAGCTGCTCTTCTTCGGGGG 78
Db 1 CCGCTTTGTTCTCCAGATGTAATAGCTCCACTATACCAAGCTGCTCTTCTTCGGGGG 60
Qy 79 ACAACGTGGGTACAGGCACAGAGAGATATTATGTCAACCTCTTGGGGTTCATCGGA 138
Db 61 ACAACGTGGGTACAGGCACAGAGAGATATTATGTCAACCTCTTGGGGTTCATCGGA 120
Qy 139 CTCCTCTGTCACATTTTTTTGGAGGTTGGAAAGTTGCTAGAGCTTTCAGAACTCCAGCC 198
Db 121 CTCCTCTGTCACATTTTTTTGGAGGTTGGAAAGTTGCTAGAGCTTTCAGAACTCCAGCC 180
Qy 199 TAATGATCCAAACTCGGGAGAAATGGCTGCTGCTCCCTGCTGGCTG---TGGTGTGCTGC 255
Db 181 TAATGATCCAAACTCGGGAGAAATGGCTGCTGCTCCCTGCTGGCTGCTGCTGCTGCTGC 240
Qy 256 TGGTGGAGCGCGCATGTTCTCTCAACCTCCCGCCCGCGCGCTGTAGAGAAAGTCT 315
Db 241 TGGTGGAGCGCGCATGTTCTCTCAACCTCCCGCCCGCGCGCTGTAGAGAAAGTCT 300
Qy 316 TCCAGTACATTTGACCTCCATCAGATGAATTTGTGCAGACGCTGAAGAGTGGGTGGCCA 375
Db 301 TCCAGTACATTTGACCTCCATCAGATGAATTTGTGCAGACGCTGAAGAGTGGGTGGCCA 360
Qy 376 TCGAGAGCGACTCTGTCCAGCTGTGCTGCTGTTCAGACAAGAGCTTTCAGAAATGATGG 435
Db 361 TCGAGAGCGACTCTGTCCAGCTGTGCTGCTGTTCAGACAAGAGCTTTCAGAAATGATGG 420
Qy 436 CCGTGGCTCGGACACGCTGCAGCGCTGGGGCGCGTGGCTCGGTGCAGATGGTGC 495
Db 421 CCGTGGCTCGGACACGCTGCAGCGCTGGGGCGCGTGGCTCGGTGCAGATGGTGC 480
Qy 496 CTCAGAGCTGCCCGATGGTTCAGATGTTCCAAATACCTCCCGTCATCTGGCCGAACTGG 555
Db 481 CTCAGAGCTGCCCGATGGTTCAGATGTTCCAAATACCTCCCGTCATCTGGCCGAACTGG 540
Qy 556 GGAGCGATCCAGAAAGGACCGTGTGCTTCTACGGCACTTGGAGCTGAGCTGCTG 615
Db 541 GGAGCGATCCAGAAAGGACCGTGTGCTTCTACGGCACTTGGAGCTGAGCTGCTG 600
Qy 616 ACCGGGGCGATGGTGGCTCACGAGCCCTATGCTGACGAGGTAGAGGGAACCTTT 675
Db 601 ACCGGGGCGATGGTGGCTCACGAGCCCTATGCTGACGAGGTAGAGGGAACCTTT 660
Qy 676 ATGGAGGAGGAGCGACCGAACAAAGAGGCCCTGTCTTGGCTTGGATCAATGCTGAGCG 735
Db 661 ATGGAGGAGGAGCGACCGAACAAAGAGGCCCTGTCTTGGCTTGGATCAATGCTGAGCG 720
Qy 736 CTTTCAGAGCCCTGGAGCAAGATCTTCTGTGAATATCAAAATTCATCATTTAGGGGATGG 795
Db 721 CTTTCAGAGCCCTGGAGCAAGATCTTCTGTGAATATCAAAATTCATCATTTAGGGGATGG 780
Qy 796 AGAGGCTGGCTGTGTTGCCCTGGAGAACTTCTGGAAGAAAGAAAGGACCGATCTTCT 855
Db 781 AGAGGCTGGCTGTGTTGCCCTGGAGAACTTCTGGAAGAAAGAAAGGACCGATCTTCT 840
Qy 856 CTGGTGTGGAATACTATTGTAATTTTCAGATAAATCTGTGGATCAGCAAAAGGAGCCAGCA 915

Db 841 CTGGTGTGACTACATTTGTTAAATTTTCAGATAAACCCTGTGGATCAGCCAAAGGACGACAA 900
QY 916 TCACATTATGGAACCCGGGGAAACAGCTACTTCAATGTGTGAGGTGAATTCAGAGACCAGG 975
Db 901 TCACATTATGGAACCCGGGGAAACAGCTACTTCAATGTGTGAGGTGAATTCAGAGACCAGG 960
QY 976 ATTTTCACACTCAGGAACCTTTGGTGGCATCCTTTCATGAACCAATGGCTGATCTGGTTGCTC 1035
Db 961 ATTTTCACACTCAGGAACCTTTGGTGGCATCCTTTCATGAACCAATGGCTGATCTGGTTGCTC 1020
QY 1036 TTCTCGGTAGCCCTGTGAGACTCGTCTGTGTCATATCCTCGTCCCTGGAATCTATGATGAAG 1095
Db 1021 TTCTCGGTAGCCCTGTGAGACTCGTCTGTGTCATATCCTCGTCCCTGGAATCTATGATGAAG 1080
QY 1096 TGGTTCTCTTACAGAAGAGGAATAAATACATACATAAAGCCATCCATCTAGACCTTAGAAG 1155
Db 1081 TGGTTCTCTTACAGAAGAGGAATAAATACATACATAAAGCCATCCATCTAGACCTTAGAAG 1140
QY 1156 AATACCGGAATAGCAGCCGGTTGAGAAATTTCTGTTTCGATACATAAGGAGGAGATTCTAA 1215
Db 1141 AATACCGGAATAGCAGCCGGTTGAGAAATTTCTGTTTCGATACATAAGGAGGAGATTCTAA 1200
QY 1216 TGCACCTCTGGAGGTACCCATCTCTTTCTATTATGSGATCGAGGCGGGTTTGTATGAGC 1275
Db 1201 TGCACCTCTGGAGGTACCCATCTCTTTCTATTATGSGATCGAGGCGGGTTTGTATGAGC 1260
QY 1276 CTGGAACATAACAGTCATACCTGGCCGAGTTATAGGAAATTTTCAATCCGCTAGTCC 1335
Db 1261 CTGGAACATAACAGTCATACCTGGCCGAGTTATAGGAAATTTTCAATCCGCTAGTCC 1320
QY 1336 CTCACATGAATGTCTGCGGTGGAATAAAGACAGGTGACACGACATCTTGAAGATGTGTCT 1395
Db 1321 CTCACATGAATGTCTGCGGTGGAATAAAGACAGGTGACACGACATCTTGAAGATGTGTCT 1380
QY 1396 CCAAAAGAAATAGTTCACAAAGATGGTTGTTTCCATGACTCTPAGGACTACACCCGTGA 1455
Db 1381 CCAAAAGAAATAGTTCACAAAGATGGTTGTTTCCATGACTCTPAGGACTACACCCGTGA 1440
QY 1456 TTGCAATATGATGACACCCGATCTCGCAGCAAAAGAGCGATCAGAACAGTGTG 1515
Db 1441 TTGCAATATGATGACACCCGATCTCGCAGCAAAAGAGCGATCAGAACAGTGTG 1500
QY 1516 GAACAGAACAGATATGATCCGGATGGATCCACCATTCCAAATGCAAAATGTTCCAGG 1575
Db 1501 GAACAGAACAGATATGATCCGGATGGATCCACCATTCCAAATGCAAAATGTTCCAGG 1560
QY 1576 AGATCGTCCACAGAGCGTGTCTAAATCCGCTGGGAGCTGTTGATGATGGAGAACATT 1635
Db 1561 AGATCGTCCACAGAGCGTGTCTAAATCCGCTGGGAGCTGTTGATGATGGAGAACATT 1620
QY 1636 CGCAGAAATGAGAAATCAACAGGTGGAATCCACCATTCCAATGCAAAATGTTCCGCT 1695
Db 1621 CGCAGAAATGAGAAATCAACAGGTGGAATCCACCATTCCAATGCAAAATGTTCCGCT 1680
QY 1696 TTTTCTTAGAGATGGCCAGCTCCATTAATCAAGAACCTTCTAGTCTGATCTGATCCA 1755
Db 1681 TTTTCTTAGAGATGGCCAGCTCCATTAATCAAGAACCTTCTAGTCTGATCTGATCCA 1740
QY 1756 CTGACAGATTACCTCCCCACATCCCTAGACAGGATGGAATGTAATATCCAGAGAT 1815
Db 1741 CTGACAGATTACCTCCCCACATCCCTAGACAGGATGGAATGTAATATCCAGAGAT 1800
QY 1816 TTGGGCTAGTAGTAGTACATTTTCCCTCCATTTAAATGCTCTGGGATCTGGATCAG 1875
Db 1801 TTGGGCTAGTAGTAGTACATTTTCCCTCCATTTAAATGCTCTGGGATCTGGATCAG 1860
QY 1876 TAATAAAATATTTCAAAGGCACAGATGTTGGAATGTTTAAGGTCCTCCCACTGCACAC 1935
Db 1861 TAATAAAATATTTCAAAGGCACAGATGTTGGAATGTTTAAGGTCCTCCCACTGCACAC 1920
QY 1936 TTCCTCAAGTCATAGTCTTGACAGCACTTGATTTTCCCAAGTCTCTGCAATAGCCCC 1995
Db 1921 TTCCTCAAGTCATAGTCTTGACAGCACTTGATTTTCCCAAGTCTCTGCAATAGCCCC 1980

QY 1996 AGGATTGGATTCCTTCCCAACCTTTTAGCATATCTCCAACCTTGCATTTGATTGGCATAA 2055
Db 1981 AGGATTGGATTCCTTCCCAACCTTTTAGCATATCTCCAACCTTGCATTTGATTGGCATAA 2040
QY 2056 TCACCTCCGGTTTGTCTTTCTAGTCTCTCAAGTCTCGTGACACATAATCATTCATCCCAAT 2115
Db 2041 TCACCTCCGGTTTGTCTTTCTAGTCTCTCAAGTCTCGTGACACATAATCATTCATCCCAAT 2100
QY 2116 GATCGCCTTGTCTTACCACTCTTCTCTTTTATCTTTATATAAAATGTTG 2167
Db 2101 GATCGCCTTGTCTTACCACTCTTCTCTTTTATCTTTATATAAAATGTTG 2152

RESULT 17

ACC50470

ID ACC50470 standard; cDNA; 2152 BP.

XX ACC50470;

DT 12-JUN-2003 (first entry)

XX Human secreted protein coding sequence, SEQ ID 137.

DE Cardiant; antiarrhythmic; antiarteriosclerotic; vasotropic; cytostatic;
XX Cardiant; antiarrhythmic; antiarteriosclerotic; vasotropic; cytostatic;
KW vulnary; antiinflammatory; nootropic; neuroprotective;
KW antiparkinsonian; gene therapy; human; cardiovascular disorder; gene; ss.
XX

OS Homo sapiens.

XX WO200295010-A2.

XX 28-NOV-2002.

XX 19-MAR-2002; 2002WO-US009785.

XX 21-MAR-2001; 2001US-0277340P.

PR 19-JUL-2001; 2001US-0306171P.

PR 13-NOV-2001; 2001US-0331287P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM;

PI WPI; 2003-129429/12.

XX Novel human secreted proteins, useful for detecting, preventing,
PT diagnosing, prognosticating, treating and/or ameliorating cardiovascular
PT disorders such as arrhythmia.

XX Claim 21; SEQ ID NO 137; 1881pp; English.

XX The present invention relates to novel human secreted proteins (ABR47633-
CC ABR48145) and their coding sequences (ACC50856). The proteins
CC and their coding sequences are useful for the preparation of a diagnostic
CC or pharmaceutical composition for diagnosing or treating a cardiovascular
CC disorder (e.g., arrhythmia, tachycardia, cardiac arrest, coronary
CC arteriosclerosis and myocardial ischaemia), neural disorders, immune
CC system disorders, muscular disorders, reproductive disorders,
CC gastrointestinal disorders, pulmonary disorders, renal disorders,
CC proliferative disorders and/or cancerous diseases and conditions, for
CC wound healing and epithelial cell proliferation, to treat inflammation or
CC infection, for treating thrombosis and arteriosclerosis, for treating or
CC preventing neural damage which occurs in neuronal disorders or
CC neurodegenerative conditions such as Alzheimer's disease and Parkinson's
CC disease, to enhance bone and periodontal regeneration and aid in tissue
CC transplants or bone grafts, to prevent skin aging or hair loss, to
CC stimulate growth and differentiation of haematopoietic cells and bone
CC marrow cells when used in combination with other cytokines, to maintain
CC organs before transplantation or for supporting cell culture of primary
CC tissues, to increase or decrease differentiation or proliferation of
CC embryonic stem cells, or to modulate mammalian characteristics or
CC metabolism. Note: The sequence data for this patent was published in

CC electronic format and is available from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 2152 BP; 541 A; 526 C; 531 G; 553 T; 0 U; 1 Other;

Query Match 95.3%; Score 2135.6; DB 8; Length 2152;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 2148; Conservative 1; Mismatches 0; Indels 3; Gaps 1;

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QY 19 CCGCTTTGTTCTCCAGATGTAATGCTCCACTATACCAGCTCGTCTTCTCCGGGG 78
DB 1 CCGCTTTGTTCTCCAGATGTAATGCTCCACTATACCAGCTCGTCTTCTCCGGGG 60
QY 79 ACAACGTGGGTTCAGGACAGAGAGATATTAATGTCACCTCTTGGGGCTTTCATGGGA 138
DB 61 ACAACGTGGGTTCAGGACAGAGAGATATTAATGTCACCTCTTGGGGCTTTCATGGGA 120
QY 139 CTCCTCTGCCACATTTTTCAGAGTGGGAAAGTGTAGAGCTTCAGAACTCCAGCC 198
DB 121 CTCCTCTGCCACATTTTTCAGAGTGGGAAAGTGTAGAGCTTCAGAACTCCAGCC 180
QY 199 TAATGGATCCCAACTCGGAGATGGCTGCTCCCTGCTGGCTGCTGCTGCTGCTG 255
DB 181 TAATGGATCCCAACTCGGAGATGGCTGCTCCCTGCTGGCTGCTGCTGCTGCTG 240
QY 256 TGCTGGAGCGGCGATGTTCTCTCACCTCCCGCCCCCGCGCTGTAGAGAAAGTCT 315
DB 241 TGCTGGAGCGGCGATGTTCTCTCACCTCCCGCCCCCGCGCTGTAGAGAAAGTCT 300
QY 316 TCCAGTACATGACCTCCATCAGATGAATTTGTGACAGCGCTGAAGAGTGGTGCCA 375
DB 301 TCCAGTACATGACCTCCATCAGATGAATTTGTGACAGCGCTGAAGAGTGGTGCCA 360
QY 376 TCGAGAGCGACTGTCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 435
DB 361 TCGAGAGCGACTGTCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
QY 436 CCGTGGCTGGGGACACGCTGACGCGCTGGGGGCGCTGCTGCTGCTGCTGCTG 495
DB 421 CCGTGGCTGGGGACACGCTGACGCGCTGGGGGCGCTGCTGCTGCTGCTGCTG 480
QY 496 CTCAGAGCTGCCCGATGGTTCAGAGTCTTCAATACCTCCGCTCATCTCGGCCAATGG 555
DB 481 CTCAGAGCTGCCCGATGGTTCAGAGTCTTCAATACCTCCGCTCATCTCGGCCAATGG 540
QY 556 GGAGCGATCCCAAGAGGACCGTGTCTTACGCGCACTTGGAGCTGCGAGCTGCTG 615
DB 541 GGAGCGATCCCAAGAGGACCGTGTCTTACGCGCACTTGGAGCTGCGAGCTGCTG 600
QY 616 ACCGGGCGATGGGTGGCTCACGACCCCTATGTGCTGACGGAGGTAGACGGGAACTTT 675
DB 601 ACCGGGCGATGGGTGGCTCACGACCCCTATGTGCTGACGGAGGTAGACGGGAACTTT 660
QY 676 ATGACAGAGGACCGACGACAAAGAGCCCTGCTTGGTGTGATCAATGCTGTAGCG 735
DB 661 ATGACAGAGGACCGACGACAAAGAGCCCTGCTTGGTGTGATCAATGCTGTAGCG 720
QY 736 CTTTCAGAGCCCTGGAGCAGATCTTCTGATATCAAAATTCATATTCAGGGGATGG 795
DB 721 CTTTCAGAGCCCTGGAGCAGATCTTCTGATATCAAAATTCATATTCAGGGGATGG 780
QY 796 AAGAGGCTGGCTCTGTTGCCCTGGAGAACTTGTGGAAAGAAAGGACCGATTCTTCT 855
DB 781 AAGAGGCTGGCTCTGTTGCCCTGGAGAACTTGTGGAAAGAAAGGACCGATTCTTCT 840
QY 856 CTGCTGTGGACTACATTTGTAATTTTCAGATCACTGTGGATCAGCAAGGAGCCAGCA 915
DB 841 CTGCTGTGGACTACATTTGTAATTTTCAGATCACTGTGGATCAGCAAGGAGCCAGCA 900
QY 916 TCACATTAGNACCCGGGGACAGCTACTTCATGCTGGAGGTGAATGACAGACCAG 975
DB 901 TCACATTAGNACCCGGGGACAGCTACTTCATGCTGGAGGTGAATGACAGACCAG 960
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QY 976 ATTTTCACTCAGGAACCTTTGGTGGCATCTTTCATGAACCAATGGCTGATCTGGTGTCT 1035
DB 961 ATTTTCACTCAGGAACCTTTGGTGGCATCTTTCATGAACCAATGGCTGATCTGGTGTCT 1020
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DB 1021 TTCTCGGTAGCTCGGTAGACTCGTCTGGTCAATATCTCTGGTCCCTGGAAATCTATGATGAAG 1080
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DB 1081 TGGTTCCTCTTACAGAGAGGAATAAATACATACAAAGCCATCCATCTAGACCTAGAG 1140
QY 1156 AATACCCGAATAGCAGCCGGGTTGAGAAATTTCTGTTTCGATACCTAAGGAGGAGATTTCTAA 1215
DB 1141 AATACCCGAATAGCAGCCGGGTTGAGAAATTTCTGTTTCGATACCTAAGGAGGAGATTTCTAA 1200
QY 1216 TGCACCTCTGGAGTACCCATCTCTTTCTATATTCATGAGGATCGAGGGCGGTTTATGATGAGC 1275
DB 1201 TGCACCTCTGGAGTACCCATCTCTTTCTATATTCATGAGGATCGAGGGCGGTTTATGATGAGC 1260
QY 1276 CTGGAACCTAAACAGTCATACCTGCGCGAGTTATAGGAAATTTTCAATCCGCTTAGTCC 1335
DB 1261 CTGGAACCTAAACAGTCATACCTGCGCGAGTTATAGGAAATTTTCAATCCGCTTAGTCC 1320
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DB 1321 CTCAATGAATGTCTGCGGTGGAATAACAGAGTGACACGACATCTTTGAAGATGTGTTCT 1380
QY 1396 CCAAGAAATAGTTCCAAAGATGTTGTTTCATATGATGACTCTAGGACTACACCCGTGGA 1455
DB 1381 CCAAGAAATAGTTCCAAAGATGTTGTTTCATATGATGACTCTAGGACTACACCCGTGGA 1440
QY 1456 TTGCAATATTTGATGACACCCAGTATCTCGCAGCAAAAGAGCGATCAGAACAGTGTG 1515
DB 1441 TTGCAATATTTGATGACACCCAGTATCTCGCAGCAAAAGAGCGATCAGAACAGTGTG 1500
QY 1516 GAACAGAACAGATATGATCCGGGATGGATCCACATTTCCAAATTCGCAAAATGTTCCAGG 1575
DB 1501 GAACAGAACAGATATGATCCGGGATGGATCCACATTTCCAAATTCGCAAAATGTTCCAGG 1560
QY 1576 AGATCGTCCAAGAGCGTGGTGTCTTCCGCTGGAGCTGTTGATGATGAGGAAACATTT 1635
DB 1561 AGATCGTCCAAGAGCGTGGTGTCTTCCGCTGGAGCTGTTGATGATGAGGAAACATTT 1620
QY 1636 CGCAGATAGAAATAACAAGGTGGAACCTACATAGAGGAAACCAATATTTCTGCTGCT 1695
DB 1621 CGCAGATAGAAATAACAAGGTGGAACCTACATAGAGGAAACCAATATTTCTGCTGCT 1680
QY 1696 TTTTCTTAGAGATGGCCAGCTCCATTAATCAAGAAACCTTTCTAGTCTGATCTGATCCA 1755
DB 1681 TTTTCTTAGAGATGGCCAGCTCCATTAATCAAGAAACCTTTCTAGTCTGATCTGATCCA 1740
QY 1756 CTGACAGATTCACCTCCCCACATCCCTAGACAGGATGGAATGTAATATTCAGAGAAAT 1815
DB 1741 CTGACAGATTCACCTCCCCACATCCCTAGACAGGATGGAATGTAATATTCAGAGAAAT 1800
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DB 1801 TTGSGTCTAGTATAGTACATTTTCCCTTCCATTTAAATGTTTGGGATATCTGGATCAG 1860
QY 1876 TAATAAAATATTTCAAAGGACAGATGTTGGAATGTTTAAAGTCCCCCACTGCACACC 1935
DB 1861 TAATAAAATATTTCAAAGGACAGATGTTGGAATGTTTAAAGTCCCCCACTGCACACC 1920
QY 1936 TTCTCAAGTCATAGTCTGTCAGGAACTTTGATTTTCCCAAGTCTCTGTGCAATAGCCCC 1995
DB 1921 TTCTCAAGTCATAGTCTGTCAGGAACTTTGATTTTCCCAAGTCTCTGTGCAATAGCCCC 1980
QY 1996 AGGATTTGGATTTCTTCAACCTTTTACCATATCTCCAACTTTCGAAATTTGATTTGGCATA 2055
DB 1981 AGGATTTGGATTTCTTCAACCTTTTACCATATCTCCAACTTTCGAAATTTGATTTGGCATA 2040
QY 2056 TCACTCCGGTTTCTTCTAGGTCCTCAAGTCTGTCGACACATAATCAATTCATCCATCAAT 2115
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[illegible]

Db	2101	GATCGCCTTGGCTTTACCAVCTCTTCCTTTATCTTATTAATAAAATGTTG	2152
RESULT 19			
ADB91167			
ID	ADB91167	standard; cDNA; 2152 BP.	
XX	XX		
AC	ADB91167;		
XX	XX		
DT	04-DEC-2003	(first entry)	
XX	XX		
DE	Human secreted protein cDNA #SEQ ID 113.		
XX	XX		
KW	Secreted protein; gene therapy; antidiabetic; diabetes; human; ss.		
XX	XX		
OS	Homo sapiens.		
XX	XX		
FN	WO2003004622-A2.		
XX	XX		
PD	16-JAN-2003.		
XX	XX		
PF	19-MAR-2002; 2002WO-US008124.		
XX	XX		
PR	21-MAR-2001; 2001US-0277340P.		
PR	19-JUL-2001; 2001US-0306171P.		
PR	13-NOV-2001; 2001US-0331287P.		
XX	XX		
PA	(HUMA-) HUMAN GENOME SCI INC.		
XX	XX		
PI	Rosen CA, Ruben SM;		
XX	XX		
DR	WPI; 2003-229407/22.		
XX	XX		
PT	Nucleic acid encoding a human secreted protein is useful in diagnosing or		
PT	treating diabetes or conditions related to diabetes.		
XX	XX		
PS	Claim 9; SEQ ID NO 113; 1537pp; English.		
XX	XX		
CC	The invention relates to isolated nucleic acid molecules ADB91065-		
CC	ADB91448 and ADB91935-ADB91911 encoding human secreted proteins ADB91449-		
CC	ADB91834. Also disclosed is a recombinant vector comprising a		
CC	polynucleotide of the invention, and a recombinant host cell comprising		
CC	the recombinant vector. The polypeptide of the invention is useful in		
CC	identifying a binding partner by contacting the polypeptide with a		
CC	binding partner; and determining whether the binding partner increases or		
CC	decreases activity of the polypeptide. The polypeptide, polynucleotide,		
CC	antibody or its fragment, agonist or antagonist are useful for preparing		
CC	a pharmaceutical composition for diagnosing or treating diabetes or		
CC	conditions related to diabetes. The present sequence is that of the human		
CC	immunoglobulin Fc portion used to generate fusion proteins, increasing		
CC	the stability of the fused protein as compared to the secreted protein		
CC	only. Note: The sequence data for this patent did not form part of the		
CC	printed specification, but was obtained in electronic format directly		
CC	from WIPO at ftp.wipo.int/pub/published_pct_sequences.		
XX	XX		
SQ	Sequence 2152 BP; 541 A; 526 C; 531 G; 553 T; 0 U; 1 Other;		

Qy 2116 GATCGCCTTGGCTTTACCACTCTTTCCTTTATCTTATTAATAAAAAATGTTG 2167


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PR 17-AUG-1998; 98US-0096768P.
PR 17-AUG-1998; 98US-0096773P.
PR 17-AUG-1998; 98US-0096791P.
PR 17-AUG-1998; 98US-0096867P.
PR 17-AUG-1998; 98US-0096891P.
PR 17-AUG-1998; 98US-0096894P.
PR 17-AUG-1998; 98US-0096897P.
PR 17-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096950P.
PR 18-AUG-1998; 98US-0096959P.
PR 18-AUG-1998; 98US-0096960P.
PR 18-AUG-1998; 98US-0097022P.
PR 19-AUG-1998; 98US-0097141P.
PR 20-AUG-1998; 98US-0097218P.
PR 24-AUG-1998; 98US-0097661P.
PR 26-AUG-1998; 98US-0097952P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097955P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097974P.
PR 26-AUG-1998; 98US-0097978P.
PR 26-AUG-1998; 98US-0097979P.
PR 26-AUG-1998; 98US-0097986P.
PR 26-AUG-1998; 98US-0098014P.
PR 31-AUG-1998; 98US-0098525P.
PR 16-SEP-1998; 98US-0100634P.
PR 16-SEP-1998; 98WO-US013330.
PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 22-DEC-1998; 98US-0113296P.
PR 05-JAN-1999; 98WO-US000106.
PR 08-MAR-1999; 98WO-US005028.
PR 12-MAR-1999; 98US-0123957P.
PR 02-JUN-1999; 98WO-US012252.
PR 23-JUN-1999; 98US-0141037P.
PR 07-JUL-1999; 98US-0143048P.
PR 20-JUL-1999; 98US-0144758P.
PR 26-JUL-1999; 98US-0145698P.
PR 28-JUL-1999; 98US-0146222P.
PR 17-AUG-1999; 98US-0149396P.
PR 15-SEP-1999; 98WO-US021090.
PR 15-SEP-1999; 98WO-US021547.
PR 08-OCT-1999; 98US-0158663P.
PR 30-NOV-1999; 98WO-US028313.
PR 01-DEC-1999; 98WO-US028301.
PR 01-DEC-1999; 98WO-US028634.
PR 16-DEC-1999; 98WO-US030095.
PR 20-DEC-1999; 98WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-JUN-2000; 2000US-0213637P.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.

Query Match 3.0%; Score 66.6; DB 8; Length 2846;
Best Local Similarity 71.3%; Pred. No. 0.00023;
Matches 87; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 2121 CCTTTGCTTTACCACTCTTTCTTTATCTTATTAATAAAATGTTGGTCTCCACCACGTG 2180
Db 2653 CCTTTTCTTCCCATCTCTTGTACACATTTTAAATAAATAAGGGTTGGCTTCTGAACATA 2712
QY 2181 NCTCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2240
Db 2713 CAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2772
QY 2241 AA 2242
Db 2773 AA 2774

RESULT 353
ACA72548
ID ACA72548 standard; cDNA; 2846 BP.
XX ACA72548;
DT 02-JUL-2003 (first entry)
DE Human PRO polynucleotide #85.
KW Human; PRO; Gene; ss; secreted polypeptide; transmembrane polypeptide;
KW cancer; adrenal tumour; lung tumour; colon tumour; breast tumour;
KW prostate tumour; rectal tumour; cervical tumour; liver tumour; TNF-alpha;
KW tumour necrosis factor-alpha; chondrocyte cell.
XX Homo sapiens.
XX US2003022295-A1.
XX 30-JAN-2003.
XX 19-JUN-2002; 2002US-00175752.
XX 18-SEP-1997; 97US-0059263P.
XX 18-SEP-1997; 97US-0059266P.
XX 17-OCT-1997; 97US-0062250P.
XX 21-OCT-1997; 97US-0063486P.
XX 24-OCT-1997; 97US-0063120P.
XX 24-OCT-1997; 97US-0063121P.
XX 28-OCT-1997; 97US-0063540P.
XX 28-OCT-1997; 97US-0063541P.
XX 28-OCT-1997; 97US-0063544P.
XX 29-OCT-1997; 97US-0063734P.
XX 31-OCT-1997; 97US-0063870P.
XX 31-OCT-1997; 97US-0064103P.
XX 13-NOV-1997; 97US-0065311P.
XX 21-NOV-1997; 97US-0066120P.
XX 24-NOV-1997; 97US-0066466P.
XX 24-NOV-1997; 97US-0066772P.
XX 11-DEC-1997; 97US-0069335P.
XX 12-DEC-1997; 97US-0069425P.
XX 17-DEC-1997; 97US-0069870P.
XX 18-DEC-1997; 97US-0068017P.
XX 10-MAR-1998; 98US-0077450P.
XX 11-MAR-1998; 98US-0077632P.
XX 11-MAR-1998; 98US-0077649P.
XX 20-MAR-1998; 98US-0078886P.
XX 20-MAR-1998; 98US-0078939P.
XX 27-MAR-1998; 98US-0079664P.
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XX 31-MAR-1998; 98US-0080107P.
XX 31-MAR-1998; 98US-0080194P.
XX 01-APR-1998; 98US-0080327P.
XX 01-APR-1998; 98US-0080333P.
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[illegible]